

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/06371

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

genebank

search terms: structures provided by specifically claimed SEQ ID NO. which encode the claimed polynucleotides.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-7, 24-33, drawn to no fewer than 694 different isolated polynucleotides, vectors containing the polynucleotides, host cells comprising said polynucleotide and methods of producing polypeptides.

Group II, claim(s) 8-11, drawn to no fewer than 682 different polypeptides encoded by the polynucleotides.

Group III, claim(s) 12-20, drawn to compositions comprising a single polypeptide, an antiseecretory agent, a bismuth salt or a combination thereof.

Group IV, claims 21-23, drawn to compositions comprising two *Helicobacter* polypeptides.

Group V, claim 34, drawn to a composition comprising antibodies to a polypeptide.

The polypeptide encoding polynucleotides, vectors containing them, organisms transformed with them and methods of polypeptide production are materially different from each other and therefore independent and distinct from the polypeptides and compositions of Groups II, III, and IV, as well as the protein antibodies of Group V.

This application contains claims directed to more than one species of generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be examined the appropriate additional examination fees must be paid. the species are as follows: Group I contains separate polynucleotide species for each sequence mentioned. Therefore, there is a minimum of 694 different species. Group II contains at least one polypeptide for each polynucleotide sequence mentioned. Therefore, there is a minimum of 682 species in Group II. For the Group that applicant elects, a total of 10(ten) specified sequences will be searched and no more than 4(four) specified sequences will be searched for each additional fee paid. The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: There is no relationship between or among the various nucleotide and polypeptide amino acid sequences mentioned in the claims.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/06371

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-7,24-33;species SEQ ID NO:26,56,198,212,264,278,490,838,1220,1292

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/06371

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : A01N 43/04; A61K 31/70

US CL : 514/44

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 514/44

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P	TOMB, J.-F. et al. The complete genome sequence of the gastric pathogen <i>Helicobacter pylori</i> . Nature. 07 August 1997, Vol. 388, pages 539-547, see entire document.	1-7, 24-33



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

17 JUNE 1998

Date of mailing of the international search report

08 July 1998 (08.07.98)

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

GINNY PORTNER

Telephone No. (703) 308-0196

-2049-

the compound of claim 8, 9, or 10 admixed with a physiologically acceptable diluent or carrier.

-2048-

29. A composition that comprises a bacterial vector comprising a DNA molecule of claim 3, said DNA molecule being placed under conditions for expression and said bacterial vector being admixed with a physiologically acceptable diluent or carrier.

5 30. The composition of claim 29, wherein said vector is selected from the group consisting of *Shigella*, *Salmonella*, *Vibrio cholerae*, *Lactobacillus*, *Bacille bilié de Calmette-Guérin*, and *Streptococcus*.

10 31. The composition of claim 24, wherein said polynucleotide is a DNA molecule that is inserted in a plasmid that is unable to replicate and to substantially integrate in a mammalian genome and is placed under conditions for expression in a mammalian cell.

15 32. An expression cassette comprising a DNA molecule of claim 3, said DNA molecule being placed under conditions for expression in a procaryotic or eucaryotic cell.

20 33. A process for producing a compound of claim 8, which comprises culturing a procaryotic or eucaryotic cell transformed or transfected with an expression cassette of claim 32, and recovering said compound from the cell culture.

25 34. A pharmaceutical composition for preventing or treating *Helicobacter* infection in a mammal, said composition comprising a prophylactically or therapeutically effective amount of an antibody that binds to

-2047-

22. The composition of claim 21, wherein the second *Helicobacter* polypeptide is a *Helicobacter* urease, or a subunit or a derivative thereof.

23. The composition of claim 11, further comprising an adjuvant.

5 24. A pharmaceutical composition for preventing or treating *Helicobacter* infection in a mammal, said composition comprising a prophylactically or therapeutically effective amount of a polynucleotide of claim 1 or 2 admixed with a physiologically acceptable diluent or carrier.

10 25. A pharmaceutical composition for preventing or treating *Helicobacter* infection in a mammal, said composition comprising a prophylactically or therapeutically effective amount of a polynucleotide of claim 4, 5, or 6 admixed with a physiologically acceptable diluent or carrier.

15 26. A pharmaceutical composition for preventing or treating *Helicobacter* infection in a mammal, said composition comprising a prophylactically or therapeutically effective amount of a polynucleotide of claim 7 admixed with a physiologically acceptable diluent or carrier.

20 27. A composition comprising a viral vector, in the genome of which is inserted a DNA molecule of claim 3, said DNA molecule being placed under conditions for expression in a mammalian cell and said viral vector being admixed with a physiologically acceptable diluent or carrier.

25 28. The composition of claim 27, wherein said viral vector is a poxvirus.

-2046-

14. The composition of claim 12, wherein said bismuth salt is selected from the group consisting of bismuth subcitrate and bismuth subsalicylate.

15. The composition of claim 12, wherein said antisecretory agent is a proton pump inhibitor.

5

16. The composition of claim 15, wherein said proton pump inhibitor is selected from the group consisting of omeprazole, lansoprazole, and pantoprazole.

10

17. The composition of claim 12, wherein said antisecretory agent is an H₂-receptor antagonist.

15

18. The composition of claim 17, wherein said H₂-receptor antagonist is selected from the group consisting of ranitidine, cimetidine, famotidine, nizatidine, and roxatidine.

19. The composition of claim 12, wherein said antisecretory agent is a prostaglandin analog.

20

20. The composition of claim 19, wherein said prostaglandin analog is misoprostil or enprostil.

25

21. The composition of claim 11, further comprising a prophylactically or therapeutically effective amount of a second *Helicobacter* polypeptide or a derivative thereof.

-2045-

GHPO 1723 (SEQ ID NO:1342), GHPO 1732 (SEQ ID NO:1344), GHPO 1739 (SEQ ID NO:1346), GHPO 1741 (SEQ ID NO:1348), GHPO 1747 (SEQ ID NO:1350), GHPO 1749 (SEQ ID NO:1352), GHPO 1750 (SEQ ID NO:1354), GHPO 1751 (SEQ ID NO:1356), GHPO 1755 (SEQ ID NO:1358), GHPO 1771 (SEQ ID NO:1360), GHPO 1786 (SEQ ID NO:1362), and GHPO 1789 (SEQ ID NO:1364); or

(ii) a derivative of said *Helicobacter* polypeptide.

9. The compound of claim 8, which is the mature form or a derivative of a polypeptide encoded by a DNA molecule of claim 4.

10. The compound of claim 8, which is the mature form or a derivative of a polypeptide encoded by a DNA molecule of claim 5.

11. A pharmaceutical composition for preventing or treating *Helicobacter* infection in a mammal, said composition comprising a prophylactically or therapeutically effective amount of a compound of claim 8, 9, or 10 admixed with a physiologically acceptable diluent or carrier.

12. The composition of claim 11, further comprising an antibiotic, an antisecretory agent, a bismuth salt, or a combination thereof.

13. The composition of claim 12, wherein said antibiotic is selected from the group consisting of amoxicillin, clarithromycin, tetracycline, metronidazole, and erythromycin.

-2044-

1351 (SEQ ID NO:1220), GHPO 1354 (SEQ ID NO:1222), GHPO 1363 (SEQ
ID NO:1224), GHPO 1371 (SEQ ID NO:1226), GHPO 1381 (SEQ ID
NO:1228), GHPO 1401 (SEQ ID NO:1230), GHPO 1402 (SEQ ID NO:1232),
GHPO 1403 (SEQ ID NO:1234), GHPO 1408 (SEQ ID NO:1236), GHPO
1416 (SEQ ID NO:1238), GHPO 1420 (SEQ ID NO:1240), GHPO 1428 (SEQ
ID NO:1242), GHPO 1437 (SEQ ID NO:1244), GHPO 1439 (SEQ ID
NO:1246), GHPO 1460 (SEQ ID NO:1248), GHPO 1463 (SEQ ID NO:1250),
GHPO 1472 (SEQ ID NO:1252), GHPO 1474 (SEQ ID NO:1254), GHPO
1484 (SEQ ID NO:1256), GHPO 1489 (SEQ ID NO:1258), GHPO 1494 (SEQ
ID NO:1260), GHPO 1495 (SEQ ID NO:1262), GHPO 1498 (SEQ ID
NO:1264), GHPO 1499 (SEQ ID NO:1266), GHPO 1500 (SEQ ID NO:1268),
GHPO 1503 (SEQ ID NO:1270), GHPO 1504 (SEQ ID NO:1272), GHPO
1510 (SEQ ID NO:1274), GHPO 1518 (SEQ ID NO:1276), GHPO 1533 (SEQ
ID NO:1278), GHPO 1541 (SEQ ID NO:1280), GHPO 1544 (SEQ ID
NO:1282), GHPO 1548 (SEQ ID NO:1284), GHPO 1565 (SEQ ID NO:1286),
GHPO 1575 (SEQ ID NO:1288), GHPO 1582 (SEQ ID NO:1290), GHPO
1595 (SEQ ID NO:1292), GHPO 1597 (SEQ ID NO:1294), GHPO 1599 (SEQ
ID NO:1296), GHPO 1601 (SEQ ID NO:1298), GHPO 1609 (SEQ ID
NO:1300), GHPO 1613 (SEQ ID NO:1302), GHPO 1614 (SEQ ID NO:1304),
GHPO 1626 (SEQ ID NO:1306), GHPO 1628 (SEQ ID NO:1308), GHPO
1639 (SEQ ID NO:1310), GHPO 1640 (SEQ ID NO:1312), GHPO 1641 (SEQ
ID NO:1314), GHPO 1646 (SEQ ID NO:1316), GHPO 1662 (SEQ ID
NO:1318), GHPO 1667 (SEQ ID NO:1320), GHPO 1668 (SEQ ID NO:1322),
GHPO 1670 (SEQ ID NO:1324), GHPO 1671 (SEQ ID NO:1326), GHPO
1672 (SEQ ID NO:1328), GHPO 1678 (SEQ ID NO:1330), GHPO 1684 (SEQ
ID NO:1332), GHPO 1695 (SEQ ID NO:1334), GHPO 1697 (SEQ ID
NO:1336), GHPO 1701 (SEQ ID NO:1338), GHPO 1719 (SEQ ID NO:1340),

-2043-

ID NO:1098), GHPO 1043 (SEQ ID NO:1100), GHPO 1044 (SEQ ID NO:1102), GHPO 1051 (SEQ ID NO:1104), GHPO 1058 (SEQ ID NO:1106), GHPO 1060 (SEQ ID NO:1108), GHPO 1075 (SEQ ID NO:1110), GHPO 1077 (SEQ ID NO:1112), GHPO 1082 (SEQ ID NO:1114), GHPO 1083 (SEQ ID NO:1116), GHPO 1086 (SEQ ID NO:1118), GHPO 1087 (SEQ ID NO:1120), GHPO 1090 (SEQ ID NO:1122), GHPO 1097 (SEQ ID NO:1124), GHPO 1098 (SEQ ID NO:1126), GHPO 1103 (SEQ ID NO:1128), GHPO 1113 (SEQ ID NO:1130), GHPO 1116 (SEQ ID NO:1132), GHPO 1123 (SEQ ID NO:1134), GHPO 1125 (SEQ ID NO:1136), GHPO 1129 (SEQ ID NO:1138), GHPO 1130 (SEQ ID NO:1140), GHPO 1134 (SEQ ID NO:1142), GHPO 1161 (SEQ ID NO:1144), GHPO 1166 (SEQ ID NO:1146), GHPO 1170 (SEQ ID NO:1148), GHPO 1175 (SEQ ID NO:1150), GHPO 1181 (SEQ ID NO:1152), GHPO 1186 (SEQ ID NO:1154), GHPO 1188 (SEQ ID NO:1156), GHPO 1191 (SEQ ID NO:1158), GHPO 1193 (SEQ ID NO:1160), GHPO 1196 (SEQ ID NO:1162), GHPO 1204 (SEQ ID NO:1164), GHPO 1210 (SEQ ID NO:1166), GHPO 1211 (SEQ ID NO:1168), GHPO 1216 (SEQ ID NO:1170), GHPO 1218 (SEQ ID NO:1172), GHPO 1220 (SEQ ID NO:1174), GHPO 1223 (SEQ ID NO:1176), GHPO 1226 (SEQ ID NO:1178), GHPO 1240 (SEQ ID NO:1180), GHPO 1246 (SEQ ID NO:1182), GHPO 1251 (SEQ ID NO:1184), GHPO 1252 (SEQ ID NO:1186), GHPO 1261 (SEQ ID NO:1188), GHPO 1265 (SEQ ID NO:1190), GHPO 1267 (SEQ ID NO:1192), GHPO 1278 (SEQ ID NO:1194), GHPO 1282 (SEQ ID NO:1196), GHPO 1283 (SEQ ID NO:1198), GHPO 1287 (SEQ ID NO:1200), GHPO 1292 (SEQ ID NO:1202), GHPO 1293 (SEQ ID NO:1204), GHPO 1302 (SEQ ID NO:1206), GHPO 1309 (SEQ ID NO:1208), GHPO 1317 (SEQ ID NO:1210), GHPO 1318 (SEQ ID NO:1212), GHPO 1321 (SEQ ID NO:1214), GHPO 1325 (SEQ ID NO:1216), GHPO 1341 (SEQ ID NO:1218), GHPO

-2042-

NO:970), GHPO 597 (SEQ ID NO:972), GHPO 598 (SEQ ID NO:974), GHPO
604 (SEQ ID NO:976), GHPO 606 (SEQ ID NO:978), GHPO 611 (SEQ ID
NO:980), GHPO 612 (SEQ ID NO:982), GHPO 615 (SEQ ID NO:984), GHPO
632 (SEQ ID NO:986), GHPO 633 (SEQ ID NO:988), GHPO 637 (SEQ ID
NO:990), GHPO 651 (SEQ ID NO:992), GHPO 663 (SEQ ID NO:994), GHPO
5 686 (SEQ ID NO:996), GHPO 693 (SEQ ID NO:998), GHPO 698 (SEQ ID
NO:1000), GHPO 703 (SEQ ID NO:1002), GHPO 704 (SEQ ID NO:1004),
GHPO 705 (SEQ ID NO:1006), GHPO 707 (SEQ ID NO:1008), GHPO 721
(SEQ ID NO:1010), GHPO 727 (SEQ ID NO:1012), GHPO 728 (SEQ ID
NO:1014), GHPO 733 (SEQ ID NO:1016), GHPO 758 (SEQ ID NO:1018),
10 GHPO 763 (SEQ ID NO:1020), GHPO 771 (SEQ ID NO:1022), GHPO 774
(SEQ ID NO:1024), GHPO 776 (SEQ ID NO:1026), GHPO 783 (SEQ ID
NO:1028), GHPO 800 (SEQ ID NO:1030), GHPO 806 (SEQ ID NO:1032),
GHPO 807 (SEQ ID NO:1034), GHPO 808 (SEQ ID NO:1036), GHPO 809
(SEQ ID NO:1038), GHPO 811 (SEQ ID NO:1040), GHPO 815 (SEQ ID
15 NO:1042), GHPO 819 (SEQ ID NO:1044), GHPO 841 (SEQ ID NO:1046),
GHPO 843 (SEQ ID NO:1048), GHPO 846 (SEQ ID NO:1050), GHPO 875
(SEQ ID NO:1052), GHPO 892 (SEQ ID NO:1054), GHPO 902 (SEQ ID
NO:1056), GHPO 904 (SEQ ID NO:1058), GHPO 906 (SEQ ID NO:1060),
GHPO 908 (SEQ ID NO:1062), GHPO 921 (SEQ ID NO:1064), GHPO 923
20 (SEQ ID NO:1066), GHPO 926 (SEQ ID NO:1068), GHPO 933 (SEQ ID
NO:1070), GHPO 939 (SEQ ID NO:1072), GHPO 940 (SEQ ID NO:1074),
GHPO 943 (SEQ ID NO:1076), GHPO 951 (SEQ ID NO:1078), GHPO 961
(SEQ ID NO:1080), GHPO 965 (SEQ ID NO:1082), GHPO 990 (SEQ ID
NO:1084), GHPO 991 (SEQ ID NO:1086), GHPO 998 (SEQ ID NO:1088),
25 GHPO 1001 (SEQ ID NO:1090), GHPO 1005 (SEQ ID NO:1092), GHPO
1033 (SEQ ID NO:1094), GHPO 1039 (SEQ ID NO:1096), GHPO 1041 (SEQ

-2041-

231 (SEQ ID NO:836), GHPO 236 (SEQ ID NO:838), GHPO 239 (SEQ ID
NO:840), GHPO 245 (SEQ ID NO:842), GHPO 246 (SEQ ID NO:844), GHPO
248 (SEQ ID NO:846), GHPO 253 (SEQ ID NO:848), GHPO 265 (SEQ ID
NO:850), GHPO 266 (SEQ ID NO:852), GHPO 271 (SEQ ID NO:854), GHPO
272 (SEQ ID NO:856), GHPO 286 (SEQ ID NO:858), GHPO 291 (SEQ ID
5 NO:860), GHPO 292 (SEQ ID NO:862), GHPO 297 (SEQ ID NO:864), GHPO
304 (SEQ ID NO:866), GHPO 307 (SEQ ID NO:868), GHPO 324 (SEQ ID
NO:870), GHPO 326 (SEQ ID NO:872), GHPO 331 (SEQ ID NO:874), GHPO
343 (SEQ ID NO:876), GHPO 345 (SEQ ID NO:878), GHPO 346 (SEQ ID
NO:880), GHPO 352 (SEQ ID NO:882), GHPO 355 (SEQ ID NO:884), GHPO
10 363 (SEQ ID NO:886), GHPO 369 (SEQ ID NO:888), GHPO 376 (SEQ ID
NO:890), GHPO 378 (SEQ ID NO:892), GHPO 388 (SEQ ID NO:894), GHPO
396 (SEQ ID NO:896), GHPO 403 (SEQ ID NO:898), GHPO 410 (SEQ ID
NO:900), GHPO 415 (SEQ ID NO:902), GHPO 421 (SEQ ID NO:904), GHPO
439 (SEQ ID NO:906), GHPO 441 (SEQ ID NO:908), GHPO 443 (SEQ ID
15 NO:910), GHPO 453 (SEQ ID NO:912), GHPO 455 (SEQ ID NO:914), GHPO
464 (SEQ ID NO:916), GHPO 467 (SEQ ID NO:918), GHPO 468 (SEQ ID
NO:920), GHPO 470 (SEQ ID NO:922), GHPO 486 (SEQ ID NO:924), GHPO
487 (SEQ ID NO:926), GHPO 488 (SEQ ID NO:928), GHPO 489 (SEQ ID
NO:930), GHPO 498 (SEQ ID NO:932), GHPO 501 (SEQ ID NO:934), GHPO
20 504 (SEQ ID NO:936), GHPO 512 (SEQ ID NO:938), GHPO 517 (SEQ ID
NO:940), GHPO 520 (SEQ ID NO:942), GHPO 528 (SEQ ID NO:944), GHPO
530 (SEQ ID NO:946), GHPO 532 (SEQ ID NO:948), GHPO 548 (SEQ ID
NO:950), GHPO 561 (SEQ ID NO:952), GHPO 564 (SEQ ID NO:954), GHPO
572 (SEQ ID NO:956), GHPO 573 (SEQ ID NO:958), GHPO 574 (SEQ ID
25 NO:960), GHPO 577 (SEQ ID NO:962), GHPO 579 (SEQ ID NO:964), GHPO
583 (SEQ ID NO:966), GHPO 588 (SEQ ID NO:968), GHPO 593 (SEQ ID

-2040-

NO:702), GHPO 1629 (SEQ ID NO:704), GHPO 1642 (SEQ ID NO:706),
GHPO 1654 (SEQ ID NO:708), GHPO 1661 (SEQ ID NO:710), GHPO 1673
(SEQ ID NO:712), GHPO 1687 (SEQ ID NO:714), GHPO 1692 (SEQ ID
NO:716), GHPO 1693 (SEQ ID NO:718), GHPO 1699 (SEQ ID NO:720),
GHPO 1738 (SEQ ID NO:722), GHPO 1745 (SEQ ID NO:724), GHPO 1746
(SEQ ID NO:726), GHPO 1754 (SEQ ID NO:728), GHPO 1792 (SEQ ID
NO:730), GHPO 1795 (SEQ ID NO:732), GHPO 1796 (SEQ ID NO:734),
GHPO 7 (SEQ ID NO:736), GHPO 8 (SEQ ID NO:738), GHPO 9 (SEQ ID
NO:740), GHPO 10 (SEQ ID NO:742), GHPO 12 (SEQ ID NO:744), GHPO
25 (SEQ ID NO:746), GHPO 27 (SEQ ID NO:748), GHPO 29 (SEQ ID
NO:750), GHPO 30 (SEQ ID NO:752), GHPO 37 (SEQ ID NO:754), GHPO
49 (SEQ ID NO:756), GHPO 51 (SEQ ID NO:758), GHPO 54 (SEQ ID
NO:760), GHPO 65 (SEQ ID NO:762), GHPO 66 (SEQ ID NO:764), GHPO
68 (SEQ ID NO:766), GHPO 70 (SEQ ID NO:768), GHPO 77 (SEQ ID
NO:770), GHPO 83 (SEQ ID NO:772), GHPO 85 (SEQ ID NO:774), GHPO
87 (SEQ ID NO:776), GHPO 91 (SEQ ID NO:778), GHPO 92 (SEQ ID
NO:780), GHPO 96 (SEQ ID NO:782), GHPO 97 (SEQ ID NO:784), GHPO
111 (SEQ ID NO:786), GHPO 115 (SEQ ID NO:788), GHPO 117 (SEQ ID
NO:790), GHPO 123 (SEQ ID NO:792), GHPO 124 (SEQ ID NO:794), GHPO
126 (SEQ ID NO:796), GHPO 127 (SEQ ID NO:798), GHPO 128 (SEQ ID
NO:800), GHPO 131 (SEQ ID NO:802), GHPO 133 (SEQ ID NO:804), GHPO
140 (SEQ ID NO:806), GHPO 141 (SEQ ID NO:808), GHPO 145 (SEQ ID
NO:810), GHPO 147 (SEQ ID NO:812), GHPO 166 (SEQ ID NO:814), GHPO
181 (SEQ ID NO:816), GHPO 187 (SEQ ID NO:818), GHPO 188 (SEQ ID
NO:820), GHPO 192 (SEQ ID NO:822), GHPO 202 (SEQ ID NO:824), GHPO
204 (SEQ ID NO:826), GHPO 205 (SEQ ID NO:828), GHPO 212 (SEQ ID
NO:830), GHPO 218 (SEQ ID NO:832), GHPO 226 (SEQ ID NO:834), GHPO

-2039-

NO:576), GHPO 1034 (SEQ ID NO:578), GHPO 1038 (SEQ ID NO:580),
GHPO 1059 (SEQ ID NO:582), GHPO 1065 (SEQ ID NO:584), GHPO 1072
(SEQ ID NO:586), GHPO 1073 (SEQ ID NO:588), GHPO 1088 (SEQ ID
NO:590), GHPO 1091 (SEQ ID NO:592), GHPO 1105 (SEQ ID NO:594),
GHPO 1115 (SEQ ID NO:596), GHPO 1159 (SEQ ID NO:598), GHPO 1177
(SEQ ID NO:600), GHPO 1187 (SEQ ID NO:602), GHPO 1192 (SEQ ID
NO:604), GHPO 1195 (SEQ ID NO:606), GHPO 1224 (SEQ ID NO:608),
GHPO 1225 (SEQ ID NO:610), GHPO 1228 (SEQ ID NO:612), GHPO 1229
(SEQ ID NO:614), GHPO 1231 (SEQ ID NO:616), GHPO 1236 (SEQ ID
NO:618), GHPO 1242 (SEQ ID NO:620), GHPO 1248 (SEQ ID NO:622),
GHPO 1270 (SEQ ID NO:624), GHPO 1271 (SEQ ID NO:626), GHPO 1298
(SEQ ID NO:628), GHPO 1301 (SEQ ID NO:630), GHPO 1304 (SEQ ID
NO:632), GHPO 1315 (SEQ ID NO:634), GHPO 1319 (SEQ ID NO:636),
GHPO 1323 (SEQ ID NO:638), GHPO 1331 (SEQ ID NO:640), GHPO 1332
(SEQ ID NO:642), GHPO 1347 (SEQ ID NO:644), GHPO 1373 (SEQ ID
NO:646), GHPO 1376 (SEQ ID NO:648), GHPO 1380 (SEQ ID NO:650),
GHPO 1394 (SEQ ID NO:652), GHPO 1407 (SEQ ID NO:654), GHPO 1415
(SEQ ID NO:656), GHPO 1425 (SEQ ID NO:658), GHPO 1427 (SEQ ID
NO:660), GHPO 1444 (SEQ ID NO:662), GHPO 1449 (SEQ ID NO:664),
GHPO 1465 (SEQ ID NO:666), GHPO 1475 (SEQ ID NO:668), GHPO 1479
(SEQ ID NO:670), GHPO 1483 (SEQ ID NO:672), GHPO 1488 (SEQ ID
NO:674), GHPO 1496 (SEQ ID NO:676), GHPO 1524 (SEQ ID NO:678),
GHPO 1536 (SEQ ID NO:680), GHPO 1539 (SEQ ID NO:682), GHPO 1540
(SEQ ID NO:684), GHPO 1542 (SEQ ID NO:686), GHPO 1555 (SEQ ID
NO:688), GHPO 1560 (SEQ ID NO:690), GHPO 1564 (SEQ ID NO:692),
GHPO 1570 (SEQ ID NO:694), GHPO 1588 (SEQ ID NO:696), GHPO 1604
(SEQ ID NO:698), GHPO 1605 (SEQ ID NO:700), GHPO 1619 (SEQ ID

-2038-

342 (SEQ ID NO:442), GHPO 344 (SEQ ID NO:444), GHPO 358 (SEQ ID NO:446), GHPO 373 (SEQ ID NO:448), GHPO 382 (SEQ ID NO:450), GHPO 384 (SEQ ID NO:452), GHPO 398 (SEQ ID NO:454), GHPO 409 (SEQ ID NO:456), GHPO 422 (SEQ ID NO:458), GHPO 430 (SEQ ID NO:460), GHPO 446 (SEQ ID NO:462), GHPO 447 (SEQ ID NO:464), GHPO 450 (SEQ ID NO:466), GHPO 451 (SEQ ID NO:468), GHPO 452 (SEQ ID NO:470), GHPO 456 (SEQ ID NO:472), GHPO 461 (SEQ ID NO:474), GHPO 476 (SEQ ID NO:476), GHPO 478 (SEQ ID NO:478), GHPO 491 (SEQ ID NO:480), GHPO 511 (SEQ ID NO:482), GHPO 519 (SEQ ID NO:484), GHPO 526 (SEQ ID NO:486), GHPO 534 (SEQ ID NO:488), GHPO 536 (SEQ ID NO:490), GHPO 542 (SEQ ID NO:492), GHPO 544 (SEQ ID NO:494), GHPO 576 (SEQ ID NO:496), GHPO 578 (SEQ ID NO:498), GHPO 580 (SEQ ID NO:500), GHPO 585 (SEQ ID NO:502), GHPO 599 (SEQ ID NO:504), GHPO 639 (SEQ ID NO:506), GHPO 642 (SEQ ID NO:508), GHPO 647 (SEQ ID NO:510), GHPO 654 (SEQ ID NO:512), GHPO 669 (SEQ ID NO:514), GHPO 710 (SEQ ID NO:516), GHPO 713 (SEQ ID NO:518), GHPO 716 (SEQ ID NO:520), GHPO 718 (SEQ ID NO:522), GHPO 726 (SEQ ID NO:524), GHPO 734 (SEQ ID NO:526), GHPO 740 (SEQ ID NO:528), GHPO 770 (SEQ ID NO:530), GHPO 782 (SEQ ID NO:532), GHPO 786 (SEQ ID NO:534), GHPO 792 (SEQ ID NO:536), GHPO 797 (SEQ ID NO:538), GHPO 816 (SEQ ID NO:540), GHPO 828 (SEQ ID NO:542), GHPO 839 (SEQ ID NO:544), GHPO 840 (SEQ ID NO:546), GHPO 842 (SEQ ID NO:548), GHPO 885 (SEQ ID NO:550), GHPO 889 (SEQ ID NO:552), GHPO 903 (SEQ ID NO:554), GHPO 912 (SEQ ID NO:556), GHPO 946 (SEQ ID NO:558), GHPO 958 (SEQ ID NO:560), GHPO 968 (SEQ ID NO:562), GHPO 987 (SEQ ID NO:564), GHPO 992 (SEQ ID NO:566), GHPO 996 (SEQ ID NO:568), GHPO 997 (SEQ ID NO:570), GHPO 1002 (SEQ ID NO:572), GHPO 1026 (SEQ ID NO:574), GHPO 1028 (SEQ ID

-2037-

798 (SEQ ID NO:310), GHPO 1102 (SEQ ID NO:312), GHPO 1114 (SEQ ID
NO:314), GHPO 1152 (SEQ ID NO:316), GHPO 1272 (SEQ ID NO:318),
GHPO 1345 (SEQ ID NO:320), GHPO 1377 (SEQ ID NO:322), GHPO 1424
(SEQ ID NO:324), GHPO 1430 (SEQ ID NO:326), GHPO 1502 (SEQ ID
NO:328), GHPO 1600 (SEQ ID NO:330), GHPO 1714 (SEQ ID NO:332),
5 GHPO 359 (SEQ ID NO:334), GHPO 678 (SEQ ID NO:336), GHPO 708
(SEQ ID NO:338), GHPO 759 (SEQ ID NO:340), GHPO 847 (SEQ ID
NO:342), GHPO 1050 (SEQ ID NO:344), GHPO 1101 (SEQ ID NO:346),
GHPO 1120 (SEQ ID NO:348), GHPO 1138 (SEQ ID NO:350), GHPO 1310
(SEQ ID NO:352), GHPO 1320 (SEQ ID NO:354), GHPO 1375 (SEQ ID
10 NO:356), GHPO 1432 (SEQ ID NO:358), GHPO 21 (SEQ ID NO:360), GHPO
282 (SEQ ID NO:362), GHPO 1089 (SEQ ID NO:364), GHPO 1141 (SEQ ID
NO:366), GHPO 1280 (SEQ ID NO:368), GHPO 1608 (SEQ ID NO:370),
GHPO 15 (SEQ ID NO:372), GHPO 16 (SEQ ID NO:374), GHPO 36 (SEQ ID
NO:376), GHPO 38 (SEQ ID NO:378), GHPO 52 (SEQ ID NO:380), GHPO
15 57 (SEQ ID NO:382), GHPO 64 (SEQ ID NO:384), GHPO 79 (SEQ ID
NO:386), GHPO 84 (SEQ ID NO:388), GHPO 86 (SEQ ID NO:390), GHPO
99 (SEQ ID NO:392), GHPO 106 (SEQ ID NO:394), GHPO 118 (SEQ ID
NO:396), GHPO 122 (SEQ ID NO:398), GHPO 128 (SEQ ID NO:400), GHPO
138 (SEQ ID NO:402), GHPO 153 (SEQ ID NO:404), GHPO 160 (SEQ ID
20 NO:406), GHPO 168 (SEQ ID NO:408), GHPO 179 (SEQ ID NO:410), GHPO
189 (SEQ ID NO:412), GHPO 229 (SEQ ID NO:414), GHPO 243 (SEQ ID
NO:416), GHPO 244 (SEQ ID NO:418), GHPO 251 (SEQ ID NO:420), GHPO
267 (SEQ ID NO:422), GHPO 269 (SEQ ID NO:424), GHPO 279 (SEQ ID
NO:426), GHPO 284 (SEQ ID NO:428), GHPO 296 (SEQ ID NO:430), GHPO
25 300 (SEQ ID NO:432), GHPO 305 (SEQ ID NO:434), GHPO 319 (SEQ ID
NO:436), GHPO 330 (SEQ ID NO:438), GHPO 340 (SEQ ID NO:440), GHPO

-2036-

GHPO 1574 (SEQ ID NO:180), GHPO 1627 (SEQ ID NO:182), GHPO 1657
(SEQ ID NO:184), GHPO 1664 (SEQ ID NO:186), GHPO 1694 (SEQ ID
NO:188), GHPO 1704 (SEQ ID NO:190), GHPO 1763 (SEQ ID NO:192),
GHPO 616 (SEQ ID NO:194), GHPO 76 (SEQ ID NO:196), GHPO 109 (SEQ
ID NO:198), GHPO 163 (SEQ ID NO:200), GHPO 169 (SEQ ID NO:202),
5 GHPO 208 (SEQ ID NO:204), GHPO 219 (SEQ ID NO:206), GHPO 445
(SEQ ID NO:208), GHPO 479 (SEQ ID NO:210), GHPO 525 (SEQ ID
NO:212), GHPO 535 (SEQ ID NO:214), GHPO 731 (SEQ ID NO:216), GHPO
836 (SEQ ID NO:218), GHPO 879 (SEQ ID NO:220), GHPO 881 (SEQ ID
NO:222), GHPO 886 (SEQ ID NO:224), GHPO 893 (SEQ ID NO:226), GHPO
10 894 (SEQ ID NO:228), GHPO 976 (SEQ ID NO:230), GHPO 1011 (SEQ ID
NO:232), GHPO 1024 (SEQ ID NO:234), GHPO 1084 (SEQ ID NO:236),
GHPO 1329 (SEQ ID NO:238), GHPO 1330 (SEQ ID NO:240), GHPO 1346
(SEQ ID NO:242), GHPO 1360 (SEQ ID NO:244), GHPO 1388 (SEQ ID
NO:246), GHPO 1411 (SEQ ID NO:248), GHPO 1419 (SEQ ID NO:250),
15 GHPO 1446 (SEQ ID NO:252), GHPO 1469 (SEQ ID NO:254), GHPO 1501
(SEQ ID NO:256), GHPO 1505 (SEQ ID NO:258), GHPO 1522 (SEQ ID
NO:260), GHPO 1525 (SEQ ID NO:262), GHPO 1615 (SEQ ID NO:264),
GHPO 1689 (SEQ ID NO:266), GHPO 1733 (SEQ ID NO:268), GHPO 18
(SEQ ID NO:270), GHPO 139 (SEQ ID NO:272), GHPO 142 (SEQ ID
20 NO:274), GHPO 250 (SEQ ID NO:276), GHPO 257 (SEQ ID NO:278), GHPO
325 (SEQ ID NO:280), GHPO 355 (SEQ ID NO:282), GHPO 357 (SEQ ID
NO:284), GHPO 454 (SEQ ID NO:286), GHPO 475 (SEQ ID NO:288), GHPO
515 (SEQ ID NO:290), GHPO 527 (SEQ ID NO:292), GHPO 551 (SEQ ID
NO:294), GHPO 602 (SEQ ID NO:296), GHPO 626 (SEQ ID NO:298), GHPO
25 646 (SEQ ID NO:300), GHPO 653 (SEQ ID NO:302), GHPO 655 (SEQ ID
NO:304), GHPO 670 (SEQ ID NO:306), GHPO 739 (SEQ ID NO:308), GHPO

-2035-

NO:46), GHPO 937 (SEQ ID NO:48), GHPO 1027 (SEQ ID NO:50), GHPO 1099 (SEQ ID NO:52), GHPO 1151 (SEQ ID NO:54), GHPO 1275 (SEQ ID NO:56), GHPO 1365 (SEQ ID NO:58), GHPO 1578 (SEQ ID NO:60), GHPO 22 (SEQ ID NO:62), GHPO 58 (SEQ ID NO:64), GHPO 200 (SEQ ID NO:66), GHPO 558 (SEQ ID NO:68), GHPO 563 (SEQ ID NO:70), GHPO 695 (SEQ ID NO:72), GHPO 699 (SEQ ID NO:74), GHPO 702 (SEQ ID NO:76), GHPO 709 (SEQ ID NO:78), GHPO 741 (SEQ ID NO:80), GHPO 762 (SEQ ID NO:82), GHPO 827 (SEQ ID NO:84), GHPO 852 (SEQ ID NO:86), GHPO 1013 (SEQ ID NO:88), GHPO 1020 (SEQ ID NO:90), GHPO 1031 (SEQ ID NO:92), GHPO 1052 (SEQ ID NO:94), GHPO 1127 (SEQ ID NO:96), GHPO 1149 (SEQ ID NO:98), GHPO 1176 (SEQ ID NO:100), GHPO 1250 (SEQ ID NO:102), GHPO 1312 (SEQ ID NO:104), GHPO 1358 (SEQ ID NO:106), GHPO 1490 (SEQ ID NO:108), GHPO 1559 (SEQ ID NO:110), GHPO 1651 (SEQ ID NO:112), GHPO 1726 (SEQ ID NO:114), GHPO 1780 (SEQ ID NO:116), GHPO 895 (SEQ ID NO:118), GHPO 1447 (SEQ ID NO:120), GHPO 28 (SEQ ID NO:122), GHPO 86 (SEQ ID NO:124), GHPO 155 (SEQ ID NO:126), GHPO 157 (SEQ ID NO:128), GHPO 237 (SEQ ID NO:130), GHPO 290 (SEQ ID NO:132), GHPO 293 (SEQ ID NO:134), GHPO 335 (SEQ ID NO:136), GHPO 374 (SEQ ID NO:138), GHPO 442 (SEQ ID NO:140), GHPO 480 (SEQ ID NO:142), GHPO 523 (SEQ ID NO:144), GHPO 610 (SEQ ID NO:146), GHPO 675 (SEQ ID NO:148), GHPO 690 (SEQ ID NO:150), GHPO 829 (SEQ ID NO:152), GHPO 850 (SEQ ID NO:154), GHPO 876 (SEQ ID NO:156), GHPO 984 (SEQ ID NO:158), GHPO 989 (SEQ ID NO:160), GHPO 1111 (SEQ ID NO:162), GHPO 1145 (SEQ ID NO:164), GHPO 1256 (SEQ ID NO:166), GHPO 1264 (SEQ ID NO:168), GHPO 1316 (SEQ ID NO:170), GHPO 1368 (SEQ ID NO:172), GHPO 1442 (SEQ ID NO:174), GHPO 1506 (SEQ ID NO:176), GHPO 1543 (SEQ ID NO:178),

-2034-

4. The isolated polynucleotide of claim 1, which is a DNA molecule that can be amplified by polymerase chain reaction from a *Helicobacter* genome.

5. The isolated DNA molecule of claim 4, which can be amplified by the polymerase chain reaction from a *Helicobacter pylori* genome.

6. The isolated polynucleotide of claim 1, which is a DNA molecule that encodes the mature form or a derivative of a polypeptide encoded by the DNA molecule of claim 4.

7. The isolated polynucleotide of claim 1, which is a DNA molecule that encodes the mature form or a derivative of a polypeptide encoded by the DNA molecule of claim 5.

8. A compound, in a substantially purified form, that is the mature form or a derivative of a polypeptide comprising an amino acid sequence that is homologous to a *Helicobacter* polypeptide selected from the group consisting of GHPO 35 (SEQ ID NO:2), GHPO 55 (SEQ ID NO:4), GHPO 78 (SEQ ID NO:6), GHPO 89 (SEQ ID NO:8), GHPO 129 (SEQ ID NO:10), GHPO 541 (SEQ ID NO:12), GHPO 607 (SEQ ID NO:14), GHPO 635 (SEQ ID NO:16), GHPO 701 (SEQ ID NO:18), GHPO 712 (SEQ ID NO:20), GHPO 761 (SEQ ID NO:22), GHPO 838 (SEQ ID NO:24), GHPO 1034 (SEQ ID NO:26), GHPO 1085 (SEQ ID NO:28), GHPO 1213 (SEQ ID NO:30), GHPO 1255 (SEQ ID NO:32), GHPO 1308 (SEQ ID NO:34), GHPO 1389 (SEQ ID NO:36), GHPO 1706 (SEQ ID NO:38), GHPO 234 (SEQ ID NO:40), GHPO 314 (SEQ ID NO:42), GHPO 510 (SEQ ID NO:44), GHPO 603 (SEQ ID

-2033-

GHPO 1575 (SEQ ID NO:1288), GHPO 1582 (SEQ ID NO:1290), GHPO 1595 (SEQ ID NO:1292), GHPO 1597 (SEQ ID NO:1294), GHPO 1599 (SEQ ID NO:1296), GHPO 1601 (SEQ ID NO:1298), GHPO 1609 (SEQ ID NO:1300), GHPO 1613 (SEQ ID NO:1302), GHPO 1614 (SEQ ID NO:1304), GHPO 1626 (SEQ ID NO:1306), GHPO 1628 (SEQ ID NO:1308), GHPO 1639 (SEQ ID NO:1310), GHPO 1640 (SEQ ID NO:1312), GHPO 1641 (SEQ ID NO:1314), GHPO 1646 (SEQ ID NO:1316), GHPO 1662 (SEQ ID NO:1318), GHPO 1667 (SEQ ID NO:1320), GHPO 1668 (SEQ ID NO:1322), GHPO 1670 (SEQ ID NO:1324), GHPO 1671 (SEQ ID NO:1326), GHPO 1672 (SEQ ID NO:1328), GHPO 1678 (SEQ ID NO:1330), GHPO 1684 (SEQ ID NO:1332), GHPO 1695 (SEQ ID NO:1334), GHPO 1697 (SEQ ID NO:1336), GHPO 1701 (SEQ ID NO:1338), GHPO 1719 (SEQ ID NO:1340), GHPO 1723 (SEQ ID NO:1342), GHPO 1732 (SEQ ID NO:1344), GHPO 1739 (SEQ ID NO:1346), GHPO 1741 (SEQ ID NO:1348), GHPO 1747 (SEQ ID NO:1350), GHPO 1749 (SEQ ID NO:1352), GHPO 1750 (SEQ ID NO:1354), GHPO 1751 (SEQ ID NO:1356), GHPO 1755 (SEQ ID NO:1358), GHPO 1771 (SEQ ID NO:1360), GHPO 1786 (SEQ ID NO:1362), and GHPO 1789 (SEQ ID NO:1364); or

(ii) a derivative of said *Helicobacter* polypeptide.

2. The isolated polynucleotide of claim 1, which encodes a mature form of said *Helicobacter* polypeptide.

3. The isolated polynucleotide of claim 1 or 2, wherein the polynucleotide is a DNA molecule.

-2032-

1210 (SEQ ID NO:1166), GHPO 1211 (SEQ ID NO:1168), GHPO 1216 (SEQ
ID NO:1170), GHPO 1218 (SEQ ID NO:1172), GHPO 1220 (SEQ ID
NO:1174), GHPO 1223 (SEQ ID NO:1176), GHPO 1226 (SEQ ID NO:1178),
GHPO 1240 (SEQ ID NO:1180), GHPO 1246 (SEQ ID NO:1182), GHPO
1251 (SEQ ID NO:1184), GHPO 1252 (SEQ ID NO:1186), GHPO 1261 (SEQ
ID NO:1188), GHPO 1265 (SEQ ID NO:1190), GHPO 1267 (SEQ ID
NO:1192), GHPO 1278 (SEQ ID NO:1194), GHPO 1282 (SEQ ID NO:1196),
GHPO 1283 (SEQ ID NO:1198), GHPO 1287 (SEQ ID NO:1200), GHPO
1292 (SEQ ID NO:1202), GHPO 1293 (SEQ ID NO:1204), GHPO 1302 (SEQ
ID NO:1206), GHPO 1309 (SEQ ID NO:1208), GHPO 1317 (SEQ ID
NO:1210), GHPO 1318 (SEQ ID NO:1212), GHPO 1321 (SEQ ID NO:1214),
GHPO 1325 (SEQ ID NO:1216), GHPO 1341 (SEQ ID NO:1218), GHPO
1351 (SEQ ID NO:1220), GHPO 1354 (SEQ ID NO:1222), GHPO 1363 (SEQ
ID NO:1224), GHPO 1371 (SEQ ID NO:1226), GHPO 1381 (SEQ ID
NO:1228), GHPO 1401 (SEQ ID NO:1230), GHPO 1402 (SEQ ID NO:1232),
GHPO 1403 (SEQ ID NO:1234), GHPO 1408 (SEQ ID NO:1236), GHPO
1416 (SEQ ID NO:1238), GHPO 1420 (SEQ ID NO:1240), GHPO 1428 (SEQ
ID NO:1242), GHPO 1437 (SEQ ID NO:1244), GHPO 1439 (SEQ ID
NO:1246), GHPO 1460 (SEQ ID NO:1248), GHPO 1463 (SEQ ID NO:1250),
GHPO 1472 (SEQ ID NO:1252), GHPO 1474 (SEQ ID NO:1254), GHPO
1484 (SEQ ID NO:1256), GHPO 1489 (SEQ ID NO:1258), GHPO 1494 (SEQ
ID NO:1260), GHPO 1495 (SEQ ID NO:1262), GHPO 1498 (SEQ ID
NO:1264), GHPO 1499 (SEQ ID NO:1266), GHPO 1500 (SEQ ID NO:1268),
GHPO 1503 (SEQ ID NO:1270), GHPO 1504 (SEQ ID NO:1272), GHPO
1510 (SEQ ID NO:1274), GHPO 1518 (SEQ ID NO:1276), GHPO 1533 (SEQ
ID NO:1278), GHPO 1541 (SEQ ID NO:1280), GHPO 1544 (SEQ ID
NO:1282), GHPO 1548 (SEQ ID NO:1284), GHPO 1565 (SEQ ID NO:1286),

-2031-

NO:1042), GHPO 819 (SEQ ID NO:1044), GHPO 841 (SEQ ID NO:1046),
GHPO 843 (SEQ ID NO:1048), GHPO 846 (SEQ ID NO:1050), GHPO 875
(SEQ ID NO:1052), GHPO 892 (SEQ ID NO:1054), GHPO 902 (SEQ ID
NO:1056), GHPO 904 (SEQ ID NO:1058), GHPO 906 (SEQ ID NO:1060),
GHPO 908 (SEQ ID NO:1062), GHPO 921 (SEQ ID NO:1064), GHPO 923
5 (SEQ ID NO:1066), GHPO 926 (SEQ ID NO:1068), GHPO 933 (SEQ ID
NO:1070), GHPO 939 (SEQ ID NO:1072), GHPO 940 (SEQ ID NO:1074),
GHPO 943 (SEQ ID NO:1076), GHPO 951 (SEQ ID NO:1078), GHPO 961
(SEQ ID NO:1080), GHPO 965 (SEQ ID NO:1082), GHPO 990 (SEQ ID
NO:1084), GHPO 991 (SEQ ID NO:1086), GHPO 998 (SEQ ID NO:1088),
10 GHPO 1001 (SEQ ID NO:1090), GHPO 1005 (SEQ ID NO:1092), GHPO
1033 (SEQ ID NO:1094), GHPO 1039 (SEQ ID NO:1096), GHPO 1041 (SEQ
ID NO:1098), GHPO 1043 (SEQ ID NO:1100), GHPO 1044 (SEQ ID
NO:1102), GHPO 1051 (SEQ ID NO:1104), GHPO 1058 (SEQ ID NO:1106),
GHPO 1060 (SEQ ID NO:1108), GHPO 1075 (SEQ ID NO:1110), GHPO
15 1077 (SEQ ID NO:1112), GHPO 1082 (SEQ ID NO:1114), GHPO 1083 (SEQ
ID NO:1116), GHPO 1086 (SEQ ID NO:1118), GHPO 1087 (SEQ ID
NO:1120), GHPO 1090 (SEQ ID NO:1122), GHPO 1097 (SEQ ID NO:1124),
GHPO 1098 (SEQ ID NO:1126), GHPO 1103 (SEQ ID NO:1128), GHPO
1113 (SEQ ID NO:1130), GHPO 1116 (SEQ ID NO:1132), GHPO 1123 (SEQ
20 ID NO:1134), GHPO 1125 (SEQ ID NO:1136), GHPO 1129 (SEQ ID
NO:1138), GHPO 1130 (SEQ ID NO:1140), GHPO 1134 (SEQ ID NO:1142),
GHPO 1161 (SEQ ID NO:1144), GHPO 1166 (SEQ ID NO:1146), GHPO
1170 (SEQ ID NO:1148), GHPO 1175 (SEQ ID NO:1150), GHPO 1181 (SEQ
ID NO:1152), GHPO 1186 (SEQ ID NO:1154), GHPO 1188 (SEQ ID
25 NO:1156), GHPO 1191 (SEQ ID NO:1158), GHPO 1193 (SEQ ID NO:1160),
GHPO 1196 (SEQ ID NO:1162), GHPO 1204 (SEQ ID NO:1164), GHPO

-2030-

NO:910), GHPO 453 (SEQ ID NO:912), GHPO 455 (SEQ ID NO:914), GHPO
464 (SEQ ID NO:916), GHPO 467 (SEQ ID NO:918), GHPO 468 (SEQ ID
NO:920), GHPO 470 (SEQ ID NO:922), GHPO 486 (SEQ ID NO:924), GHPO
487 (SEQ ID NO:926), GHPO 488 (SEQ ID NO:928), GHPO 489 (SEQ ID
NO:930), GHPO 498 (SEQ ID NO:932), GHPO 501 (SEQ ID NO:934), GHPO
5 504 (SEQ ID NO:936), GHPO 512 (SEQ ID NO:938), GHPO 517 (SEQ ID
NO:940), GHPO 520 (SEQ ID NO:942), GHPO 528 (SEQ ID NO:944), GHPO
530 (SEQ ID NO:946), GHPO 532 (SEQ ID NO:948), GHPO 548 (SEQ ID
NO:950), GHPO 561 (SEQ ID NO:952), GHPO 564 (SEQ ID NO:954), GHPO
572 (SEQ ID NO:956), GHPO 573 (SEQ ID NO:958), GHPO 574 (SEQ ID
10 NO:960), GHPO 577 (SEQ ID NO:962), GHPO 579 (SEQ ID NO:964), GHPO
583 (SEQ ID NO:966), GHPO 588 (SEQ ID NO:968), GHPO 593 (SEQ ID
NO:970), GHPO 597 (SEQ ID NO:972), GHPO 598 (SEQ ID NO:974), GHPO
604 (SEQ ID NO:976), GHPO 606 (SEQ ID NO:978), GHPO 611 (SEQ ID
NO:980), GHPO 612 (SEQ ID NO:982), GHPO 615 (SEQ ID NO:984), GHPO
15 632 (SEQ ID NO:986), GHPO 633 (SEQ ID NO:988), GHPO 637 (SEQ ID
NO:990), GHPO 651 (SEQ ID NO:992), GHPO 663 (SEQ ID NO:994), GHPO
686 (SEQ ID NO:996), GHPO 693 (SEQ ID NO:998), GHPO 698 (SEQ ID
NO:1000), GHPO 703 (SEQ ID NO:1002), GHPO 704 (SEQ ID NO:1004),
GHPO 705 (SEQ ID NO:1006), GHPO 707 (SEQ ID NO:1008), GHPO 721
20 (SEQ ID NO:1010), GHPO 727 (SEQ ID NO:1012), GHPO 728 (SEQ ID
NO:1014), GHPO 733 (SEQ ID NO:1016), GHPO 758 (SEQ ID NO:1018),
GHPO 763 (SEQ ID NO:1020), GHPO 771 (SEQ ID NO:1022), GHPO 774
(SEQ ID NO:1024), GHPO 776 (SEQ ID NO:1026), GHPO 783 (SEQ ID
NO:1028), GHPO 800 (SEQ ID NO:1030), GHPO 806 (SEQ ID NO:1032),
25 GHPO 807 (SEQ ID NO:1034), GHPO 808 (SEQ ID NO:1036), GHPO 809
(SEQ ID NO:1038), GHPO 811 (SEQ ID NO:1040), GHPO 815 (SEQ ID

-2029-

87 (SEQ ID NO:776), GHPO 91 (SEQ ID NO:778), GHPO 92 (SEQ ID
NO:780), GHPO 96 (SEQ ID NO:782), GHPO 97 (SEQ ID NO:784), GHPO
111 (SEQ ID NO:786), GHPO 115 (SEQ ID NO:788), GHPO 117 (SEQ ID
NO:790), GHPO 123 (SEQ ID NO:792), GHPO 124 (SEQ ID NO:794), GHPO
126 (SEQ ID NO:796), GHPO 127 (SEQ ID NO:798), GHPO 128 (SEQ ID
5 NO:800), GHPO 131 (SEQ ID NO:802), GHPO 133 (SEQ ID NO:804), GHPO
140 (SEQ ID NO:806), GHPO 141 (SEQ ID NO:808), GHPO 145 (SEQ ID
NO:810), GHPO 147 (SEQ ID NO:812), GHPO 166 (SEQ ID NO:814), GHPO
181 (SEQ ID NO:816), GHPO 187 (SEQ ID NO:818), GHPO 188 (SEQ ID
NO:820), GHPO 192 (SEQ ID NO:822), GHPO 202 (SEQ ID NO:824), GHPO
10 204 (SEQ ID NO:826), GHPO 205 (SEQ ID NO:828), GHPO 212 (SEQ ID
NO:830), GHPO 218 (SEQ ID NO:832), GHPO 226 (SEQ ID NO:834), GHPO
231 (SEQ ID NO:836), GHPO 236 (SEQ ID NO:838), GHPO 239 (SEQ ID
NO:840), GHPO 245 (SEQ ID NO:842), GHPO 246 (SEQ ID NO:844), GHPO
248 (SEQ ID NO:846), GHPO 253 (SEQ ID NO:848), GHPO 265 (SEQ ID
15 NO:850), GHPO 266 (SEQ ID NO:852), GHPO 271 (SEQ ID NO:854), GHPO
272 (SEQ ID NO:856), GHPO 286 (SEQ ID NO:858), GHPO 291 (SEQ ID
NO:860), GHPO 292 (SEQ ID NO:862), GHPO 297 (SEQ ID NO:864), GHPO
304 (SEQ ID NO:866), GHPO 307 (SEQ ID NO:868), GHPO 324 (SEQ ID
NO:870), GHPO 326 (SEQ ID NO:872), GHPO 331 (SEQ ID NO:874), GHPO
20 343 (SEQ ID NO:876), GHPO 345 (SEQ ID NO:878), GHPO 346 (SEQ ID
NO:880), GHPO 352 (SEQ ID NO:882), GHPO 355 (SEQ ID NO:884), GHPO
363 (SEQ ID NO:886), GHPO 369 (SEQ ID NO:888), GHPO 376 (SEQ ID
NO:890), GHPO 378 (SEQ ID NO:892), GHPO 388 (SEQ ID NO:894), GHPO
396 (SEQ ID NO:896), GHPO 403 (SEQ ID NO:898), GHPO 410 (SEQ ID
25 NO:900), GHPO 415 (SEQ ID NO:902), GHPO 421 (SEQ ID NO:904), GHPO
439 (SEQ ID NO:906), GHPO 441 (SEQ ID NO:908), GHPO 443 (SEQ ID

-2028-

NO:646), GHPO 1376 (SEQ ID NO:648), GHPO 1380 (SEQ ID NO:650),
GHPO 1394 (SEQ ID NO:652), GHPO 1407 (SEQ ID NO:654), GHPO 1415
(SEQ ID NO:656), GHPO 1425 (SEQ ID NO:658), GHPO 1427 (SEQ ID
NO:660), GHPO 1444 (SEQ ID NO:662), GHPO 1449 (SEQ ID NO:664),
GHPO 1465 (SEQ ID NO:666), GHPO 1475 (SEQ ID NO:668), GHPO 1479
5 (SEQ ID NO:670), GHPO 1483 (SEQ ID NO:672), GHPO 1488 (SEQ ID
NO:674), GHPO 1496 (SEQ ID NO:676), GHPO 1524 (SEQ ID NO:678),
GHPO 1536 (SEQ ID NO:680), GHPO 1539 (SEQ ID NO:682), GHPO 1540
(SEQ ID NO:684), GHPO 1542 (SEQ ID NO:686), GHPO 1555 (SEQ ID
NO:688), GHPO 1560 (SEQ ID NO:690), GHPO 1564 (SEQ ID NO:692),
10 GHPO 1570 (SEQ ID NO:694), GHPO 1588 (SEQ ID NO:696), GHPO 1604
(SEQ ID NO:698), GHPO 1605 (SEQ ID NO:700), GHPO 1619 (SEQ ID
NO:702), GHPO 1629 (SEQ ID NO:704), GHPO 1642 (SEQ ID NO:706),
GHPO 1654 (SEQ ID NO:708), GHPO 1661 (SEQ ID NO:710), GHPO 1673
(SEQ ID NO:712), GHPO 1687 (SEQ ID NO:714), GHPO 1692 (SEQ ID
15 NO:716), GHPO 1693 (SEQ ID NO:718), GHPO 1699 (SEQ ID NO:720),
GHPO 1738 (SEQ ID NO:722), GHPO 1745 (SEQ ID NO:724), GHPO 1746
(SEQ ID NO:726), GHPO 1754 (SEQ ID NO:728), GHPO 1792 (SEQ ID
NO:730), GHPO 1795 (SEQ ID NO:732), GHPO 1796 (SEQ ID NO:734),
GHPO 7 (SEQ ID NO:736), GHPO 8 (SEQ ID NO:738), GHPO 9 (SEQ ID
20 NO:740), GHPO 10 (SEQ ID NO:742), GHPO 12 (SEQ ID NO:744), GHPO
25 (SEQ ID NO:746), GHPO 27 (SEQ ID NO:748), GHPO 29 (SEQ ID
NO:750), GHPO 30 (SEQ ID NO:752), GHPO 37 (SEQ ID NO:754), GHPO
49 (SEQ ID NO:756), GHPO 51 (SEQ ID NO:758), GHPO 54 (SEQ ID
NO:760), GHPO 65 (SEQ ID NO:762), GHPO 66 (SEQ ID NO:764), GHPO
25 68 (SEQ ID NO:766), GHPO 70 (SEQ ID NO:768), GHPO 77 (SEQ ID
NO:770), GHPO 83 (SEQ ID NO:772), GHPO 85 (SEQ ID NO:774), GHPO

-2027-

NO:516), GHPO 713 (SEQ ID NO:518), GHPO 716 (SEQ ID NO:520), GHPO
718 (SEQ ID NO:522), GHPO 726 (SEQ ID NO:524), GHPO 734 (SEQ ID
NO:526), GHPO 740 (SEQ ID NO:528), GHPO 770 (SEQ ID NO:530), GHPO
782 (SEQ ID NO:532), GHPO 786 (SEQ ID NO:534), GHPO 792 (SEQ ID
NO:536), GHPO 797 (SEQ ID NO:538), GHPO 816 (SEQ ID NO:540), GHPO
5 828 (SEQ ID NO:542), GHPO 839 (SEQ ID NO:544), GHPO 840 (SEQ ID
NO:546), GHPO 842 (SEQ ID NO:548), GHPO 885 (SEQ ID NO:550), GHPO
889 (SEQ ID NO:552), GHPO 903 (SEQ ID NO:554), GHPO 912 (SEQ ID
NO:556), GHPO 946 (SEQ ID NO:558), GHPO 958 (SEQ ID NO:560), GHPO
968 (SEQ ID NO:562), GHPO 987 (SEQ ID NO:564), GHPO 992 (SEQ ID
10 NO:566), GHPO 996 (SEQ ID NO:568), GHPO 997 (SEQ ID NO:570), GHPO
1002 (SEQ ID NO:572), GHPO 1026 (SEQ ID NO:574), GHPO 1028 (SEQ ID
NO:576), GHPO 1034 (SEQ ID NO:578), GHPO 1038 (SEQ ID NO:580),
GHPO 1059 (SEQ ID NO:582), GHPO 1065 (SEQ ID NO:584), GHPO 1072
(SEQ ID NO:586), GHPO 1073 (SEQ ID NO:588), GHPO 1088 (SEQ ID
15 NO:590), GHPO 1091 (SEQ ID NO:592), GHPO 1105 (SEQ ID NO:594),
GHPO 1115 (SEQ ID NO:596), GHPO 1159 (SEQ ID NO:598), GHPO 1177
(SEQ ID NO:600), GHPO 1187 (SEQ ID NO:602), GHPO 1192 (SEQ ID
NO:604), GHPO 1195 (SEQ ID NO:606), GHPO 1224 (SEQ ID NO:608),
GHPO 1225 (SEQ ID NO:610), GHPO 1228 (SEQ ID NO:612), GHPO 1229
20 (SEQ ID NO:614), GHPO 1231 (SEQ ID NO:616), GHPO 1236 (SEQ ID
NO:618), GHPO 1242 (SEQ ID NO:620), GHPO 1248 (SEQ ID NO:622),
GHPO 1270 (SEQ ID NO:624), GHPO 1271 (SEQ ID NO:626), GHPO 1298
(SEQ ID NO:628), GHPO 1301 (SEQ ID NO:630), GHPO 1304 (SEQ ID
NO:632), GHPO 1315 (SEQ ID NO:634), GHPO 1319 (SEQ ID NO:636),
25 GHPO 1323 (SEQ ID NO:638), GHPO 1331 (SEQ ID NO:640), GHPO 1332
(SEQ ID NO:642), GHPO 1347 (SEQ ID NO:644), GHPO 1373 (SEQ ID

-2026-

57 (SEQ ID NO:382), GHPO 64 (SEQ ID NO:384), GHPO 79 (SEQ ID
NO:386), GHPO 84 (SEQ ID NO:388), GHPO 86 (SEQ ID NO:390), GHPO
99 (SEQ ID NO:392), GHPO 106 (SEQ ID NO:394), GHPO 118 (SEQ ID
NO:396), GHPO 122 (SEQ ID NO:398), GHPO 128 (SEQ ID NO:400), GHPO
138 (SEQ ID NO:402), GHPO 153 (SEQ ID NO:404), GHPO 160 (SEQ ID
NO:406), GHPO 168 (SEQ ID NO:408), GHPO 179 (SEQ ID NO:410), GHPO
189 (SEQ ID NO:412), GHPO 229 (SEQ ID NO:414), GHPO 243 (SEQ ID
NO:416), GHPO 244 (SEQ ID NO:418), GHPO 251 (SEQ ID NO:420), GHPO
267 (SEQ ID NO:422), GHPO 269 (SEQ ID NO:424), GHPO 279 (SEQ ID
NO:426), GHPO 284 (SEQ ID NO:428), GHPO 296 (SEQ ID NO:430), GHPO
300 (SEQ ID NO:432), GHPO 305 (SEQ ID NO:434), GHPO 319 (SEQ ID
NO:436), GHPO 330 (SEQ ID NO:438), GHPO 340 (SEQ ID NO:440), GHPO
342 (SEQ ID NO:442), GHPO 344 (SEQ ID NO:444), GHPO 358 (SEQ ID
NO:446), GHPO 373 (SEQ ID NO:448), GHPO 382 (SEQ ID NO:450), GHPO
384 (SEQ ID NO:452), GHPO 398 (SEQ ID NO:454), GHPO 409 (SEQ ID
NO:456), GHPO 422 (SEQ ID NO:458), GHPO 430 (SEQ ID NO:460), GHPO
446 (SEQ ID NO:462), GHPO 447 (SEQ ID NO:464), GHPO 450 (SEQ ID
NO:466), GHPO 451 (SEQ ID NO:468), GHPO 452 (SEQ ID NO:470), GHPO
456 (SEQ ID NO:472), GHPO 461 (SEQ ID NO:474), GHPO 476 (SEQ ID
NO:476), GHPO 478 (SEQ ID NO:478), GHPO 491 (SEQ ID NO:480), GHPO
511 (SEQ ID NO:482), GHPO 519 (SEQ ID NO:484), GHPO 526 (SEQ ID
NO:486), GHPO 534 (SEQ ID NO:488), GHPO 536 (SEQ ID NO:490), GHPO
542 (SEQ ID NO:492), GHPO 544 (SEQ ID NO:494), GHPO 576 (SEQ ID
NO:496), GHPO 578 (SEQ ID NO:498), GHPO 580 (SEQ ID NO:500), GHPO
585 (SEQ ID NO:502), GHPO 599 (SEQ ID NO:504), GHPO 639 (SEQ ID
NO:506), GHPO 642 (SEQ ID NO:508), GHPO 647 (SEQ ID NO:510), GHPO
654 (SEQ ID NO:512), GHPO 669 (SEQ ID NO:514), GHPO 710 (SEQ ID

-2025-

GHPO 1446 (SEQ ID NO:252), GHPO 1469 (SEQ ID NO:254), GHPO 1501
(SEQ ID NO:256), GHPO 1505 (SEQ ID NO:258), GHPO 1522 (SEQ ID
NO:260), GHPO 1525 (SEQ ID NO:262), GHPO 1615 (SEQ ID NO:264),
GHPO 1689 (SEQ ID NO:266), GHPO 1733 (SEQ ID NO:268), GHPO 18
(SEQ ID NO:270), GHPO 139 (SEQ ID NO:272), GHPO 142 (SEQ ID
5 NO:274), GHPO 250 (SEQ ID NO:276), GHPO 257 (SEQ ID NO:278), GHPO
325 (SEQ ID NO:280), GHPO 355 (SEQ ID NO:282), GHPO 357 (SEQ ID
NO:284), GHPO 454 (SEQ ID NO:286), GHPO 475 (SEQ ID NO:288), GHPO
515 (SEQ ID NO:290), GHPO 527 (SEQ ID NO:292), GHPO 551 (SEQ ID
NO:294), GHPO 602 (SEQ ID NO:296), GHPO 626 (SEQ ID NO:298), GHPO
10 646 (SEQ ID NO:300), GHPO 653 (SEQ ID NO:302), GHPO 655 (SEQ ID
NO:304), GHPO 670 (SEQ ID NO:306), GHPO 739 (SEQ ID NO:308), GHPO
798 (SEQ ID NO:310), GHPO 1102 (SEQ ID NO:312), GHPO 1114 (SEQ ID
NO:314), GHPO 1152 (SEQ ID NO:316), GHPO 1272 (SEQ ID NO:318),
GHPO 1345 (SEQ ID NO:320), GHPO 1377 (SEQ ID NO:322), GHPO 1424
15 (SEQ ID NO:324), GHPO 1430 (SEQ ID NO:326), GHPO 1502 (SEQ ID
NO:328), GHPO 1600 (SEQ ID NO:330), GHPO 1714 (SEQ ID NO:332),
GHPO 359 (SEQ ID NO:334), GHPO 678 (SEQ ID NO:336), GHPO 708
(SEQ ID NO:338), GHPO 759 (SEQ ID NO:340), GHPO 847 (SEQ ID
NO:342), GHPO 1050 (SEQ ID NO:344), GHPO 1101 (SEQ ID NO:346),
20 GHPO 1120 (SEQ ID NO:348), GHPO 1138 (SEQ ID NO:350), GHPO 1310
(SEQ ID NO:352), GHPO 1320 (SEQ ID NO:354), GHPO 1375 (SEQ ID
NO:356), GHPO 1432 (SEQ ID NO:358), GHPO 21 (SEQ ID NO:360), GHPO
282 (SEQ ID NO:362), GHPO 1089 (SEQ ID NO:364), GHPO 1141 (SEQ ID
NO:366), GHPO 1280 (SEQ ID NO:368), GHPO 1608 (SEQ ID NO:370),
25 GHPO 15 (SEQ ID NO:372), GHPO 16 (SEQ ID NO:374), GHPO 36 (SEQ ID
NO:376), GHPO 38 (SEQ ID NO:378), GHPO 52 (SEQ ID NO:380), GHPO

-2024-

5 NO:120), GHPO 28 (SEQ ID NO:122), GHPO 86 (SEQ ID NO:124), GHPO
155 (SEQ ID NO:126), GHPO 157 (SEQ ID NO:128), GHPO 237 (SEQ ID
NO:130), GHPO 290 (SEQ ID NO:132), GHPO 293 (SEQ ID NO:134), GHPO
335 (SEQ ID NO:136), GHPO 374 (SEQ ID NO:138), GHPO 442 (SEQ ID
NO:140), GHPO 480 (SEQ ID NO:142), GHPO 523 (SEQ ID NO:144), GHPO
610 (SEQ ID NO:146), GHPO 675 (SEQ ID NO:148), GHPO 690 (SEQ ID
NO:150), GHPO 829 (SEQ ID NO:152), GHPO 850 (SEQ ID NO:154), GHPO
876 (SEQ ID NO:156), GHPO 984 (SEQ ID NO:158), GHPO 989 (SEQ ID
NO:160), GHPO 1111 (SEQ ID NO:162), GHPO 1145 (SEQ ID NO:164),
GHPO 1256 (SEQ ID NO:166), GHPO 1264 (SEQ ID NO:168), GHPO 1316
10 (SEQ ID NO:170), GHPO 1368 (SEQ ID NO:172), GHPO 1442 (SEQ ID
NO:174), GHPO 1506 (SEQ ID NO:176), GHPO 1543 (SEQ ID NO:178),
GHPO 1574 (SEQ ID NO:180), GHPO 1627 (SEQ ID NO:182), GHPO 1657
(SEQ ID NO:184), GHPO 1664 (SEQ ID NO:186), GHPO 1694 (SEQ ID
NO:188), GHPO 1704 (SEQ ID NO:190), GHPO 1763 (SEQ ID NO:192),
15 GHPO 616 (SEQ ID NO:194), GHPO 76 (SEQ ID NO:196), GHPO 109 (SEQ
ID NO:198), GHPO 163 (SEQ ID NO:200), GHPO 169 (SEQ ID NO:202),
GHPO 208 (SEQ ID NO:204), GHPO 219 (SEQ ID NO:206), GHPO 445
(SEQ ID NO:208), GHPO 479 (SEQ ID NO:210), GHPO 525 (SEQ ID
NO:212), GHPO 535 (SEQ ID NO:214), GHPO 731 (SEQ ID NO:216), GHPO
20 836 (SEQ ID NO:218), GHPO 879 (SEQ ID NO:220), GHPO 881 (SEQ ID
NO:222), GHPO 886 (SEQ ID NO:224), GHPO 893 (SEQ ID NO:226), GHPO
894 (SEQ ID NO:228), GHPO 976 (SEQ ID NO:230), GHPO 1011 (SEQ ID
NO:232), GHPO 1024 (SEQ ID NO:234), GHPO 1084 (SEQ ID NO:236),
GHPO 1329 (SEQ ID NO:238), GHPO 1330 (SEQ ID NO:240), GHPO 1346
25 (SEQ ID NO:242), GHPO 1360 (SEQ ID NO:244), GHPO 1388 (SEQ ID
NO:246), GHPO 1411 (SEQ ID NO:248), GHPO 1419 (SEQ ID NO:250),

-2023-

1. An isolated polynucleotide that encodes:

(i) a polypeptide comprising an amino acid sequence that is homologous to the amino acid sequence of a *Helicobacter* polypeptide selected from the group consisting of GHPO 35 (SEQ ID NO:2), GHPO 55 (SEQ ID NO:4), GHPO 78 (SEQ ID NO:6), GHPO 89 (SEQ ID NO:8), GHPO 129 (SEQ ID NO:10), GHPO 541 (SEQ ID NO:12), GHPO 607 (SEQ ID NO:14), GHPO 635 (SEQ ID NO:16), GHPO 701 (SEQ ID NO:18), GHPO 712 (SEQ ID NO:20), GHPO 761 (SEQ ID NO:22), GHPO 838 (SEQ ID NO:24), GHPO 1034 (SEQ ID NO:26), GHPO 1085 (SEQ ID NO:28), GHPO 1213 (SEQ ID NO:30), GHPO 1255 (SEQ ID NO:32), GHPO 1308 (SEQ ID NO:34), GHPO 1389 (SEQ ID NO:36), GHPO 1706 (SEQ ID NO:38), GHPO 234 (SEQ ID NO:40), GHPO 314 (SEQ ID NO:42), GHPO 510 (SEQ ID NO:44), GHPO 603 (SEQ ID NO:46), GHPO 937 (SEQ ID NO:48), GHPO 1027 (SEQ ID NO:50), GHPO 1099 (SEQ ID NO:52), GHPO 1151 (SEQ ID NO:54), GHPO 1275 (SEQ ID NO:56), GHPO 1365 (SEQ ID NO:58), GHPO 1578 (SEQ ID NO:60), GHPO 22 (SEQ ID NO:62), GHPO 58 (SEQ ID NO:64), GHPO 200 (SEQ ID NO:66), GHPO 558 (SEQ ID NO:68), GHPO 563 (SEQ ID NO:70), GHPO 695 (SEQ ID NO:72), GHPO 699 (SEQ ID NO:74), GHPO 702 (SEQ ID NO:76), GHPO 709 (SEQ ID NO:78), GHPO 741 (SEQ ID NO:80), GHPO 762 (SEQ ID NO:82), GHPO 827 (SEQ ID NO:84), GHPO 852 (SEQ ID NO:86), GHPO 1013 (SEQ ID NO:88), GHPO 1020 (SEQ ID NO:90), GHPO 1031 (SEQ ID NO:92), GHPO 1052 (SEQ ID NO:94), GHPO 1127 (SEQ ID NO:96), GHPO 1149 (SEQ ID NO:98), GHPO 1176 (SEQ ID NO:100), GHPO 1250 (SEQ ID NO:102), GHPO 1312 (SEQ ID NO:104), GHPO 1358 (SEQ ID NO:106), GHPO 1490 (SEQ ID NO:108), GHPO 1559 (SEQ ID NO:110), GHPO 1651 (SEQ ID NO:112), GHPO 1726 (SEQ ID NO:114), GHPO 1780 (SEQ ID NO:116), GHPO 895 (SEQ ID NO:118), GHPO 1447 (SEQ ID

-2022-

Other embodiments are within the following claims.

What is claimed is:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

CGCGGATCCG AGGAAATAGC ATGTTAATAA CC

32

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

CCGCTCGAGT CACTGCTTGC ATGACTTATT CCA

33

GCGGATCCTT TTCTTCAATG TTG

24

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

CCGCTCGAGT CAAAGTTTTA AACAAATTC

29

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

CCGAATTCGG TTATAAAGCC CCT

23

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

CCGCTCGAGT TAAGGCTGAT TTAA

24

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CGCGGATCCG AAGACATGTG CAACCGATG

29

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

CCGCTCGAGC TAAAAGTTTT GCAAAATCAC

30

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

CGCGGATCCG ATTTTACTTG AAAAATTAA AC

32

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

CCGCTCGAGT TAGAAAGTGT AGTTCAAATA C

31

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

Met	Leu	Gly	Ser	Lys	Thr	Tyr	Ser	Val	Leu	Arg	Ser	Tyr	Glu	Lys	Thr
1				5					10					15	
Phe	Ser	Pro	Glu	Leu	Cys	Ile	Leu	Met	Gly	Lys	Thr	Tyr	Glu	Tyr	
			20				25					30			
Pro	Ile	Met	Leu	Lys	Glu	Leu	Leu	Met	Leu	Leu	Ala	Asn	Ala	Arg	Gly
		35					40					45			
Leu	Leu	Glu	Ala	Leu	Lys	Val	Ile	Phe	Asn	Met	Leu	Gly	Leu	Ser	Lys
	50					55					60				
Leu	Lys	Asp	Lys	Ser	Pro	Phe	Ser	Leu	Arg	Val	Leu	Ser	Ser	Phe	Lys
65					70				75						80
Glu	Ser	Lys	Arg	Pro	Ile	Thr									
					85										

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

CTGAATTCGA ATGAAAAGAA TTTTAGTCTC T

31

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

CCGCTCGAGT TAAAACTCAT AATTCAAAT

29

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...290
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

```

AACCATGCCT TTTCATCGTC TCTATCAAA ATG TTA GGG TCT AAA ACA TAT TCC      53
                Met Leu Gly Ser Lys Thr Tyr Ser
                1                      5

GTT TTA AGA TCG TAT GAA AAA ACA TTC TCG CCT GAA GAG CTT TGC ATT      101
Val Leu Arg Ser Tyr Glu Lys Thr Phe Ser Pro Glu Glu Leu Cys Ile
    10                15                20

TTA ATG GGC AAA ACA TAC GAA TAC CCC ATC ATG CTT AAA GAA TTA TTG      149
Leu Met Gly Lys Thr Tyr Glu Tyr Pro Ile Met Leu Lys Glu Leu Leu
    25                30                35                40

ATG CTT TTG GCA AAC GCT AGG GGA TTG CTT GAA GCC TTG AAA GTG ATT      197
Met Leu Leu Ala Asn Ala Arg Gly Leu Leu Glu Ala Leu Lys Val Ile
                45                50                55

TTC AAC ATG CTT GGC TTG TCA AAA TTA AAA GAC AAA AGC CCG TTT TCT      245
Phe Asn Met Leu Gly Leu Ser Lys Leu Lys Asp Lys Ser Pro Phe Ser
                60                65                70

TTG AGA GTG TTG AGC AGT TTC AAG GAA TCC AAA CGC CCC ATT ACA TAGAA      295
Leu Arg Val Leu Ser Ser Phe Lys Glu Ser Lys Arg Pro Ile Thr
                75                80                85

AGCCTTACGA TTTTAAACA AACGCTCTAA AAAAAGCTTG TTCGTATGA      344

```

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Glu His Glu Gly Leu Ser Lys Lys Ile Leu Ala Lys Met Asp Thr Ile
 190 195 200

TTG AGC GTA AAA ATG CGA AGA GAT TTT GAT TCG CTC AAT GTG AGC GTG 676
 Leu Ser Val Lys Met Arg Arg Asp Phe Asp Ser Leu Asn Val Ser Val
 205 210 215

GCA GCA GGG ATC TTA ATG GAT AAA ATC AAC TAGGTGGTCA ATTGAATGGA ACA 729
 Ala Ala Gly Ile Leu Met Asp Lys Ile Asn
 220 225

GAATAAA 736

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

Met Gln Ala Val Ile Tyr Gly Lys Gln Val Ile Met His Leu Leu Asn
 1 5 10 15
 Ser His Gln Glu Lys Leu Gln Glu Ile Tyr Leu Ser Lys Glu Ile Asp
 20 25 30
 Lys Lys Leu Phe Phe Ala Leu Lys Lys Ala Cys Pro Asn Ile Ile Lys
 35 40 45
 Val Asp Asn Lys Lys Ala Gln Ser Leu Ala Lys Gly Gly Asn His Gln
 50 55 60
 Gly Val Leu Ala Lys Val Glu Leu Pro Leu Ala Val Ser Leu Lys Glu
 65 70 75 80
 Val Lys Lys Ala Gln Lys Leu Leu Val Leu Cys Gly Ile Thr Asp Val
 85 90 95
 Gly Asn Ile Gly Gly Ile Phe Arg Ser Ala Tyr Cys Leu Gly Met Gly
 100 105 110
 Gly Val Ile Leu Asp Phe Ala Lys Glu Leu Ala Tyr Glu Gly Ile Val
 115 120 125
 Arg Ser Ser Leu Gly Leu Met Tyr Asp Leu Pro Phe Ser Val Met Pro
 130 135 140
 Asn Thr Leu Asp Leu Ile Asn Glu Leu Lys Thr Ser Gly Phe Leu Cys
 145 150 155 160
 Leu Gly Ala Ser Met Gln Gly Ser Ser Gln Ile Glu Asn Leu Ser Leu
 165 170 175
 Lys Lys Cys Ala Leu Phe Leu Gly Ser Glu His Glu Gly Leu Ser Lys
 180 185 190
 Lys Ile Leu Ala Lys Met Asp Thr Ile Leu Ser Val Lys Met Arg Arg
 195 200 205
 Asp Phe Asp Ser Leu Asn Val Ser Val Ala Ala Gly Ile Leu Met Asp
 210 215 220
 Lys Ile Asn
 225

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

AAAAAATCAA TAAAAGGGGT TTAGC ATG CAA GCA GTA ATT TAT GGC AAG CAA	52
Met Gln Ala Val Ile Tyr Gly Lys Gln	
1 5	
GTG ATT ATG CAC CTT CTA AAC TCT CAT CAA GAA AAA TTG CAA GAA ATC	100
Val Ile Met His Leu Leu Asn Ser His Gln Glu Lys Leu Gln Glu Ile	
10 15 20 25	
TAT CTT TCT AAA GAA ATA GAC AAG AAA CTT TTT TTC GCG CTC AAA AAA	148
Tyr Leu Ser Lys Glu Ile Asp Lys Lys Leu Phe Phe Ala Leu Lys Lys	
30 35 40	
GCA TGC CCT AAT ATC ATC AAA GTG GAT AAT AAA AAA GCG CAA AGC TTG	196
Ala Cys Pro Asn Ile Ile Lys Val Asp Asn Lys Lys Ala Gln Ser Leu	
45 50 55	
GCT AAG GGG GGG AAT CAT CAA GGG GTT TTG GCT AAG GTG GAA CTG CCC	244
Ala Lys Gly Gly Asn His Gln Gly Val Leu Ala Lys Val Glu Leu Pro	
60 65 70	
TTA GCG GTT TCT TTA AAA GAG GTT AAA AAA GCT CAA AAA CTT TTG GTG	292
Leu Ala Val Ser Leu Lys Glu Val Lys Lys Ala Gln Lys Leu Leu Val	
75 80 85	
CTT TGC GGG ATT ACG GAT GTG GGG AAT ATT GGA GGT ATT TTT AGG AGC	340
Leu Cys Gly Ile Thr Asp Val Gly Asn Ile Gly Gly Ile Phe Arg Ser	
90 95 100 105	
GCG TAT TGC TTA GGA ATG GGT GGC GTT ATT TTA GAT TTT GCT AAA GAA	388
Ala Tyr Cys Leu Gly Met Gly Gly Val Ile Leu Asp Phe Ala Lys Glu	
110 115 120	
TTG GCT TAT GAG GGG ATT GTG CGA TCC AGC TTG GGG CTT ATG TAT GAT	436
Leu Ala Tyr Glu Gly Ile Val Arg Ser Ser Leu Gly Leu Met Tyr Asp	
125 130 135	
TTG CCT TTT AGC GTT ATG CCT AAC ACG CTG GAT TTA ATC AAT GAA TTG	484
Leu Pro Phe Ser Val Met Pro Asn Thr Leu Asp Leu Ile Asn Glu Leu	
140 145 150	
AAA ACG AGC GGG TTT TTA TGT TTG GGC GCG AGC ATG CAA GGC TCT AGT	532
Lys Thr Ser Gly Phe Leu Cys Leu Gly Ala Ser Met Gln Gly Ser Ser	
155 160 165	
CAA ATA GAA AAT CTA TCC TTA AAA AAA TGC GCT CTT TTT TTG GGG AGC	580
Gln Ile Glu Asn Leu Ser Leu Lys Lys Cys Ala Leu Phe Leu Gly Ser	
170 175 180 185	
GAG CAT GAG GGG TTG TCT AAA AAA ATC CTT GCT AAA ATG GAT ACT ATA	628

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

```

Met Lys Gln Ser Leu Arg Glu Gln Lys Leu Leu Lys Ile Leu Glu Asn
 1           5           10           15
Asp Val Leu Thr Ile Leu Asp Ser Phe Ser Asn Tyr Leu Phe Glu Leu
          20           25           30
Arg Glu Glu Leu Asp Phe Ile Glu Glu Glu Met Glu Gly Glu Ile Thr
          35           40           45
Glu Gln Asn Leu Thr Ala Leu Tyr Asp Phe Ser Asn Phe Leu Glu Asp
          50           55           60
His Val Asn Val Phe Tyr Glu Asn Val Leu Asn Ile Asp Asp Val Lys
65           70           75           80
Thr Glu His Leu Tyr Ser Gly Leu Ile Asp Ser Leu Asn Ala Asn Leu
          85           90           95
His Phe Val Lys Ser Phe Leu Ser Asn Gln Asp Leu Asp Phe Arg Phe
          100          105          110
Phe Lys Glu Ile Asn Asp Gly Gln Asp Pro Gln Lys Thr Leu Ser Arg
          115          120          125
Leu Ile Pro Leu Gln Ser Gly Lys Asn Asp Ala Ser Ser Phe Lys Ala
          130          135          140
Asn Asn Ser Phe Val Ser Leu Val Tyr Val Tyr Val Tyr Phe Met Leu
145          150          155          160
Glu Thr Ile Met Gln Ser Tyr Arg Ile Leu Arg Leu Leu Glu Lys Pro
          165          170          175
Ile Asn Asn Asn Ile Ser Glu Asp Met Gln Asn Asp Ile Glu Asn Phe
          180          185          190
Phe Val Gln Ala Asn Phe Leu Glu Tyr Tyr Val Gln Asn Lys Ile Tyr
          195          200          205
Pro Thr Asn His Ala Tyr Asp Phe Thr His Leu Ile Met Asp Ser Ile
          210          215          220
Ile Pro Asn Trp Ile Gln Thr Asp Met Ser Val Glu Ala Lys Lys Lys
225          230          235          240
Glu Leu Phe Glu Lys Tyr Phe Gln Asn Ile Asp Glu Val Thr Asn Lys
          245          250          255
Met Leu Asp Gln Lys Xaa Gln Asn Lys Ser Asn Asp
          260          265

```

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 26...706

AGT CTT AAC GCT AAT CTT CAC TTT GTC AAG TCA TTT CTC AGT AAT CAG	339
Ser Leu Asn Ala Asn Leu His Phe Val Lys Ser Phe Leu Ser Asn Gln	
95 100 105	
GAT TTA GAC TTC CGC TTT TTT AAG GAA ATA AAC GAT GGG CAA GAT CCC	387
Asp Leu Asp Phe Arg Phe Phe Lys Glu Ile Asn Asp Gly Gln Asp Pro	
110 115 120	
CAA AAA ACA TTA TCA AGA TTA ATT CCT CTT CAA AGT GGG AAA AAT GAT	435
Gln Lys Thr Leu Ser Arg Leu Ile Pro Leu Gln Ser Gly Lys Asn Asp	
125 130 135	
GCA AGC TCG TTT AAA GCC AAT AAT TCT TTT GTT TCA TTA GTT TAT GTT	483
Ala Ser Ser Phe Lys Ala Asn Asn Ser Phe Val Ser Leu Val Tyr Val	
140 145 150	
TAT GTT TAC TTC ATG CTA GAA ACT ATC ATG CAG TCG TAT AGG ATT CTC	531
Tyr Val Tyr Phe Met Leu Glu Thr Ile Met Gln Ser Tyr Arg Ile Leu	
155 160 165 170	
AGA TTG CTA GAA AAA CCT ATC AAT AAC AAC ATA AGC GAG GAC ATG CAG	579
Arg Leu Leu Glu Lys Pro Ile Asn Asn Asn Ile Ser Glu Asp Met Gln	
175 180 185	
AAC GAT ATA GAG AAT TTT TTT GTT CAA GCG AAT TTT TTA GAA TAC TAT	627
Asn Asp Ile Glu Asn Phe Phe Val Gln Ala Asn Phe Leu Glu Tyr Tyr	
190 195 200	
GTT CAG AAC AAA ATA TAC CCA ACC AAT CAT GCC TAT GAC TTC ACG CAT	675
Val Gln Asn Lys Ile Tyr Pro Thr Asn His Ala Tyr Asp Phe Thr His	
205 210 215	
TTG ATC ATG GAC TCC ATT ATT CCT AAT TGG ATT CAA ACT GAT ATG AGC	723
Leu Ile Met Asp Ser Ile Ile Pro Asn Trp Ile Gln Thr Asp Met Ser	
220 225 230	
GTT GAA GCT AAA AAG AAA GAG CTT TTT GAA AAA TAT TTT CAA AAC ATT	771
Val Glu Ala Lys Lys Lys Glu Leu Phe Glu Lys Tyr Phe Gln Asn Ile	
235 240 245 250	
GAT GAA GTA ACA AAC AAA ATG CTC GAT CAA AAA ANT CAA AAC AAA AGT	819
Asp Glu Val Thr Asn Lys Met Leu Asp Gln Lys Xaa Gln Asn Lys Ser	
255 260 265	
AAC GAT TGAGTGGCGT TAATGCGCTA GAATAGTGCT AAAAATAAGA ATAAAGGAGT CA	877
Asn Asp	

877

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

```

Thr Pro Glu Phe Asn Tyr Ala Leu Gly Gln Ala Ile Asn Gly Ser Met
  1650                      1655                      1660
Gln Ser Ser Ala Gln Met Ser Asn Gln Ile Leu Gly Gln Leu Met Asn
665                      1670                      1675                      1680
Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly Asp Ser Ile Lys Ile Leu
                      1685                      1690                      1695
Thr Met Asp Asp Ile Asp Phe Ser Gly Val Tyr Asp Val Lys Ile Thr
                      1700                      1705                      1710
Asn Lys Ser Val Val Asp Glu Ile Ile Lys Gln Ser Thr Lys Thr Leu
                      1715                      1720                      1725
Ser Arg Glu His Glu Glu Ile Thr Thr Ser Pro Lys Gly Gly Asn
                      1730                      1735                      1740

```

(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...825
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

```

AACAAATAAA GGAGTATTAA A ATG AAA CAA AGT TTG CGC GAA CAA AAA TTA      51
                      Met Lys Gln Ser Leu Arg Glu Gln Lys Leu
                      1                      5                      10

TTG AAA ATT TTA GAA AAT GAT GTC TTG ACG ATT TTG GAT AGT TTT TCT      99
Leu Lys Ile Leu Glu Asn Asp Val Leu Thr Ile Leu Asp Ser Phe Ser
                      15                      20                      25

AAT TAT CTT TTT GAA CTG AGA GAA GAG TTG GAC TTC ATA GAA GAA GAA      147
Asn Tyr Leu Phe Glu Leu Arg Glu Glu Leu Asp Phe Ile Glu Glu Glu
                      30                      35                      40

ATG GAA GGT GAA ATC ACC GAA CAA AAC CTT ACC GCT CTT TAT GAT TTT      195
Met Glu Gly Glu Ile Thr Glu Gln Asn Leu Thr Ala Leu Tyr Asp Phe
                      45                      50                      55

TCT AAT TTC TTA GAA GAC CAT GTC AAT GTA TTT TAT GAG AAT GTT TTG      243
Ser Asn Phe Leu Glu Asp His Val Asn Val Phe Tyr Glu Asn Val Leu
                      60                      65                      70

AAT ATA GAT GAT GTC AAA ACA GAA CAC CTT TAT TCA GGT CTC ATA GAT      291
Asn Ile Asp Asp Val Lys Thr Glu His Leu Tyr Ser Gly Leu Ile Asp
75                      80                      85                      90

```

```

1205          1210          1215
Asn Asp Arg Ala Ala Ile Met Lys Cys Leu Asp Gly Leu Ser Asp Glu
1220          1225          1230
Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg Glu Lys Ala Val Ala Asp
1235          1240          1245
Cys Leu Ala Met Ala Lys Thr Asp Glu Glu Lys Arg Lys Cys Gln Asn
1250          1255          1260
Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln Asn Lys Arg Thr Gln Asn
265          1270          1275          1280
Lys Gln Asn Gln Leu Ser Lys Thr Glu Arg Leu His Gln Ala Ser Glu
1285          1290          1295
Cys Leu Asp Asn Leu Asp Asp Pro Thr Asp Gln Glu Ala Ile Glu Gln
1300          1305          1310
Cys Leu Glu Gly Leu Ser Asp Ser Glu Arg Ala Leu Ile Leu Gly Ile
1315          1320          1325
Lys Arg Gln Ala Asp Glu Val Asp Leu Ile Tyr Ser Asp Leu Arg Asn
1330          1335          1340
Arg Lys Thr Phe Asp Asn Met Ala Ala Lys Gly Tyr Pro Leu Leu Pro
345          1350          1355          1360
Met Asp Phe Lys Asn Gly Gly Asp Ile Ala Thr Ile Asn Ala Thr Asn
1365          1370          1375
Val Asp Ala Asp Lys Ile Ala Ser Asp Asn Pro Ile Tyr Ala Ser Ile
1380          1385          1390
Glu Pro Asp Ile Ala Lys Gln Tyr Glu Thr Glu Lys Thr Ile Lys Asp
1395          1400          1405
Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala Leu Gly Gly Asn Lys Lys
1410          1415          1420
Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser Thr Ala Glu Ala Lys Ala
425          1430          1435          1440
Glu Asn Asn Lys Ile Asp Lys Asp Val Ala Glu Thr Ala Lys Asn Ile
1445          1450          1455
Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu Lys Ser Gly Glu Phe Val
1460          1465          1470
Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys Lys Lys Ala Glu Lys Gln
1475          1480          1485
Asp Glu Thr Ser Pro Val Lys Gln Ala Phe Ile Gly Lys Ser Asp Pro
1490          1495          1500
Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile Glu Ile Thr Leu Thr Ser
505          1510          1515          1520
Lys Val Asp Ala Thr Leu Thr Gly Ile Val Ser Gly Val Val Ala Lys
1525          1530          1535
Asp Val Trp Asn Met Asn Gly Thr Met Ile Leu Leu Asp Lys Gly Thr
1540          1545          1550
Lys Val Tyr Gly Asn Tyr Gln Ser Val Lys Gly Gly Thr Pro Ile Met
1555          1560          1565
Thr Arg Leu Met Ile Val Phe Thr Lys Ala Ile Thr Pro Asp Gly Val
1570          1575          1580
Ile Ile Pro Leu Ala Asn Ala Gln Ala Ala Gly Met Leu Gly Glu Ala
585          1590          1595          1600
Gly Val Asp Gly Tyr Val Asn Asn His Phe Met Lys Arg Ile Gly Phe
1605          1610          1615
Ala Val Ile Ala Ser Val Val Asn Ser Phe Leu Gln Thr Ala Pro Ile
1620          1625          1630
Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly Lys Gly Arg Ser Glu Arg
1635          1640          1645

```


Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu
 770 775 780
 Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys Leu Leu Glu Gln Gln
 785 790 795 800
 Ala Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp Lys Glu Arg Lys Lys
 805 810 815
 Cys Leu Lys Asp Leu Pro Lys Asp Leu Gln Lys Lys Val Leu Ala Lys
 820 825 830
 Glu Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Gln Ala Lys Thr Glu
 835 840 845
 Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys
 850 855 860
 Leu Leu Glu Glu Ala Lys Lys Ser Val Lys Ala Xaa Leu Asp Cys Val
 865 870 875 880
 Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu
 885 890 895
 Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu Ala Lys Glu Ser Val Lys
 900 905 910
 Ala Tyr Lys Asp Cys Val Ser Lys Ala Arg Asn Glu Lys Glu Lys Lys
 915 920 925
 Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys Leu Leu Glu Gln
 930 935 940
 Gln Val Leu Asp Cys Leu Lys Asn Ala Lys Thr Glu Ala Asp Lys Lys
 945 950 955 960
 Arg Cys Val Lys Asp Leu Pro Lys Asp Leu Gln Lys Lys Val Leu Ala
 965 970 975
 Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn
 980 985 990
 Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys
 995 1000 1005
 Lys Leu Leu Glu Glu Ala Lys Glu Ser Leu Lys Ala Tyr Lys Asp Cys
 1010 1015 1020
 Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu Lys Leu
 025 1030 1035 1040
 Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu Val Lys Lys Ser
 1045 1050 1055
 Ile Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu
 1060 1065 1070
 Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Phe Leu
 1075 1080 1085
 Ala Lys Gln Val Leu Asn Cys Leu Glu Lys Ala Gly Asn Glu Glu Glu
 1090 1095 1100
 Arg Lys Ala Cys Leu Lys Asn Leu Pro Lys Asp Leu Gln Glu Asn Ile
 105 1110 1115 1120
 Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys Asp Cys Leu Ser Gln Ala
 1125 1130 1135
 Arg Asn Glu Glu Arg Arg Ala Cys Glu Lys Leu Leu Thr Pro Glu
 1140 1145 1150
 Ala Arg Lys Leu Leu Glu Gln Glu Val Lys Lys Ser Val Lys Ala Tyr
 1155 1160 1165
 Leu Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys
 1170 1175 1180
 Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Phe Leu Ala Lys Glu Leu
 185 1190 1195 1200
 Gln Gln Lys Asp Lys Ala Ile Lys Asp Cys Leu Lys Asn Ala Asp Pro

-2009-

TCGGTTCTTT ACAAATAAAA AGACAAAACC AACAAACAGGC TCT

5334

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1743 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

```

Met Asn Glu Glu Asn Asp Lys Leu Glu Thr Ser Lys Lys Ala Gln Gln
 1           5           10           15
Asp Ser Pro Gln Asp Leu Ser Asn Glu Glu Ala Thr Glu Ala Asn His
          20           25           30
Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu Ser Ser Asp His His Leu
          35           40           45
Asp Asn Pro Thr Glu Thr Gln Thr His Phe Asp Gly Asp Lys Ser Glu
          50           55           60
Glu Thr Gln Thr Gln Met Asp Ser Glu Gly Asn Glu Thr Ser Glu Ser
65           70           75           80
Ser Asn Gly Ser Leu Ala Asp Lys Leu Phe Lys Lys Ala Arg Lys Leu
          85           90           95
Val Asp Asn Lys Lys Pro Phe Thr Gln Lys Lys Asn Leu Asp Glu Glu
          100          105          110
Thr Gln Glu Leu Asn Glu Glu Asp Gln Glu Asn Asn Glu Tyr Gln
          115          120          125
Glu Glu Thr Gln Thr Asp Leu Ile Asp Asp Glu Thr Ser Lys Lys Thr
          130          135          140
Gln Gln His Ser Pro Gln Asp Leu Ser Asn Glu Glu Ala Thr Glu Ala
145          150          155          160
Asn His Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu Ser Ser Asp His
          165          170          175
His Leu Asp Asn Pro Thr Glu Thr Gln Thr Asn Phe Asp Gly Asp Lys
          180          185          190
Ser Glu Glu Thr Gln Thr Gln Met Asp Ser Glu Gly Asn Glu Thr Ser
          195          200          205
Glu Ser Ser Asn Gly Ser Leu Ala Asp Lys Leu Phe Lys Lys Ala Arg
          210          215          220
Lys Leu Val Asp Asn Lys Lys Pro Phe Thr Gln Gln Lys Asn Leu Asp
225          230          235          240
Glu Glu Thr Gln Glu Leu Asn Glu Glu Asp Asp Gln Glu Asn Asn Glu
          245          250          255
Tyr Gln Glu Glu Thr Gln Thr Asp Leu Ile Asp Asp Glu Thr Ser Lys
          260          265          270
Lys Thr Gln Gln His Ser Pro Gln Asp Leu Ser Asn Glu Glu Ala Thr
          275          280          285
Glu Ala Asn His Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu Ser Ser
          290          295          300
Asp His His Leu Asp Asn Pro Thr Glu Thr Gln Thr Asn Phe Asp Gly
305          310          315          320
Asp Lys Ser Glu Glu Ile Thr Asp Asp Ser Asn Asp Gln Glu Ile Ile

```

AGT GGG GTT GTA GCC AAA GAT GTA TGG AAC ATG AAC GGC ACT ATG ATC	4659
Ser Gly Val Val Ala Lys Asp Val Trp Asn Met Asn Gly Thr Met Ile	
1535 1540 1545	
TTA TTA GAC AAA GGC ACT AAG GTG TAT GGG AAT TAT CAA AGC GTG AAA	4707
Leu Leu Asp Lys Gly Thr Lys Val Tyr Gly Asn Tyr Gln Ser Val Lys	
1550 1555 1560	
GGT GGC ACA CCC ATT ATG ACA CGC TTA ATG ATA GTC TTT ACT AAA GCC	4755
Gly Gly Thr Pro Ile Met Thr Arg Leu Met Ile Val Phe Thr Lys Ala	
1565 1570 1575	
ATT ACG CCT GAT GGT GTG ATA ATA CCT CTA GCA AAC GCT CAA GCA GCA	4803
Ile Thr Pro Asp Gly Val Ile Ile Pro Leu Ala Asn Ala Gln Ala Ala	
1580 1585 1590	
GGC ATG TTG GGT GAA GCA GGG GTA GAT GGC TAT GTG AAT AAT CAC TTT	4851
Gly Met Leu Gly Glu Ala Gly Val Asp Gly Tyr Val Asn Asn His Phe	
1595 1600 1605 1610	
ATG AAG CGC ATA GGC TTT GCT GTG ATA GCA AGC GTG GTT AAT AGC TTC	4899
Met Lys Arg Ile Gly Phe Ala Val Ile Ala Ser Val Val Asn Ser Phe	
1615 1620 1625	
TTG CAA ACT GCG CCT ATC ATA GCT CTA GAT AAA CTC ATA GGC CTT GGC	4947
Leu Gln Thr Ala Pro Ile Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly	
1630 1635 1640	
AAA GGT AGA AGT GAA AGG ACA CCT GAA TTT AAT TAC GCT TTG GGT CAA	4995
Lys Gly Arg Ser Glu Arg Thr Pro Glu Phe Asn Tyr Ala Leu Gly Gln	
1645 1650 1655	
GCT ATC AAT GGT AGC ATG CAA AGT TCA GCT CAG ATG TCT AAT CAA ATT	5043
Ala Ile Asn Gly Ser Met Gln Ser Ser Ala Gln Met Ser Asn Gln Ile	
1660 1665 1670	
CTA GGG CAA CTG ATG AAT ATC CCC CCA AGT TTT TAC AAA AAC GAG GGC	5091
Leu Gly Gln Leu Met Asn Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly	
1675 1680 1685 1690	
GAT AGT ATT AAG ATT CTC ACA ATG GAC GAT ATT GAT TTT AGC GGT GTG	5139
Asp Ser Ile Lys Ile Leu Thr Met Asp Asp Ile Asp Phe Ser Gly Val	
1695 1700 1705	
TAT GAT GTT AAA ATT ACT AAC AAA TCT GTG GTA GAT GAA ATT ATC AAA	5187
Tyr Asp Val Lys Ile Thr Asn Lys Ser Val Val Asp Glu Ile Ile Lys	
1710 1715 1720	
CAA AGC ACC AAA ACT TTG TCT AGA GAA CAT GAA GAA ATC ACC ACA AGC	5235
Gln Ser Thr Lys Thr Leu Ser Arg Glu His Glu Glu Ile Thr Thr Ser	
1725 1730 1735	
CCC AAA GGT GGC AAT TAATTCAAGA GAAAGGATAA AATATATTCA TGTTACTAAA C	5291
Pro Lys Gly Gly Asn	
1740	

CAA GAG GCC ATA GAG CAA TGT TTA GAG GGC TTG AGC GAT AGT GAA AGG	3987
Gln Glu Ala Ile Glu Gln Cys Leu Glu Gly Leu Ser Asp Ser Glu Arg	
1310 1315 1320	
GCG CTA ATT CTA GGA ATT AAA CGA CAA GCT GAT GAA GTG GAT CTG ATT	4035
Ala Leu Ile Leu Gly Ile Lys Arg Gln Ala Asp Glu Val Asp Leu Ile	
1325 1330 1335	
TAT AGC GAT CTA AGA AAC CGT AAA ACC TTT GAT AAC ATG GCG GCT AAA	4083
Tyr Ser Asp Leu Arg Asn Arg Lys Thr Phe Asp Asn Met Ala Ala Lys	
1340 1345 1350	
GGT TAT CCA TTG TTA CCA ATG GAT TTC AAA AAT GGC GGC GAT ATT GCC	4131
Gly Tyr Pro Leu Leu Pro Met Asp Phe Lys Asn Gly Gly Asp Ile Ala	
1355 1360 1365 1370	
ACT ATT AAC GCC ACT AAT GTT GAT GCG GAC AAA ATA GCT AGC GAT AAT	4179
Thr Ile Asn Ala Thr Asn Val Asp Ala Asp Lys Ile Ala Ser Asp Asn	
1375 1380 1385	
CCT ATT TAT GCT TCC ATA GAG CCT GAT ATT GCC AAG CAA TAC GAA ACA	4227
Pro Ile Tyr Ala Ser Ile Glu Pro Asp Ile Ala Lys Gln Tyr Glu Thr	
1390 1395 1400	
GAA AAA ACC ATT AAG GAT AAG AAT TTA GAA GCT AAA TTA GCT AAG GCT	4275
Glu Lys Thr Ile Lys Asp Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala	
1405 1410 1415	
TTA GGT GGC AAT AAA AAA GAT GAC GAT AAA GAA AAA AGT AAA AAA TCC	4323
Leu Gly Gly Asn Lys Lys Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser	
1420 1425 1430	
ACA GCA GAA GCT AAA GCA GAA AAC AAT AAG ATA GAC AAA GAT GTC GCA	4371
Thr Ala Glu Ala Lys Ala Glu Asn Asn Lys Ile Asp Lys Asp Val Ala	
1435 1440 1445 1450	
GAA ACT GCC AAG AAT ATC AGT GAA ATC GCT CTT AAG AAC AAA AAA GAA	4419
Glu Thr Ala Lys Asn Ile Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu	
1455 1460 1465	
AAG AGT GGG GAA TTT GTA GAT GAA AAT GGT AAT CCC ATT GAT GAC AAA	4467
Lys Ser Gly Glu Phe Val Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys	
1470 1475 1480	
AAG AAA GCA GAA AAA CAA GAT GAA ACA AGC CCT GTC AAA CAG GCC TTT	4515
Lys Lys Ala Glu Lys Gln Asp Glu Thr Ser Pro Val Lys Gln Ala Phe	
1485 1490 1495	
ATA GGC AAG AGT GAT CCC ACA TTT GTT TTA GCG CAA TAC ACC CCC ATT	4563
Ile Gly Lys Ser Asp Pro Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile	
1500 1505 1510	
GAA ATC ACT CTG ACT TCT AAA GTA GAT GCC ACT CTC ACA GGT ATA GTG	4611
Glu Ile Thr Leu Thr Ser Lys Val Asp Ala Thr Leu Thr Gly Ile Val	
1515 1520 1525 1530	

GAA GCG AGA AAA TTT TTA GCG AAG CAA GTG CTA AAT TGT TTG GAA AAA	3315
Glu Ala Arg Lys Phe Leu Ala Lys Gln Val Leu Asn Cys Leu Glu Lys	
1085 1090 1095	
GCT GGA AAT GAA GAA GAA AGA AAA GCA TGT CTT AAA AAT CTC CCT AAA	3363
Ala Gly Asn Glu Glu Glu Arg Lys Ala Cys Leu Lys Asn Leu Pro Lys	
1100 1105 1110	
GAC TTA CAG GAA AAT ATT TTA GCT AAA GAG AGT CTT AAA GCT TAT AAA	3411
Asp Leu Gln Glu Asn Ile Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys	
1115 1120 1125 1130	
GAC TGC CTC TCT CAA GCT AGA AAT GAA GAA GAA AGG AGA GCT TGC GAG	3459
Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu	
1135 1140 1145	
AAA CTA CTC ACG CCT GAA GCG AGA AAA CTC TTA GAG CAA GAA GTT AAG	3507
Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu Val Lys	
1150 1155 1160	
AAA AGC GTT AAG GCT TAT TTG GAC TGC GTA TCA AGA GCT AGG AAT GAA	3555
Lys Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu	
1165 1170 1175	
AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT GAA GCG AGA AAA	3603
Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys	
1180 1185 1190	
TTT TTA GCG AAA GAA CTC CAA CAA AAA GAT AAA GCG ATC AAA GAT TGC	3651
Phe Leu Ala Lys Glu Leu Gln Gln Lys Asp Lys Ala Ile Lys Asp Cys	
1195 1200 1205 1210	
TTG AAA AAC GCC GAT CCT AAC GAC AGA GCG GCT ATC ATG AAG TGT TTG	3699
Leu Lys Asn Ala Asp Pro Asn Asp Arg Ala Ala Ile Met Lys Cys Leu	
1215 1220 1225	
GAT GGT TTG AGC GAT GAA GAG AAG CTC AAA TAC CTG CAA GAA GCT AGA	3747
Asp Gly Leu Ser Asp Glu Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg	
1230 1235 1240	
GAA AAG GCT GTT GCG GAT TGT TTG GCT ATG GCT AAA ACC GAT GAA GAA	3795
Glu Lys Ala Val Ala Asp Cys Leu Ala Met Ala Lys Thr Asp Glu Glu	
1245 1250 1255	
AAA AGG AAA TGC CAA AAC CTT TAT AGC GAT TTG ATC CAA GAA ATC CAA	3843
Lys Arg Lys Cys Gln Asn Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln	
1260 1265 1270	
AAT AAA AGG ACA CAA AAC AAA CAA AAT CAA TTG AGT AAA ACA GAA AGG	3891
Asn Lys Arg Thr Gln Asn Lys Gln Asn Gln Leu Ser Lys Thr Glu Arg	
1275 1280 1285 1290	
TTG CAT CAA GCA AGC GAG TGC TTG GAT AAC TTA GAT GAC CCT ACT GAT	3939
Leu His Gln Ala Ser Glu Cys Leu Asp Asn Leu Asp Asp Pro Thr Asp	
1295 1300 1305	

ACC	CCT	GAA	GCG	AGA	AAA	CTT	TTA	GAA	GAA	GCT	AAA	AAA	AGC	GTT	AAG	2643
Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Lys	Ser	Val	Lys	
	860					865					870					
GCT	TAY	TTG	GAT	TGC	GTA	TCT	CAA	GCC	AAA	ACT	GAA	GCT	GAG	AAA	AAA	2691
Ala	Xaa	Leu	Asp	Cys	Val	Ser	Gln	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Lys	
	875				880					885					890	
GAA	TGC	GAG	AAA	TTA	CTC	ACC	CCT	GAA	GCG	AGA	AAA	CTC	TTA	GAA	GAA	2739
Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Glu	
				895					900					905		
GCT	AAA	GAG	AGC	GTT	AAA	GCT	TAT	AAA	GAC	TGC	GTA	TCA	AAA	GCT	AGG	2787
Ala	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Lys	Asp	Cys	Val	Ser	Lys	Ala	Arg	
			910					915					920			
AAT	GAA	AAA	GAG	AAA	AAA	GAA	TGC	GAG	AAA	TTA	CTC	ACG	CCT	GAA	GCG	2835
Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	
		925					930					935				
AAA	AAA	CTT	TTA	GAG	CAA	CAA	GTG	CTA	GAT	TGT	TTG	AAA	AAC	GCT	AAA	2883
Lys	Lys	Leu	Leu	Glu	Gln	Gln	Val	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	
	940					945					950					
ACC	GAA	GCT	GAT	AAA	AAA	AGG	TGT	GTC	AAA	GAT	CTC	CCT	AAA	GAC	TTG	2931
Thr	Glu	Ala	Asp	Lys	Lys	Arg	Cys	Val	Lys	Asp	Leu	Pro	Lys	Asp	Leu	
	955				960					965					970	
CAG	AAA	AAG	GTT	TTA	GCT	AAA	GAG	AGC	GTT	AAG	GCT	TAT	TTG	GAC	TGC	2979
Gln	Lys	Lys	Val	Leu	Ala	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	
			975					980						985		
GTA	TCA	AGA	GCT	AGG	AAT	GAA	AAA	GAG	AAA	AAA	GAA	TGC	GAG	AAA	TTG	3027
Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	
			990					995				1000				
CTC	ACC	CCT	GAA	GCG	AAA	AAA	CTT	TTA	GAA	GAA	GCC	AAA	GAG	AGT	CTT	3075
Leu	Thr	Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Leu	
		1005					1010					1015				
AAA	GCT	TAT	AAA	GAC	TGC	CTC	TCT	CAA	GCT	AGA	AAT	GAA	GAA	GAA	AGG	3123
Lys	Ala	Tyr	Lys	Asp	Cys	Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	
	1020					1025					1030					
AGA	GCT	TGC	GAG	AAA	CTA	CTC	ACG	CCT	GAA	GCG	AGA	AAA	CTC	TTA	GAG	3171
Arg	Ala	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	
1035					1040					1045					1050	
CAA	GAA	GTT	AAG	AAA	AGC	ATT	AAG	GCT	TAT	TTG	GAC	TGC	GTA	TCA	AGA	3219
Gln	Glu	Val	Lys	Lys	Ser	Ile	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	
			1055					1060					1065			
GCT	AGG	AAT	GAA	AAA	GAG	AAA	AAA	GAA	TGC	GAG	AAA	TTA	CTC	ACG	CCT	3267
Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	
			1070					1075					1080			

GAG AAA CAA GAA TGC GAG AAA TTG CTC ACG CCT GAA GCG AGG AAA AAG Glu Lys Gln Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Lys 635 640 645 650	1971
TTA GAA CAA CAG GTT CTA GAT TGT TTG AAA AAC GCT AAA ACC GAT GAA Leu Glu Gln Gln Val Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp Glu 655 660 665	2019
GAA CGA AAA AAG TGT TTG AAA GAT CTC CCT AAA GAC TTA CAA AGC GAT Glu Arg Lys Lys Cys Leu Lys Asp Leu Pro Lys Asp Leu Gln Ser Asp 670 675 680	2067
ATT CTA GCC AAA GAG AGC CTG AAA GCT TAT AAA GAC TGC GTA TCT CAA Ile Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys Asp Cys Val Ser Gln 685 690 695	2115
GCC AAA ACC GAA GCT GAG AAA AAA GAA TGC GAG AAA TTA CTC ACC CCT Ala Lys Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro 700 705 710	2163
GAA GCG AAA AAA CTT TTA GAA GAA GAA GCC AAA GAG AGC GTT AAG GCT Glu Ala Lys Lys Leu Leu Glu Glu Glu Ala Lys Glu Ser Val Lys Ala 715 720 725 730	2211
TAT TTG GAT TGC GTA TCT CAA GCC AAA ACC GAA GCT GAG AAA AAA GAA Tyr Leu Asp Cys Val Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys Glu 735 740 745	2259
TGC GAG AAA TTG CTC ACC CCT GAA GCG AAA AAA AAG TTA GAA GAA GCT Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys Lys Leu Glu Glu Ala 750 755 760	2307
AAA AAA AGC GTT AAA GCT TAC TTG GAT TGC GTA TCA AGA GCT AGG AAT Lys Lys Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn 765 770 775	2355
GAA AAA GAG AAA AAA GAA TGC GAG AAA TTG CTC ACC CCT GAA GCG AAA Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys 780 785 790	2403
AAA CTT TTA GAG CAA CAA GCA CTA GAT TGT TTG AAA AAC GCT AAA ACC Lys Leu Leu Glu Gln Gln Ala Leu Asp Cys Leu Lys Asn Ala Lys Thr 795 800 805 810	2451
GAT AAA GAA CGA AAA AAG TGT TTG AAA GAT CTC CCT AAA GAC TTG CAG Asp Lys Glu Arg Lys Lys Cys Leu Lys Asp Leu Pro Lys Asp Leu Gln 815 820 825	2499
AAA AAG GTT TTA GCT AAA GAA AGC GTT AAA GCT TAC TTG GAT TGC GTA Lys Lys Val Leu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys Val 830 835 840	2547
TCT CAA GCC AAA ACT GAA GCT GAG AAA AAA GAA TGC GAG AAA TTA CTC Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys Glu Cys Glu Lys Leu Leu 845 850 855	2595

AAG AAT CTT TTC TTC AAT GAC GAT CCC AAT AGA ACC TTA TAC AAC TAT	1299
Lys Asn Leu Phe Phe Asn Asp Asp Pro Asn Arg Thr Leu Tyr Asn Tyr	
415 420 425	
TTG AAT ATT GCA GAA ATT GAG GAC AAA AAC CCG TTG AGA GCC TTT TAT	1347
Leu Asn Ile Ala Glu Ile Glu Asp Lys Asn Pro Leu Arg Ala Phe Tyr	
430 435 440	
GAA TGT ATT AGT AAT GGT GGC AAC TAT GAA GAA TGT TTG AAG CTT ATC	1395
Glu Cys Ile Ser Asn Gly Gly Asn Tyr Glu Glu Cys Leu Lys Leu Ile	
445 450 455	
AAA GAC AAA AAA CTT CAA GAT CAG ATG AAA AAG ACT CTA GAG GCT TAT	1443
Lys Asp Lys Lys Leu Gln Asp Gln Met Lys Lys Thr Leu Glu Ala Tyr	
460 465 470	
AAC GAC TGC ATC AAA AAT GCC AAA ACT GAA GAA GAA AGG ATC AAG TGT	1491
Asn Asp Cys Ile Lys Asn Ala Lys Thr Glu Glu Glu Arg Ile Lys Cys	
475 480 485 490	
TTA GAT TTA ATC AAA GAT GAA AAC CTA AAA AAA AGC TTA CTG AAC CAA	1539
Leu Asp Leu Ile Lys Asp Glu Asn Leu Lys Lys Ser Leu Leu Asn Gln	
495 500 505	
CAA AAA GTT CAA GTG GCG CTA GAT TGT TTG AAA AAC GCT AAA ACC GAT	1587
Gln Lys Val Gln Val Ala Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp	
510 515 520	
GAA GAA CGA AAC GAG TGC CTA AAA CTC ATA AAT GAC CCT GAG ATT AGA	1635
Glu Glu Arg Asn Glu Cys Leu Lys Leu Ile Asn Asp Pro Glu Ile Arg	
525 530 535	
GAG AAA TTC CGT AAG GAA TTA GAG CTT CAA AAA GAG CTT CAA GAG TAT	1683
Glu Lys Phe Arg Lys Glu Leu Glu Leu Gln Lys Glu Leu Gln Glu Tyr	
540 545 550	
AAG GAT TGT ATC AAA AAC GCC AAA ACA GAA GCT GAG AAA AAC AAA TGC	1731
Lys Asp Cys Ile Lys Asn Ala Lys Thr Glu Ala Glu Lys Asn Lys Cys	
555 560 565 570	
TTG AAA GGC TTG TCT AAA GAA GCT ATA GAG AGA TTG AAA CAG CAA GCG	1779
Leu Lys Gly Leu Ser Lys Glu Ala Ile Glu Arg Leu Lys Gln Gln Ala	
575 580 585	
CTA GAT TGT TTG AAA AAC GCT AAA ACC GAT GAA GAA CGA AAC GAG TGC	1827
Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp Glu Glu Arg Asn Glu Cys	
590 595 600	
TTG AAA AAT ATT CCC CAA GAC TTG CAA AAA GAA CTA TTA GCT GAT ATG	1875
Leu Lys Asn Ile Pro Gln Asp Leu Gln Lys Glu Leu Leu Ala Asp Met	
605 610 615	
AGC GTC AAG GCT TAC AAG GAT TGC GTA TCA AAA GCT AGA AAT GAA AAA	1923
Ser Val Lys Ala Tyr Lys Asp Cys Val Ser Lys Ala Arg Asn Glu Lys	
620 625 630	

Asn Phe Asp Gly Asp Lys Ser Glu Glu Thr Gln Thr Gln Met Asp Ser	
190 195 200	
GAA GGT AAT GAA ACT TCA GAA TCT AGC AAT GGC AGT CTA GCA GAC AAG	675
Glu Gly Asn Glu Thr Ser Glu Ser Ser Asn Gly Ser Leu Ala Asp Lys	
205 210 215	
TTA TTC AAA AAA GCC AGA AAA TTA GTT GAT AAT AAA AAA CCT TTC ACT	723
Leu Phe Lys Lys Ala Arg Lys Leu Val Asp Asn Lys Lys Pro Phe Thr	
220 225 230	
CAG CAA AAG AAT TTA GAT GAA GAA ACC CAA GAA CTG AAC GAA GAA GAC	771
Gln Gln Lys Asn Leu Asp Glu Glu Thr Gln Glu Leu Asn Glu Glu Asp	
235 240 245 250	
GAT CAA GAA AAT AAT GAG TAT CAA GAA GAA ACT CAA ACG GAC TTA ATT	819
Asp Gln Glu Asn Asn Glu Tyr Gln Glu Glu Thr Gln Thr Asp Leu Ile	
255 260 265	
GAT GAT GAA ACT TCT AAA AAA ACC CAA CAA CAT TCA CCC CAA GAT TTA	867
Asp Asp Glu Thr Ser Lys Lys Thr Gln Gln His Ser Pro Gln Asp Leu	
270 275 280	
TCC AAT GAA GAA GCA ACA GAA GCC AAT CAT TTT GAA AAT CTT TTA AAA	915
Ser Asn Glu Glu Ala Thr Glu Ala Asn His Phe Glu Asn Leu Leu Lys	
285 290 295	
GAA TCC AAA GAA AGC TCA GAT CAT CAT CTT GAC AAC CCC ACA GAA ACT	963
Glu Ser Lys Glu Ser Ser Asp His His Leu Asp Asn Pro Thr Glu Thr	
300 305 310	
CAA ACC AAT TTT GAT GGA GAC AAG TCA GAA GAA ATA ACT GAC GAC TCT	1011
Gln Thr Asn Phe Asp Gly Asp Lys Ser Glu Glu Ile Thr Asp Asp Ser	
315 320 325 330	
AAC GAT CAA GAG ATT ATC AAA GGA AGC AAA AAG AAA TAT ATT ATT GGT	1059
Asn Asp Gln Glu Ile Ile Lys Gly Ser Lys Lys Lys Tyr Ile Ile Gly	
335 340 345	
GGC ATT GTA GTC GCT GTT CTT ATC GTG ATT ATT TTA TTT TCT AGA AGC	1107
Gly Ile Val Val Ala Val Leu Ile Val Ile Ile Leu Phe Ser Arg Ser	
350 355 360	
ATT TTT CAC TAC TTC ATG CCT TTG GAA GAT AAA AGC TCT CGT TTT AGC	1155
Ile Phe His Tyr Phe Met Pro Leu Glu Asp Lys Ser Ser Arg Phe Ser	
365 370 375	
AAA GAC AGG AAT CTT TAT GTC AAT GAT GAA ATC CAA ATA AGG CAA GAG	1203
Lys Asp Arg Asn Leu Tyr Val Asn Asp Glu Ile Gln Ile Arg Gln Glu	
380 385 390	
TAT AAC CGA TTG CTG AAA GAA CGG AAT GAA AAA GGC AAT ATG ATC GAT	1251
Tyr Asn Arg Leu Leu Lys Glu Arg Asn Glu Lys Gly Asn Met Ile Asp	
395 400 405 410	

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

TAAATAAAAA GCGCTTAAGA C ATG AAT GAA GAA AAC GAT AAA CTT GAA ACT	51
Met Asn Glu Glu Asn Asp Lys Leu Glu Thr	
1 5 10	
TCT AAA AAA GCC CAA CAA GAT TCA CCC CAA GAT TTA TCC AAT GAA GAA	99
Ser Lys Lys Ala Gln Gln Asp Ser Pro Gln Asp Leu Ser Asn Glu Glu	
15 20 25	
GCA ACA GAA GCC AAT CAT TTT GAA AAT CTT TTA AAA GAA TCC AAA GAA	147
Ala Thr Glu Ala Asn His Phe Glu Asn Leu Leu Lys Glu Ser Lys Glu	
30 35 40	
AGC TCA GAT CAT CAT CTT GAC AAC CCC ACA GAA ACT CAA ACC CAT TTT	195
Ser Ser Asp His His Leu Asp Asn Pro Thr Glu Thr Gln Thr His Phe	
45 50 55	
GAT GGA GAC AAG TCA GAA GAA ACC CAA ACT CAA ATG GAT TCT GAA GGT	243
Asp Gly Asp Lys Ser Glu Glu Thr Gln Thr Gln Met Asp Ser Glu Gly	
60 65 70	
AAT GAA ACT TCA GAA TCT AGC AAT GGC AGT CTA GCA GAC AAG TTA TTC	291
Asn Glu Thr Ser Glu Ser Ser Asn Gly Ser Leu Ala Asp Lys Leu Phe	
75 80 85 90	
AAA AAA GCC AGA AAA TTA GTT GAT AAT AAA AAA CCT TTC ACT CAG CAA	339
Lys Lys Ala Arg Lys Leu Val Asp Asn Lys Lys Pro Phe Thr Gln Gln	
95 100 105	
AAG AAT TTA GAT GAA GAA ACC CAA GAA CTG AAC GAA GAA GAC GAT CAA	387
Lys Asn Leu Asp Glu Glu Thr Gln Glu Leu Asn Glu Glu Asp Asp Gln	
110 115 120	
GAA AAT AAT GAG TAT CAA GAA GAA ACT CAA ACG GAC TTA ATT GAT GAT	435
Glu Asn Asn Glu Tyr Gln Glu Glu Thr Gln Thr Asp Leu Ile Asp Asp	
125 130 135	
GAA ACT TCT AAA AAA ACC CAA CAA CAT TCA CCC CAA GAT TTA TCC AAT	483
Glu Thr Ser Lys Lys Thr Gln Gln His Ser Pro Gln Asp Leu Ser Asn	
140 145 150	
GAA GAA GCA ACA GAA GCC AAT CAT TTT GAA AAT CTT TTA AAA GAA TCC	531
Glu Glu Ala Thr Glu Ala Asn His Phe Glu Asn Leu Leu Lys Glu Ser	
155 160 165 170	
AAA GAA AGC TCA GAT CAT CAT CTT GAC AAC CCC ACA GAA ACT CAA ACC	579
Lys Glu Ser Ser Asp His His Leu Asp Asn Pro Thr Glu Thr Gln Thr	
175 180 185	
AAT TTT GAT GGA GAC AAG TCA GAA GAA ACC CAA ACT CAA ATG GAT TCT	627

1	5	10	15
Glu Arg Ala	Leu Lys Glu Ala Ala	Leu Asn Pro Leu Arg	His Ala Thr
20	25	30	
Glu Glu Leu Phe Gly Asp Phe	Leu Lys Met Glu Asn Ile Thr	Glu Ile	
35	40	45	
Cys Tyr Asn Gly Asn Lys Val Val Trp Val	Leu Lys Asn Asn Gly Glu		
50	55	60	
Trp Gln Pro Phe Asp Val Arg Asp Arg Lys Ala Phe Ser Leu Ser Arg			
65	70	75	80
Leu Met His Phe Ala Arg Cys Cys Ala Ser Phe Lys Lys Lys Thr Ile			
85	90	95	
Asp Asn Tyr Glu Asn Pro Ile Leu Ser Ser Asn Leu Ala Asn Gly Glu			
100	105	110	
Arg Val Gln Ile Val Leu Ser Pro Val Thr Val Asn Asp Glu Thr Ile			
115	120	125	
Ser Ile Ser Ile Arg Ile Pro Ser Lys Thr Thr Tyr Pro His Ser Phe			
130	135	140	
Phe Glu Glu Gln Gly Phe Tyr Asn Leu Leu Asp Asn Lys Glu Gln Ala			
145	150	155	160
Ile Ser Ala Ile Lys Asp Gly Ile Ala Ile Gly Lys Asn Val Ile Val			
165	170	175	
Cys Gly Gly Thr Gly Ser Gly Lys Thr Thr Tyr Ile Lys Ser Ile Met			
180	185	190	
Glu Phe Ile Pro Lys Glu Glu Arg Ile Ile Ser Ile Glu Asp Thr Glu			
195	200	205	
Glu Ile Val Phe Lys His His Lys Asn Tyr Thr Gln Leu Phe Phe Gly			
210	215	220	
Gly Asn Ile Thr Ser Ala Asp Cys Leu Lys Ser Cys Leu Arg Met Arg			
225	230	235	240
Pro Asp Arg Ile Ile Leu Gly Glu Leu Arg Ser Ser Glu Ala Tyr Asp			
245	250	255	
Phe Tyr Asn Val Leu Cys Ser Gly His Lys Gly Thr Leu Thr Thr Leu			
260	265	270	
His Ala Gly Ser Ser Glu Glu Ala Phe Ile Arg Leu Ala Asn Met Ser			
275	280	285	
Ser Ser Asn Ser Ala Ala Arg Asn Ile Lys Phe Glu Ser Leu Ile Glu			
290	295	300	
Gly Phe Lys Asp Leu Ile Asp Met Ile Val His Ile Asn His His Lys			
305	310	315	320
Gln Cys Asp Glu Phe Tyr Ile Lys His Arg			
325	330		

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...5250

AAA AAT GTG ATT GTT TGT GGT GGC ACA GGA AGC GGT AAA ACG ACT TAT	579
Lys Asn Val Ile Val Cys Gly Gly Thr Gly Ser Gly Lys Thr Thr Tyr	
175 180 185	
ATC AAA AGC ATC ATG GAG TTT ATC CCT AAA GAA GAA AGG ATC ATA TCC	627
Ile Lys Ser Ile Met Glu Phe Ile Pro Lys Glu Glu Arg Ile Ile Ser	
190 195 200	
ATT GAA GAC ACC GAA GAG ATT GTA TTC AAA CAC CAC AAA AAC TAC ACA	675
Ile Glu Asp Thr Glu Glu Ile Val Phe Lys His His Lys Asn Tyr Thr	
205 210 215	
CAG CTT TTT TTT GGT GGG AAT ATC ACC TCT GCT GAT TGC TTA AAG TCA	723
Gln Leu Phe Phe Gly Gly Asn Ile Thr Ser Ala Asp Cys Leu Lys Ser	
220 225 230 235	
TGT CTG AGA ATG CGG CCT GAT AGA ATC ATT TTA GGG GAA CTC AGA AGC	771
Cys Leu Arg Met Arg Pro Asp Arg Ile Ile Leu Gly Glu Leu Arg Ser	
240 245 250	
AGT GAG GCA TAC GAT TTT TAT AAT GTG CTT TGT AGC GGT CAT AAA GGC	819
Ser Glu Ala Tyr Asp Phe Tyr Asn Val Leu Cys Ser Gly His Lys Gly	
255 260 265	
ACA CTA ACC ACT CTG CAT GCA GGG AGC AGT GAA GAA GCG TTT ATC CGT	867
Thr Leu Thr Thr Leu His Ala Gly Ser Ser Glu Glu Ala Phe Ile Arg	
270 275 280	
TTG GCC AAC ATG AGT TCA TCT AAT AGC GCA GCA AGG AAT ATC AAG TTT	915
Leu Ala Asn Met Ser Ser Ser Asn Ser Ala Ala Arg Asn Ile Lys Phe	
285 290 295	
GAA AGT CTT ATT GAG GGC TTT AAA GAT TTG ATT GAT ATG ATT GTC CAT	963
Glu Ser Leu Ile Glu Gly Phe Lys Asp Leu Ile Asp Met Ile Val His	
300 305 310 315	
ATC AAC CAC CAC AAA CAG TGT GAT GAA TTT TAT ATC AAA CAC AGG TAGTA	1013
Ile Asn His His Lys Gln Cys Asp Glu Phe Tyr Ile Lys His Arg	
320 325 330	
GGCACAAATGG AAGACTTTTT GTAT	1037

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

Met Thr Glu Asp Arg Leu Ser Ala Glu Asp Lys Lys Phe Leu Glu Val

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 19...1008
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

TAAATTTGGA ATAAGAAC ATG ACT GAA GAC AGA TTG AGT GCA GAA GAT AAA	51
Met Thr Glu Asp Arg Leu Ser Ala Glu Asp Lys	
1 5 10	
AAG TTT CTA GAA GTA GAA AGA GCT TTA AAA GAA GCG GCA TTA AAT CCT	99
Lys Phe Leu Glu Val Glu Arg Ala Leu Lys Glu Ala Ala Leu Asn Pro	
15 20 25	
CTA AGG CAT GCT ACT GAA GAA CTT TTT GGT GAT TTT TTA AAA ATG GAA	147
Leu Arg His Ala Thr Glu Glu Leu Phe Gly Asp Phe Leu Lys Met Glu	
30 35 40	
AAT ATC ACT GAG ATT TGT TAC AAT GGG AAC AAG GTT GTA TGG GTT TTA	195
Asn Ile Thr Glu Ile Cys Tyr Asn Gly Asn Lys Val Val Trp Val Leu	
45 50 55	
AAA AAT AAT GGC GAA TGG CAA CCA TTT GAT GTG AGA GAC AGG AAA GCC	243
Lys Asn Asn Gly Glu Trp Gln Pro Phe Asp Val Arg Asp Arg Lys Ala	
60 65 70 75	
TTT AGC CTG TCT CGT TTA ATG CAT TTT GCT CGG TGT TGT GCA AGT TTT	291
Phe Ser Leu Ser Arg Leu Met His Phe Ala Arg Cys Cys Ala Ser Phe	
80 85 90	
AAG AAA AAA ACA ATA GAC AAC TAT GAA AAT CCT ATT TTG AGC AGC AAT	339
Lys Lys Lys Thr Ile Asp Asn Tyr Glu Asn Pro Ile Leu Ser Ser Asn	
95 100 105	
TTA GCG AAT GGT GAA AGG GTG CAG ATT GTC CTT TCC CCT GTT ACA GTT	387
Leu Ala Asn Gly Glu Arg Val Gln Ile Val Leu Ser Pro Val Thr Val	
110 115 120	
AAT GAT GAA ACC ATT TCC ATA TCC ATA AGG ATA CCT AGC AAA ACA ACC	435
Asn Asp Glu Thr Ile Ser Ile Ser Ile Arg Ile Pro Ser Lys Thr Thr	
125 130 135	
TAT CCT CAT AGC TTC TTT GAA GAG CAA GGT TTT TAT AAT CTA CTA GAC	483
Tyr Pro His Ser Phe Phe Glu Glu Gln Gly Phe Tyr Asn Leu Leu Asp	
140 145 150 155	
AAC AAA GAA CAA GCG ATC AGC GCG ATT AAA GAT GGT ATT GCT ATT GGT	531
Asn Lys Glu Gln Ala Ile Ser Ala Ile Lys Asp Gly Ile Ala Ile Gly	
160 165 170	

```

Glu Phe Val Lys Arg Lys Lys Ile Ile Met Pro Glu Thr Pro Thr Met
385                               390                               395                               400
Phe Phe Ile Gly Ser Met Ala Ser Gly Ile Asn Leu Ile Asp Glu Asp
                               405                               410                               415
Thr Asn Met Glu Lys Val Val Ser Leu Met Glu Phe Phe Gly Gly Glu
                               420                               425                               430
Glu Asp Lys Ser Gly Asp Asn Leu Arg Val Leu Ser Pro Ala Thr Arg
                               435                               440                               445
Asn Met Trp Asn Ser Phe Lys Thr Met Gly Gly Ala Arg Glu Thr Tyr
                               450                               455                               460
Ser Ser Val Gln Gly Val Tyr Thr Ser Ala Phe Ala Pro Tyr Asn Asn
465                               470                               475                               480
Ala Met Ile Arg Asn Phe Thr Ser Ala Asn Asp Phe Asp Phe Arg Arg
                               485                               490                               495
Leu Arg Ile Asp Glu Val Ser Ile Gly Val Ile Ala Asn Pro Lys Glu
                               500                               505                               510
Ser Thr Ile Val Gly Pro Ile Leu Glu Leu Phe Phe Asn Val Met Ile
                               515                               520                               525
Tyr Ser Asn Leu Ile Leu Pro Ile His Asp Pro Gln Cys Lys Arg Ser
                               530                               535                               540
Cys Leu Met Leu Met Asp Glu Phe Thr Leu Cys Gly Tyr Leu Glu Thr
545                               550                               555                               560
Phe Val Lys Ala Val Gly Ile Met Ala Glu Tyr Asn Met Arg Pro Ala
                               565                               570                               575
Phe Val Phe Gln Ser Lys Ala Gln Leu Glu Asn Asp Pro Pro Leu Gly
                               580                               585                               590
Tyr Gly Arg Asn Gly Ala Lys Thr Ile Leu Asp Asn Leu Ser Leu Asn
                               595                               600                               605
Met Tyr Tyr Gly Ile Asn Asn Asp Asn Tyr Tyr Glu His Phe Glu Lys
                               610                               615                               620
Leu Ser Lys Val Leu Gly Lys Tyr Thr Arg Gln Asp Val Ser Arg Ser
625                               630                               635                               640
Ile Asp Asp Asn Thr Gly Lys Thr Asn Thr Ser Ile Ser Asn Lys Glu
                               645                               650                               655
Arg Phe Leu Met Thr Pro Asp Glu Leu Met Thr Met Gly Asp Glu Leu
                               660                               665                               670
Ile Ile Leu Glu Asn Thr Leu Lys Pro Ile Lys Cys His Lys Ala Leu
                               675                               680                               685
Tyr Tyr Asp Asp Pro Phe Phe Thr Asp Glu Leu Ile Lys Val Ser Pro
                               690                               695                               700
Ser Leu Ser Lys Lys Tyr Lys Leu Gly Lys Val Pro Asn Gln Ala Thr
705                               710                               715                               720
Phe Tyr Asp Asp Leu Gln Ala Ala Lys Thr Arg Gly Glu Leu Ser Tyr
                               725                               730                               735
Asp Lys Ser Leu Val Pro Val Gly Ser Ser Glu Leu
                               740                               745

```

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1037 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

```

Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile Glu Asp Tyr Lys
 1           5           10           15
Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala Leu Phe Phe Leu
          20           25           30
Tyr Lys Phe Ile Lys Ala Gln Lys Lys Ala Phe Lys Asp Lys Ala Asn
          35           40           45
Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile Ile Asp Gly Leu
          50           55           60
Lys Glu Arg Val Lys Thr Phe Gly Phe Trp Leu Gln Ala Ile Leu Leu
          65           70           75           80
Leu Ser Tyr Ser Phe Ile Thr Ser Gly Leu Phe Phe Leu Ile Leu Leu
          85           90           95
Gly Asn Phe Tyr Asp Asp Asn Arg Ser Pro Glu Ser Asp Asp Asp Leu
          100          105          110
Phe Asp Ile Trp Ile Tyr Ala Ile Gln Asp Phe Pro Asn Tyr Tyr Phe
          115          120          125
Lys Ala Leu Gly Phe Ser Ser Leu Lys Ile Tyr Gly Phe Asn Ile Ser
          130          135          140
Leu Val Val Tyr Gly Ser Ile Leu Cys Ser Tyr Ile Phe Ile Thr Phe
          145          150          155          160
Phe Val Trp Phe Leu Lys Tyr Leu Thr Arg Thr Arg Asp Ile Gly Ala
          165          170          175
Asn Lys Lys Val Asp Asp Leu Phe Gly Ser Ala Ser Trp Glu Thr Glu
          180          185          190
Glu Lys Met Ile Lys Ala Lys Leu Ile Thr Pro Asn Asn Lys Lys Arg
          195          200          205
Ala Phe Asp Lys Arg Glu Val Ile Val Gly Arg Arg Gly Leu Gly Asp
          210          215          220
Phe Ile Ala Tyr Ala Gly Gln Ala Phe Ile Gly Leu Ile Ala Pro Thr
          225          230          235          240
Arg Ser Gly Lys Gly Val Gly Phe Ile Met Pro Asn Met Ile Asn Tyr
          245          250          255
Pro Gln Asn Ile Val Val Phe Asp Pro Lys Ala Asp Thr Met Glu Thr
          260          265          270
Cys Gly Lys Ile Arg Glu Lys Arg Phe Asn Gln Lys Val Phe Ile Tyr
          275          280          285
Glu Pro Phe Ser Leu Lys Thr His Arg Phe Asn Pro Phe Ala Tyr Val
          290          295          300
Asp Phe Gly Asn Asp Val Val Leu Thr Glu Asp Ile Leu Ser Gln Ile
          305          310          315          320
Asp Thr Arg Leu Lys Gly His Gly Met Val Ala Ser Gly Gly Asp Phe
          325          330          335
Ser Thr Gln Ile Phe Gly Leu Ala Lys Leu Val Phe Pro Glu Arg Pro
          340          345          350
Asn Glu Lys Asp Pro Phe Phe Ser Asn Gln Ala Arg Asn Leu Phe Val
          355          360          365
Ile Asn Cys Asn Ile Tyr Arg Asp Leu Met Trp Thr Lys Lys Gly Leu
          370          375          380

```


GCA GAA TAC AAC ATG CGC CCC GCT TTT GTG TTT CAA AGT AAG GCG CAA	1782
Ala Glu Tyr Asn Met Arg Pro Ala Phe Val Phe Gln Ser Lys Ala Gln	
570 575 580	
CTA GAG AAT GAC CCC CCA CTT GGT TAT GGT AGG AAT GGC GCT AAG ACT	1830
Leu Glu Asn Asp Pro Pro Leu Gly Tyr Gly Arg Asn Gly Ala Lys Thr	
585 590 595 600	
ATT TTA GAC AAC CTT TCT TTG AAT ATG TAT TAT GGG ATT AAC AAC GAT	1878
Ile Leu Asp Asn Leu Ser Leu Asn Met Tyr Tyr Gly Ile Asn Asn Asp	
605 610 615	
AAC TAC TAT GAA CAT TTT GAA AAA CTT TCT AAG GTA TTA GGG AAA TAC	1926
Asn Tyr Tyr Glu His Phe Glu Lys Leu Ser Lys Val Leu Gly Lys Tyr	
620 625 630	
ACA AGG CAA GAC GTG AGC CGA AGC ATT GAT GAT AAT ACA GGT AAG ACC	1974
Thr Arg Gln Asp Val Ser Arg Ser Ile Asp Asp Asn Thr Gly Lys Thr	
635 640 645	
AAC ACT TCT ATC AGC AAC AAA GAG CGG TTT TTG ATG ACC CCT GAT GAA	2022
Asn Thr Ser Ile Ser Asn Lys Glu Arg Phe Leu Met Thr Pro Asp Glu	
650 655 660	
TTG ATG ACT ATG GGC GAT GAG CTT ATC ATT CTA GAG AAT ACG CTC AAA	2070
Leu Met Thr Met Gly Asp Glu Leu Ile Ile Leu Glu Asn Thr Leu Lys	
665 670 675 680	
CCT ATC AAG TGC CAC AAG GCG CTT TAC TAT GAT GAT CCA TTC TTC ACC	2118
Pro Ile Lys Cys His Lys Ala Leu Tyr Tyr Asp Asp Pro Phe Phe Thr	
685 690 695	
GAT GAA CTC ATT AAG GTA AGT CCA AGC TTG AGC AAG AAA TAC AAA TTG	2166
Asp Glu Leu Ile Lys Val Ser Pro Ser Leu Ser Lys Lys Tyr Lys Leu	
700 705 710	
GGG AAA GTG CCT AAT CAA GCA ACT TTC TAT GAT GAT TTG CAA GCC GCT	2214
Gly Lys Val Pro Asn Gln Ala Thr Phe Tyr Asp Asp Leu Gln Ala Ala	
715 720 725	
AAA ACT AGA GGT GAA TTG AGT TAT GAT AAA TCT TTA GTG CCT GTG GGT	2262
Lys Thr Arg Gly Glu Leu Ser Tyr Asp Lys Ser Leu Val Pro Val Gly	
730 735 740	
TCA AGT GAA CTG TGATTAAGAC AAAATATCTT AACAAAAAGA AAATTAAAAG ATAAT	2319
Ser Ser Glu Leu	
745	
GATATAAATA	2329

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 748 amino acids

(B) TYPE: amino acid

AAG CTC GTG TTC CCT GAA AGA CCT AAT GAA AAA GAT CCT TTC TTT AGC	1110
Lys Leu Val Phe Pro Glu Arg Pro Asn Glu Lys Asp Pro Phe Phe Ser	
345 350 355 360	
AAT CAA GCG CGA AAT CTT TTT GTC ATC AAT TGC AAT ATT TAC AGG GAT	1158
Asn Gln Ala Arg Asn Leu Phe Val Ile Asn Cys Asn Ile Tyr Arg Asp	
365 370 375	
CTC ATG TGG ACT AAA AAG GGG CTT GAG TTT GTC AAA AGA AAA AAA ATC	1206
Leu Met Trp Thr Lys Lys Gly Leu Glu Phe Val Lys Arg Lys Lys Ile	
380 385 390	
ATC ATG CCT GAA ACA CCC ACG ATG TTT TTC ATA GGT TCT ATG GCA AGC	1254
Ile Met Pro Glu Thr Pro Thr Met Phe Phe Ile Gly Ser Met Ala Ser	
395 400 405	
GGG ATC AAC TTG ATT GAT GAA GAC ACA AAC ATG GAA AAA GTC GTG TCT	1302
Gly Ile Asn Leu Ile Asp Glu Asp Thr Asn Met Glu Lys Val Val Ser	
410 415 420	
TTA ATG GAA TTT TTT GGA GGT GAA GAA GAT AAG AGT GGC GAT AAT CTA	1350
Leu Met Glu Phe Phe Gly Gly Glu Glu Asp Lys Ser Gly Asp Asn Leu	
425 430 435 440	
AGA GTG CTT AGT CCT GCC ACT AGA AAC ATG TGG AAT AGC TTC AAG ACA	1398
Arg Val Leu Ser Pro Ala Thr Arg Asn Met Trp Asn Ser Phe Lys Thr	
445 450 455	
ATG GGC GGC GCT AGA GAA ACT TAT AGC TCG GTT CAA GGG GTA TAC ACT	1446
Met Gly Gly Ala Arg Glu Thr Tyr Ser Ser Val Gln Gly Val Tyr Thr	
460 465 470	
TCA GCC TTT GCG CCT TAT AAT AAC GCA ATG ATT AGA AAT TTC ACG AGC	1494
Ser Ala Phe Ala Pro Tyr Asn Asn Ala Met Ile Arg Asn Phe Thr Ser	
475 480 485	
GCC AAT GAT TTT GAT TTC AGG CGT TTA AGG ATC GAT GAA GTG AGT ATT	1542
Ala Asn Asp Phe Asp Phe Arg Arg Leu Arg Ile Asp Glu Val Ser Ile	
490 495 500	
GGT GTG ATC GCT AAT CCT AAA GAA AGC ACT ATT GTT GGA CCG ATA TTA	1590
Gly Val Ile Ala Asn Pro Lys Glu Ser Thr Ile Val Gly Pro Ile Leu	
505 510 515 520	
GAG CTG TTT TTC AAT GTG ATG ATT TAT AGC AAT TTG ATT CTG CCA ATC	1638
Glu Leu Phe Phe Asn Val Met Ile Tyr Ser Asn Leu Ile Leu Pro Ile	
525 530 535	
CAT GAT CCA CAG TGC AAA AGA AGT TGC TTG ATG CTC ATG GAC GAA TTC	1686
His Asp Pro Gln Cys Lys Arg Ser Cys Leu Met Leu Met Asp Glu Phe	
540 545 550	
ACT TTA TGT GGC TAT TTA GAG ACC TTT GTT AAA GCG GTA GGG ATT ATG	1734
Thr Leu Cys Gly Tyr Leu Glu Thr Phe Val Lys Ala Val Gly Ile Met	
555 560 565	

CAA GAT TTT CCT AAT TAC TAT TTT AAA GCG CTT GGT TTT AGT TCA CTC	438
Gln Asp Phe Pro Asn Tyr Tyr Phe Lys Ala Leu Gly Phe Ser Ser Leu	
125 130 135	
AAG ATT TAT GGG TTC AAT ATA TCC TTA GTC GTA TAT GGT TCT ATT TTA	486
Lys Ile Tyr Gly Phe Asn Ile Ser Leu Val Val Tyr Gly Ser Ile Leu	
140 145 150	
TGC TCT TAT ATC TTC ATT ACC TTT TTT GTG TGG TTC TTA AAA TAC TTA	534
Cys Ser Tyr Ile Phe Ile Thr Phe Phe Val Trp Phe Leu Lys Tyr Leu	
155 160 165	
ACT CGG ACT AGA GAT ATA GGA GCG AAT AAA AAA GTT GAT GAT CTC TTT	582
Thr Arg Thr Arg Asp Ile Gly Ala Asn Lys Lys Val Asp Asp Leu Phe	
170 175 180	
GGT AGC GCG AGT TGG GAA ACT GAA GAG AAA ATG ATC AAA GCC AAA CTC	630
Gly Ser Ala Ser Trp Glu Thr Glu Glu Lys Met Ile Lys Ala Lys Leu	
185 190 195 200	
ATC ACG CCC AAC AAT AAA AAA CGC GCC TTT GAC AAA CGA GAG GTG ATT	678
Ile Thr Pro Asn Asn Lys Lys Arg Ala Phe Asp Lys Arg Glu Val Ile	
205 210 215	
GTA GGC AGG CGT GGC TTG GGG GAT TTT ATC GCT TAC GCA GGG CAG GCG	726
Val Gly Arg Arg Gly Leu Gly Asp Phe Ile Ala Tyr Ala Gly Gln Ala	
220 225 230	
TTC ATT GGC TTG ATT GCT CCT ACT AGA AGC GGT AAG GGG GTG GGT TTC	774
Phe Ile Gly Leu Ile Ala Pro Thr Arg Ser Gly Lys Gly Val Gly Phe	
235 240 245	
ATC ATG CCC AAT ATG ATC AAT TAT CCT CAA AAT ATC GTT GTG TTT GAC	822
Ile Met Pro Asn Met Ile Asn Tyr Pro Gln Asn Ile Val Val Phe Asp	
250 255 260	
CCT AAA GCT GAC ACT ATG GAG ACT TGC GGA AAA ATC AGA GAA AAA CGC	870
Pro Lys Ala Asp Thr Met Glu Thr Cys Gly Lys Ile Arg Glu Lys Arg	
265 270 275 280	
TTC AAC CAA AAA GTG TTC ATC TAT GAA CCT TTC TCC TTA AAA ACA CAC	918
Phe Asn Gln Lys Val Phe Ile Tyr Glu Pro Phe Ser Leu Lys Thr His	
285 290 295	
CGA TTT AAT CCT TTC GCT TAT GTG GAT TTT GGT AAT GAT GTG GTT TTG	966
Arg Phe Asn Pro Phe Ala Tyr Val Asp Phe Gly Asn Asp Val Val Leu	
300 305 310	
ACC GAA GAC ATA CTC TCT CAA ATT GAC ACA CGC CTA AAA GGG CAT GGC	1014
Thr Glu Asp Ile Leu Ser Gln Ile Asp Thr Arg Leu Lys Gly His Gly	
315 320 325	
ATG GTG GCT AGT GGA GGG GAT TTT TCC ACT CAA ATC TTT GGA TTA GCA	1062
Met Val Ala Ser Gly Gly Asp Phe Ser Thr Gln Ile Phe Gly Leu Ala	
330 335 340	

			100					105				110
Lys	Phe	Arg	Cys	Ile	Tyr	Ser	Gln	Val	Arg	Tyr	Asn	Glu
		115					120				125	

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...2274
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

ATTTTATATC AAACACAGGT AGTAGGCACA	ATG GAA GAC TTT TTG TAT AAC ACC	54
	Met Glu Asp Phe Leu Tyr Asn Thr	
	1 5	
TTA TAT TTC ATA GAG GAT TAT AAG TTG GTT GTT ATT TTT AGT TTC ATA		102
Leu Tyr Phe Ile Glu Asp Tyr Lys Leu Val Val Ile Phe Ser Phe Ile		
10 15 20		
GGG TTA ATA GCG TTA TTT TTT CTT TAC AAA TTC ATA AAA GCT CAA AAA		150
Gly Leu Ile Ala Leu Phe Phe Leu Tyr Lys Phe Ile Lys Ala Gln Lys		
25 30 35 40		
AAG GCT TTT AAA GAT AAA GCT AAC CAG CCT CAA AAG AAA AAA AGC TTT		198
Lys Ala Phe Lys Asp Lys Ala Asn Gln Pro Gln Lys Lys Lys Ser Phe		
45 50 55		
AAA GAA ATC ATT ATA GAT GGG CTG AAA GAA AGG GTT AAA ACC TTT GGC		246
Lys Glu Ile Ile Ile Asp Gly Leu Lys Glu Arg Val Lys Thr Phe Gly		
60 65 70		
TTT TGG TTG CAA GCT ATA CTA TTA CTA TCC TAT TCT TTT ATC ACA TCA		294
Phe Trp Leu Gln Ala Ile Leu Leu Leu Ser Tyr Ser Phe Ile Thr Ser		
75 80 85		
GGA TTA TTT TTC TTG ATT CTC TTA GGT AAT TTT TAT GAT GAT AAT CGA		342
Gly Leu Phe Phe Leu Ile Leu Leu Gly Asn Phe Tyr Asp Asp Asn Arg		
90 95 100		
TCG CCT GAG AGC GAT GAT GAT CTT TTT GAT ATA TGG ATC TAT GCG ATA		390
Ser Pro Glu Ser Asp Asp Asp Leu Phe Asp Ile Trp Ile Tyr Ala Ile		
105 110 115 120		

CTA GGG TTG AAC AAC AGG CGA GAA AAA TCC CTT AAA GAC ACT TCT TAT 158
 Leu Gly Leu Asn Asn Arg Arg Glu Lys Ser Leu Lys Asp Thr Ser Tyr
 15 20 25 30

TCC ATG TTT CAT ATC ACC CTA AAC ACC GCT AAA AAA TTC TAC CCT ACC 206
 Ser Met Phe His Ile Thr Leu Asn Thr Ala Lys Lys Phe Tyr Pro Thr
 35 40 45

TAC TCT AAA ACG CTC CTC AAA TTC AAA TTG CTA AAC GAT GTG GGT TTT 254
 Tyr Ser Lys Thr Leu Leu Lys Phe Lys Leu Leu Asn Asp Val Gly Phe
 50 55 60

GCG ATC CAA TTA GCC AAA CAA ATT TTA AAA GAA AAT TTT GAT TAT TAC 302
 Ala Ile Gln Leu Ala Lys Gln Ile Leu Lys Glu Asn Phe Asp Tyr Tyr
 65 70 75

AAA CAA AAA CAC CCC AAC AAA AGC GTG TAT CAA TTA GTA GAA ATG GCA 350
 Lys Gln Lys His Pro Asn Lys Ser Val Tyr Gln Leu Val Glu Met Ala
 80 85 90

ATA GGC GCT TAC AAT GGG GGA ATG AAA CAC AAC CCT AAT GGC GCT TAC 398
 Ile Gly Ala Tyr Asn Gly Gly Met Lys His Asn Pro Asn Gly Ala Tyr
 95 100 105 110

GTG AAA AAA TTC CGT TGC ATT TAT TCT CAA GTG CGA TAT AAC GAG TAGAG 448
 Val Lys Lys Phe Arg Cys Ile Tyr Ser Gln Val Arg Tyr Asn Glu
 115 120 125

CATACTCATT TTATAAGCAA TCTTGATGAC ACACTTCTAC TATCTTATGA ATTTAT 504

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

Met Cys Arg Thr Leu Ile Ser Ile Ala Leu Leu Glu Ser Ser Leu Gly
 1 5 10 15
 Leu Asn Asn Arg Arg Glu Lys Ser Leu Lys Asp Thr Ser Tyr Ser Met
 20 25 30
 Phe His Ile Thr Leu Asn Thr Ala Lys Lys Phe Tyr Pro Thr Tyr Ser
 35 40 45
 Lys Thr Leu Leu Lys Phe Lys Leu Leu Asn Asp Val Gly Phe Ala Ile
 50 55 60
 Gln Leu Ala Lys Gln Ile Leu Lys Glu Asn Phe Asp Tyr Tyr Lys Gln
 65 70 75 80
 Lys His Pro Asn Lys Ser Val Tyr Gln Leu Val Glu Met Ala Ile Gly
 85 90 95
 Ala Tyr Asn Gly Gly Met Lys His Asn Pro Asn Gly Ala Tyr Val Lys

AT

450

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

```

Met Tyr Gly Gly Asn Ala Met Ala Asp Thr Ile Asn Thr Thr Glu Ala
 1             5             10             15
Thr His Glu Thr Lys Lys Pro Asn Ala Phe Val Asn Phe Phe Lys Asn
          20          25          30
Asn Leu Thr Asp Lys Arg Tyr Asp Ser Leu Gly Leu Ile Gly Ala Gly
          35          40          45
Val Leu Cys Cys Val Leu Ser Gly Ala Met Gly Ile Val Gly Ile Ile
          50          55          60
Phe Val Ala Ile Gly Ile Phe Leu Ser Phe Ser Asn Ile Asn Leu Val
65          70          75          80
Lys Leu Val Glu Lys Leu Ser Lys Lys Gln Ser Lys Val Pro Thr Thr
          85          90          95
Val Asn Asn Glu Thr Gln Lys Ser Gln Ala Thr Ser Val Thr Asn Glu
          100         105         110
Pro Thr Glu Ala Lys Glu Thr Lys Asp
          115         120

```

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 69...443
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

```

TAACCATTAG TTTCAAGCAG TATGAAAATC TTCTCCATAT CCATCAAAAA GGTTGCGACA      60
ATGAAGTG ATG TGC AGA ACG CTC ATC TCT ATC GCT TTG TTA GAA AGC TCT      110
    Met Cys Arg Thr Leu Ile Ser Ile Ala Leu Leu Glu Ser Ser
      1             5             10

```

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...396
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

TGTTTCATAG TAACAAATTG AAAATATACC ATT ATG TAT GGA GGT AAT GCT ATG	54
Met Tyr Gly Gly Asn Ala Met	
1 5	
GCT GAC ACA ATC AAT ACA ACT GAA GCA ACT CAT GAA ACA AAA AAA CCA	102
Ala Asp Thr Ile Asn Thr Thr Glu Ala Thr His Glu Thr Lys Lys Pro	
10 15 20	
AAC GCT TTT GTA AAT TTT TTC AAA AAC AAT TTG ACT GAT AAG CGT TAT	150
Asn Ala Phe Val Asn Phe Phe Lys Asn Asn Leu Thr Asp Lys Arg Tyr	
25 30 35	
GAT TCA TTA GGT CTC ATT GGA GCA GGG GTT TTA TGT TGT GTC TTG AGC	198
Asp Ser Leu Gly Leu Ile Gly Ala Gly Val Leu Cys Cys Val Leu Ser	
40 45 50 55	
GGT GCT ATG GGG ATT GTT GGG ATA ATC TTT GTC GCA ATA GGA ATC TTT	246
Gly Ala Met Gly Ile Val Gly Ile Ile Phe Val Ala Ile Gly Ile Phe	
60 65 70	
TTG TCT TTT TCT AAT ATC AAC TTA GTG AAA TTA GTT GAA AAA TTG TCC	294
Leu Ser Phe Ser Asn Ile Asn Leu Val Lys Leu Val Glu Lys Leu Ser	
75 80 85	
AAA AAA CAA TCT AAA GTG CCA ACA ACT GTC AAT AAC GAA ACT CAA AAA	342
Lys Lys Gln Ser Lys Val Pro Thr Thr Val Asn Asn Glu Thr Gln Lys	
90 95 100	
TCT CAA GCA ACA AGC GTT ACC AAC GAA CCA ACT GAA GCC AAA GAG ACT	390
Ser Gln Ala Thr Ser Val Thr Asn Glu Pro Thr Glu Ala Lys Glu Thr	
105 110 115	
AAA GAT TGAGGCAAAA CAACGATTTT GACTGAAGAA AGAATGAGAG AAAATTTCAA AA	448
Lys Asp	
120	

GAA GAC AAT AAG ATC GCT GCT ATT GGG AGT GGG GGG AAT TAC GCT TTA 435
 Glu Asp Asn Lys Ile Ala Ala Ile Gly Ser Gly Gly Asn Tyr Ala Leu
 125 130 135

AGC GCG GCT AGG GCT TTA GAT CAT TTC GCT CAT TTA GAG CCT AGA AAA 483
 Ser Ala Ala Arg Ala Leu Asp His Phe Ala His Leu Glu Pro Arg Lys
 140 145 150 155

CTT GTA GAA GAG TCC TTA AAA ATC GCA GGG GAT CTT TGC ATT TAC ACC 531
 Leu Val Glu Glu Ser Leu Lys Ile Ala Gly Asp Leu Cys Ile Tyr Thr
 160 165 170

AAC ACG AAT ATT AAA ATT TTG GAG CTT TAATGTCTAA ATTGAATATG ACCCCAC 585
 Asn Thr Asn Ile Lys Ile Leu Glu Leu
 175 180

GAGAAATTGT CGC 598

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

Met Phe Glu Ala Thr Thr Ile Leu Gly Tyr Arg Gly Glu Leu Asn His
 1 5 10 15
 Lys Lys Phe Ala Leu Ile Gly Gly Asp Gly Gln Val Thr Leu Gly Asn
 20 25 30
 Cys Val Val Lys Ala Asn Ala Thr Lys Ile Arg Ser Leu Tyr His Asn
 35 40 45
 Gln Val Leu Ser Gly Phe Ala Gly Ser Thr Ala Asp Ala Phe Ser Leu
 50 55 60
 Phe Asp Met Phe Glu Arg Ile Leu Glu Ser Lys Lys Gly Asp Leu Phe
 65 70 75 80
 Lys Ser Val Val Asp Phe Ser Lys Glu Trp Arg Lys Asp Lys Tyr Leu
 85 90 95
 Arg Arg Leu Glu Ala Met Met Ile Val Leu Asn Phe Asp His Ile Phe
 100 105 110
 Ile Leu Ser Gly Met Gly Asp Val Leu Glu Ala Glu Asp Asn Lys Ile
 115 120 125
 Ala Ala Ile Gly Ser Gly Gly Asn Tyr Ala Leu Ser Ala Ala Arg Ala
 130 135 140
 Leu Asp His Phe Ala His Leu Glu Pro Arg Lys Leu Val Glu Glu Ser
 145 150 155 160
 Leu Lys Ile Ala Gly Asp Leu Cys Ile Tyr Thr Asn Thr Asn Ile Lys
 165 170 175
 Ile Leu Glu Leu
 180

Leu Gly Leu Ile Lys Gln Ala Leu Glu Lys Gln Met Gly Gly Arg Asn
 645 650 655
 Arg Gln

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...558
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

GTGGTGGCTG AGTAGAAA ATG TTT GAA GCG ACG ACG ATT TTA GGC TAT AGA	51
Met Phe Glu Ala Thr Thr Ile Leu Gly Tyr Arg	
1 5 10	
GGG GAA TTG AAT CAT AAA AAG TTC GCG CTC ATT GGA GGC GAT GGG CAG	99
Gly Glu Leu Asn His Lys Lys Phe Ala Leu Ile Gly Gly Asp Gly Gln	
15 20 25	
GTA ACT TTG GGT AAT TGC GTG GTC AAA GCC AAT GCG ACA AAA ATC AGA	147
Val Thr Leu Gly Asn Cys Val Val Lys Ala Asn Ala Thr Lys Ile Arg	
30 35 40	
AGC TTG TAT CAC AAC CAG GTT TTA AGC GGG TTT GCC GGA AGC ACC GCG	195
Ser Leu Tyr His Asn Gln Val Leu Ser Gly Phe Ala Gly Ser Thr Ala	
45 50 55	
GAC GCT TTT AGT TTG TTT GAT ATG TTT GAA CGC ATT TTA GAG AGC AAA	243
Asp Ala Phe Ser Leu Phe Asp Met Phe Glu Arg Ile Leu Glu Ser Lys	
60 65 70 75	
AAG GGG GAT TTG TTT AAA AGC GTG GTG GAT TTC AGT AAA GAA TGG CGC	291
Lys Gly Asp Leu Phe Lys Ser Val Val Asp Phe Ser Lys Glu Trp Arg	
80 85 90	
AAA GAT AAG TAT TTA CGC CGA CTG GAA GCG ATG ATG ATC GTT TTA AAC	339
Lys Asp Lys Tyr Leu Arg Arg Leu Glu Ala Met Met Ile Val Leu Asn	
95 100 105	
TTC GAT CAC ATT TTC ATT TTG AGC GGC ATG GGC GAT GTT TTA GAA GCT	387
Phe Asp His Ile Phe Ile Leu Ser Gly Met Gly Asp Val Leu Glu Ala	
110 115 120	

```

      195              200              205
His Tyr Leu Thr Ile Lys Ile Gly Lys Ile Pro Asn Glu Lys Arg Val
  210              215              220
Tyr Glu Ala Phe Lys Asp Tyr Arg Gln Lys Lys Gly Ile Glu Ile Glu
  225              230              235              240
Asp Leu Leu Lys Asp Leu Gln Lys Tyr Cys Gly Tyr Phe Cys Gln Ile
      245              250              255
Ala Phe Lys Lys Glu Asp Asp Lys Asp Leu Asn Lys Ala Leu Ser Phe
      260              265              270
Leu Val Asn Leu Glu Met Asp Val Ile Tyr Pro Leu Leu Leu Glu Leu
      275              280              285
Tyr Ser Asp Tyr Lys Asp Gly Val Leu Ser Lys Gln Asp Phe Ile Pro
  290              295              300
Ile Ile Tyr Leu Ile Glu Ser Tyr Ile Cys Arg Arg Ala Val Cys Gly
  305              310              315              320
Leu Gly Thr Asn Ser Leu Asn Lys Val Phe Pro Ser Phe Thr Lys His
      325              330              335
Ile Gln Lys Asp Glu Tyr Phe Lys Ser Leu Lys Ala His Phe Val Cys
      340              345              350
Leu Thr Glu Lys Gln Arg Phe Pro Asn Asn Asp Glu Phe Lys Lys Leu
  355              360              365
Phe Ile Thr Ile Asp Phe Tyr Lys Phe Lys Lys Asn Lys Tyr Phe Leu
  370              375              380
Glu Arg Leu Glu Asn Phe Asp Thr Lys Glu Pro Val Asp Thr Gln Lys
  385              390              395              400
Cys Asn Ile Glu His Ile Met Pro Gln Thr Leu Thr Pro Glu Trp Gln
      405              410              415
Arg Asp Leu Gly Glu Asn Phe Gln Ala Ile His Glu Lys Tyr Leu His
      420              425              430
Thr Ile Gly Asn Leu Thr Leu Thr Gly Tyr Asn Ser Lys Tyr Ser Asn
      435              440              445
Asn Ser Phe Gln Glu Lys Arg Asp Met Glu Lys Gly Phe Lys Gln Ser
  450              455              460
Ser Leu Lys Leu Asn Gln Ser Leu Lys Asp Leu Glu Ser Phe Gly Glu
  465              470              475              480
Lys Glu Ile Glu Lys Arg Ala Ser Asp Leu Ala Asp Trp Ala Leu Lys
      485              490              495
Ile Trp Thr Tyr Pro Ile Leu Glu Ala Glu Thr Leu Glu Glu Tyr Lys
      500              505              510
Pro Lys Lys Glu Lys Lys Glu Lys Glu Lys Glu Glu Tyr Lys Leu
  515              520              525
Lys Lys Glu Lys Lys Val Tyr Asp Leu Ser Ser Tyr Lys Phe Ser Ser
  530              535              540
Asp Ser Arg Glu Leu Phe Asp Ile Leu Arg Glu Lys Ile Lys Ala Leu
  545              550              555              560
Asp Glu Arg Ile Thr Glu Lys Phe Asn Gln Lys Tyr Ile Ala Tyr Lys
      565              570              575
Phe Cys Lys Ile Ser Phe Val Asp Ile Val Val Gln Glu Lys Gly Leu
      580              585              590
Lys Leu Tyr Leu Lys Met Asn Leu Asn Glu Leu Gln Asp Glu Ile Lys
  595              600              605
Glu Lys Leu Lys Ile Arg Asp Val Ser Asn Ile Gly Arg Pro Cys Val
  610              615              620
Gly Asn Met Glu Val Glu Leu Glu Thr Lys Glu Asn Ile Pro Tyr Cys
  625              630              635              640

```

```

TTA AAA ATG AAC TTG AAT GAA TTG CAA GAT GAA ATA AAG GAA AAA CTA      1881
Leu Lys Met Asn Leu Asn Glu Leu Gln Asp Glu Ile Lys Glu Lys Leu
                               600                               605                               610

AAA ATT AGA GAC GTT TCT AAT ATC GGT CGT CCA TGC GTT GGA AAC ATG      1929
Lys Ile Arg Asp Val Ser Asn Ile Gly Arg Pro Cys Val Gly Asn Met
                               615                               620                               625

GAA GTA GAG CTA GAA ACA AAA GAA AAT ATC CCT TAT TGT TTG GGA TTG      1977
Glu Val Glu Leu Glu Thr Lys Glu Asn Ile Pro Tyr Cys Leu Gly Leu
                               630                               635                               640

ATC AAG CAG GCT TTA GAA AAA CAG ATG GGT GGT AGG AAT AGG CAA TAAAA  2027
Ile Lys Gln Ala Leu Glu Lys Gln Met Gly Gly Arg Asn Arg Gln
                               645                               650                               655

ACCCAACCTTA TTCAAAATAA AGAGTATAAT TACAAATTAC TTAC                      2071

```

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

```

Met Asn Gly His Phe Ile Gly Ser Ile Leu Tyr Val Leu Asp Ser Asn
 1           5           10           15
Thr His Ser Asn Asn Thr Leu Leu Ile Ile Asp Gly Gln Gln Arg Leu
          20           25           30
Thr Thr Ile Thr Leu Leu Leu Ile Ala Leu Arg Asn His Leu Ser Glu
          35           40           45
Glu Val Glu Ile Leu Glu Lys Phe Ser Arg Lys Glu Ile Glu Ser Tyr
          50           55           60
Leu Ile Asn Ser Asn Lys Asp Gly Asp Lys Lys Phe Arg Leu Ile Leu
          65           70           75           80
Ser Glu Ser Asp Lys Asp Thr Leu Leu Ser Leu Ile Asp Lys Asn Lys
          85           90           95
Arg Lys Pro Ser Glu Pro Ser Val Lys Ile Val Glu Asn Phe Glu Leu
          100          105          110
Phe Glu Lys Trp Ile Ser Glu Asn Thr Asp Lys Leu Glu Thr Ile Phe
          115          120          125
Lys Gly Leu Lys Lys Leu Met Ile Val Trp Ile Ser Leu Asp Lys Gly
          130          135          140
Lys Asp Asp Pro Gln Leu Ile Phe Glu Ser Met Asn Ser Lys Asp Ile
          145          150          155          160
Glu Leu Thr Gln Thr Asp Leu Ile Arg Asn Tyr Ile Val Met Glu Thr
          165          170          175
Glu Val Glu Lys Gln Glu Asp Phe Tyr Asn Gln Tyr Trp Arg Ala Met
          180          185          190
Glu Glu Arg Phe Glu Gln Asn Glu Thr Leu Phe Asn Arg Phe Val Arg

```

ATA GAT TTT TAT AAG TTT AAA AAA AAT AAA TAC TTT CTT GAA AGG TTA	1209
Ile Asp Phe Tyr Lys Phe Lys Lys Asn Lys Tyr Phe Leu Glu Arg Leu	
375 380 385	
GAA AAT TTT GAC ACA AAA GAA CCG GTC GAT ACT CAA AAA TGC AAT ATA	1257
Glu Asn Phe Asp Thr Lys Glu Pro Val Asp Thr Gln Lys Cys Asn Ile	
390 395 400	
GAA CAT ATA ATG CCT CAA ACC CTT ACT CCA GAA TGG CAA AGG GAT TTG	1305
Glu His Ile Met Pro Gln Thr Leu Thr Pro Glu Trp Gln Arg Asp Leu	
405 410 415	
GGT GAA AAT TTT CAA GCA ATA CAC GAG AAA TAC CTC CAC ACA ATA GGG	1353
Gly Glu Asn Phe Gln Ala Ile His Glu Lys Tyr Leu His Thr Ile Gly	
420 425 430 435	
AAT CTC ACT CTA ACC GGT TAT AAC TCT AAG TAT AGC AAC AAT TCT TTC	1401
Asn Leu Thr Leu Thr Gly Tyr Asn Ser Lys Tyr Ser Asn Asn Ser Phe	
440 445 450	
CAA GAA AAA AGA GAT ATG GAG AAG GGC TTT AAA CAA AGC TCA TTA AAA	1449
Gln Glu Lys Arg Asp Met Glu Lys Gly Phe Lys Gln Ser Ser Leu Lys	
455 460 465	
CTC AAT CAA AGT TTG AAA GAT TTG GAA TCT TTT GGC GAA AAA GAG ATT	1497
Leu Asn Gln Ser Leu Lys Asp Leu Glu Ser Phe Gly Glu Lys Glu Ile	
470 475 480	
GAA AAA AGG GCT AGT GAT TTA GCG GAT TGG GCT TTA AAG ATT TGG ACT	1545
Glu Lys Arg Ala Ser Asp Leu Ala Asp Trp Ala Leu Lys Ile Trp Thr	
485 490 495	
TAC CCA ATT CTA GAG GCA GAA ACA TTA GAG GAA TAT AAA CCC AAA AAA	1593
Tyr Pro Ile Leu Glu Ala Glu Thr Leu Glu Glu Tyr Lys Pro Lys Lys	
500 505 510 515	
GAA AAG AAA GAA AAG AAA GAA AAA GAG GAG TAT AAA CTC AAG AAA GAA	1641
Glu Lys Lys Glu Lys Lys Glu Lys Glu Glu Tyr Lys Leu Lys Lys Glu	
520 525 530	
AAA AAG GTT TAT GAT TTA AGC TCT TAT AAG TTT AGC TCT GAT TCA AGG	1689
Lys Lys Val Tyr Asp Leu Ser Ser Tyr Lys Phe Ser Ser Asp Ser Arg	
535 540 545	
GAA TTG TTT GAT ATT TTA AGA GAA AAG ATT AAA GCT CTT GAT GAA AGG	1737
Glu Leu Phe Asp Ile Leu Arg Glu Lys Ile Lys Ala Leu Asp Glu Arg	
550 555 560	
ATA ACT GAA AAA TTT AAT CAA AAA TAT ATA GCT TAT AAG TTT TGT AAA	1785
Ile Thr Glu Lys Phe Asn Gln Lys Tyr Ile Ala Tyr Lys Phe Cys Lys	
565 570 575	
ATA AGT TTT GTG GAT ATT GTT GTG CAA GAA AAA GGC TTA AAA TTG TAT	1833
Ile Ser Phe Val Asp Ile Val Val Gln Glu Lys Gly Leu Lys Leu Tyr	
580 585 590 595	

CCT CAA CTT ATT TTT GAG AGC ATG AAC TCA AAA GAT ATC GAA CTC ACG	537
Pro Gln Leu Ile Phe Glu Ser Met Asn Ser Lys Asp Ile Glu Leu Thr	
150 155 160	
CAA ACG GAT TTG ATC AGA AAT TAT ATC GTA ATG GAA ACG GAG GTT GAA	585
Gln Thr Asp Leu Ile Arg Asn Tyr Ile Val Met Glu Thr Glu Val Glu	
165 170 175	
AAA CAG GAA GAC TTT TAT AAT CAA TAT TGG AGG GCT ATG GAG GAG AGA	633
Lys Gln Glu Asp Phe Tyr Asn Gln Tyr Trp Arg Ala Met Glu Glu Arg	
180 185 190 195	
TTT GAA CAA AAT GAA ACA TTG TTT AAT CGG TTT GTC CGG CAT TAT CTC	681
Phe Glu Gln Asn Glu Thr Leu Phe Asn Arg Phe Val Arg His Tyr Leu	
200 205 210	
ACG ATC AAA ATA GGA AAG ATT CCC AAT GAG AAA AGA GTT TAT GAA GCT	729
Thr Ile Lys Ile Gly Lys Ile Pro Asn Glu Lys Arg Val Tyr Glu Ala	
215 220 225	
TTC AAG GAT TAC CGG CAA AAA AAG GGG ATA GAA ATA GAG GAT TTA TTA	777
Phe Lys Asp Tyr Arg Gln Lys Lys Gly Ile Glu Ile Glu Asp Leu Leu	
230 235 240	
AAA GAT TTA CAA AAA TAC TGC GGG TAT TTT TGC CAG ATT GCA TTC AAA	825
Lys Asp Leu Gln Lys Tyr Cys Gly Tyr Phe Cys Gln Ile Ala Phe Lys	
245 250 255	
AAA GAA GAC GAT AAA GAT TTA AAC AAG GCT TTA AGT TTT TTG GTG AAT	873
Lys Glu Asp Asp Lys Asp Leu Asn Lys Ala Leu Ser Phe Leu Val Asn	
260 265 270 275	
TTA GAG ATG GAT GTG ATC TAT CCG CTA CTA CTA GAG CTT TAT AGC GAT	921
Leu Glu Met Asp Val Ile Tyr Pro Leu Leu Leu Glu Leu Tyr Ser Asp	
280 285 290	
TAT AAG GAT GGC GTT TTA TCC AAG CAG GAT TTT ATC CCT ATT ATC TAT	969
Tyr Lys Asp Gly Val Leu Ser Lys Gln Asp Phe Ile Pro Ile Ile Tyr	
295 300 305	
TTA ATA GAG AGC TAT ATT TGC AGA AGG GCG GTG TGT GGG CTT GGC ACA	1017
Leu Ile Glu Ser Tyr Ile Cys Arg Ala Val Cys Gly Leu Gly Thr	
310 315 320	
AAT AGT CTC AAT AAA GTT TTT CCC TCT TTT ACA AAG CAC ATC CAA AAA	1065
Asn Ser Leu Asn Lys Val Phe Pro Ser Phe Thr Lys His Ile Gln Lys	
325 330 335	
GAT GAA TAT TTT AAA AGC CTA AAG GCG CAT TTT GTC TGT CTG ACA GAA	1113
Asp Glu Tyr Phe Lys Ser Leu Lys Ala His Phe Val Cys Leu Thr Glu	
340 345 350 355	
AAA CAA AGA TTT CCA AAC AAT GAC GAG TTT AAA AAG CTT TTT ATT ACG	1161
Lys Gln Arg Phe Pro Asn Asn Asp Glu Phe Lys Lys Leu Phe Ile Thr	
360 365 370	

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 49...2022
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

TGCGAACAAAT TATGGGATGA TATTATAAAA ATTGGTGGGA ATGATAAG ATG AAC GGA	57
Met Asn Gly	
1	
CAT TTT ATC GGT TCT ATT TTG TAT GTG CTA GAT AGT AAT ACG CAC TCT	105
His Phe Ile Gly Ser Ile Leu Tyr Val Leu Asp Ser Asn Thr His Ser	
5 10 15	
AAC AAT ACA TTA CTC ATC ATT GAC GGC CAA CAA AGG CTC ACC ACT ATC	153
Asn Asn Thr Leu Leu Ile Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile	
20 25 30 35	
ACG CTT TTA CTC ATC GCT TTA AGG AAT CAT CTA AGC GAA GAA GTT GAA	201
Thr Leu Leu Leu Ile Ala Leu Arg Asn His Leu Ser Glu Glu Val Glu	
40 45 50	
ATT TTG GAG AAA TTT TCG CGT AAA GAA ATA GAG AGC TAT CTT ATC AAC	249
Ile Leu Glu Lys Phe Ser Arg Lys Glu Ile Glu Ser Tyr Leu Ile Asn	
55 60 65	
AGC AAT AAG GAC GGC GAT AAG AAA TTC AGG CTC ATT CTT TCA GAG TCC	297
Ser Asn Lys Asp Gly Asp Lys Lys Phe Arg Leu Ile Leu Ser Glu Ser	
70 75 80	
GAT AAA GAC ACC TTG CTG TCT TTG ATT GAT AAA AAC AAA AGA AAG CCG	345
Asp Lys Asp Thr Leu Leu Ser Leu Ile Asp Lys Asn Lys Arg Lys Pro	
85 90 95	
AGC GAG CCT TCG GTA AAA ATA GTG GAA AAT TTT GAA TTG TTT GAA AAA	393
Ser Glu Pro Ser Val Lys Ile Val Glu Asn Phe Glu Leu Phe Glu Lys	
100 105 110 115	
TGG ATC AGT GAA AAC ACC GAC AAA CTA GAA ACG ATT TTT AAA GGA TTA	441
Trp Ile Ser Glu Asn Thr Asp Lys Leu Glu Thr Ile Phe Lys Gly Leu	
120 125 130	
AAA AAA CTC ATG ATA GTT TGG ATT TCT TTA GAT AAA GGA AAA GAT GAT	489
Lys Lys Leu Met Ile Val Trp Ile Ser Leu Asp Lys Gly Lys Asp Asp	
135 140 145	

CTT GAT TTT ATA ATG GAT TTT CAA TAC GCT AAA ACC ACC GGA TTG TCT 630
 Leu Asp Phe Ile Met Asp Phe Gln Tyr Ala Lys Thr Thr Gly Leu Ser
 185 190 195

TTA GCC ATT TTA TGG CAT TTA AAA AAG TTT AAA AAT GTT TAAAAGGAAT TT 681
 Leu Ala Ile Leu Trp His Leu Lys Lys Phe Lys Asn Val
 200 205 210

TATGTTAAGG CTTTTG 697

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

Met Ser Tyr Phe Lys Asn Ala Phe Asn Gln Lys Ser Leu Ile Asp Asp
 1 5 10 15
 Ser Ser Val Tyr Leu Glu Pro Cys Ser Ser Ser Asn Phe Ile Glu Leu
 20 25 30
 Lys Arg Met His Tyr Asn Glu Glu Asn Thr Lys Lys Thr Trp Asp Ile
 35 40 45
 Ile Lys Ser Leu Asp Ser Val Ala Val Leu Leu Tyr Glu Lys Glu Ser
 50 55 60
 Asp Cys Phe Val Ile Val Lys Gln Phe Arg Pro Ala Ile Tyr Ala Arg
 65 70 75 80
 Arg Phe His Phe Lys Cys Asp Gln Asp Gln Thr Ile Asp Gly Tyr Thr
 85 90 95
 Tyr Glu Leu Cys Ala Gly Leu Val Asp Lys Ala Asn Lys Ser Leu Glu
 100 105 110
 Glu Ile Ala Cys Glu Glu Ala Leu Glu Glu Cys Gly Tyr Gln Ile Ser
 115 120 125
 Pro Lys Asn Leu Glu Thr Ile Gly Gln Phe Tyr Ser Ala Thr Gly Leu
 130 135 140
 Ser Gly Ser Leu Gln Thr Leu Tyr Tyr Ala Glu Val His Lys Asn Leu
 145 150 155 160
 Lys Val Ser Lys Gly Gly Ile Asp Thr Glu Arg Ile Glu Val Leu
 165 170 175
 Phe Leu Glu Arg Ser Lys Ala Leu Asp Phe Ile Met Asp Phe Gln Tyr
 180 185 190
 Ala Lys Thr Thr Gly Leu Ser Leu Ala Ile Leu Trp His Leu Lys Lys
 195 200 205
 Phe Lys Asn Val
 210

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2071 base pairs

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 34...669
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

AAAAAATTCA TTTTATCTTT TAGAGGGTTT TTA ATG TCT TAT TTT AAG AAT GCT	54
Met Ser Tyr Phe Lys Asn Ala	
1 5	
TTC AAT CAA AAA TCT TTA ATA GAT GAT TCT AGT GTG TAT TTA GAG CCT	102
Phe Asn Gln Lys Ser Leu Ile Asp Asp Ser Ser Val Tyr Leu Glu Pro	
10 15 20	
TGT TCT AGC TCT AAT TTC ATA GAA TTA AAA CGC ATG CAT TAT AAT GAA	150
Cys Ser Ser Ser Asn Phe Ile Glu Leu Lys Arg Met His Tyr Asn Glu	
25 30 35	
GAG AAT ACT AAG AAA ACA TGG GAT ATT ATT AAG TCT TTA GAC AGC GTG	198
Glu Asn Thr Lys Lys Thr Trp Asp Ile Ile Lys Ser Leu Asp Ser Val	
40 45 50 55	
GCG GTT TTA CTC TAT GAA AAA GAA TCC GAT TGC TTT GTG ATT GTG AAA	246
Ala Val Leu Leu Tyr Glu Lys Glu Ser Asp Cys Phe Val Ile Val Lys	
60 65 70	
CAA TTC CGC CCA GCC ATT TAT GCG CGC CGT TTT CAT TTT AAG TGC GAT	294
Gln Phe Arg Pro Ala Ile Tyr Ala Arg Arg Phe His Phe Lys Cys Asp	
75 80 85	
CAA GAT CAA ACT ATT GAC GGA TAC ACT TAT GAA TTG TGC GCA GGG CTT	342
Gln Asp Gln Thr Ile Asp Gly Tyr Thr Tyr Glu Leu Cys Ala Gly Leu	
90 95 100	
GTG GAT AAA GCT AAT AAG AGT TTA GAA GAA ATC GCT TGC GAA GAA GCG	390
Val Asp Lys Ala Asn Lys Ser Leu Glu Glu Ile Ala Cys Glu Glu Ala	
105 110 115	
CTA GAA GAA TGC GGT TAT CAA ATT AGC CCT AAA AAT TTA GAA ACC ATA	438
Leu Glu Glu Cys Gly Tyr Gln Ile Ser Pro Lys Asn Leu Glu Thr Ile	
120 125 130 135	
GGC CAA TTT TAT AGC GCG ACT GGG TTG AGT GGG AGT TTG CAA ACG CTC	486
Gly Gln Phe Tyr Ser Ala Thr Gly Leu Ser Gly Ser Leu Gln Thr Leu	
140 145 150	
TAT TAC GCT GAA GTG CAT AAG AAT TTG AAA GTT TCA AAG GGT GGG GGG	534
Tyr Tyr Ala Glu Val His Lys Asn Leu Lys Val Ser Lys Gly Gly Gly	
155 160 165	
ATT GAT ACC GAA AGG ATT GAA GTG CTG TTT TTA GAG CGA TCA AAA GCT	582
Ile Asp Thr Glu Arg Ile Glu Val Leu Phe Leu Glu Arg Ser Lys Ala	
170 175 180	


```

Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr Asn Tyr Tyr
      20      25      30
Leu Arg Lys Gln Asp Leu His Ile Lys Thr Gln Asn Asp Leu Ser
      35      40      45
Asn Ser Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu His Ser Trp
      50      55      60
Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr Leu Gly Thr
      65      70      75      80
Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe Gln Trp Tyr
      85      90      95
His Pro Asn Ile Asn Pro Tyr Gln Arg Asn Glu Phe Lys Phe Gln Ile
      100      105      110
Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr Lys Gly Thr
      115      120      125
Leu Tyr Leu Ala Tyr Thr Gln Thr Asp Trp Phe Gln Ile Tyr Asn Asp
      130      135      140
Pro Gln Ser Ala Pro Met Arg Met Met Asn Phe Met Pro Glu Leu Ile
      145      150      155      160
Tyr Val Tyr Pro Ile Asn Phe Lys Pro Phe Gly Gly Lys Ile Gly Asn
      165      170      175
Phe Ser Glu Ile Trp Ile Gly Trp Gln His Ile Ser Asn Gly Val Gly
      180      185      190
Gly Ala Gln Cys Tyr Gln Pro Phe Asn Lys Glu Gly Asn Pro Glu Asn
      195      200      205
Gln Phe Pro Gly Gln Pro Val Ile Val Lys Asp Tyr Asn Gly Gln Lys
      210      215      220
Asp Val Arg Trp Gly Gly Cys Arg Ser Val Ser Ala Gly Gln Arg Pro
      225      230      235      240
Val Phe Arg Leu Val Trp Glu Lys Gly Gly Leu Lys Ile Met Val Ala
      245      250      255
Tyr Trp Pro Tyr Val Pro Tyr Asp Gln Ser Asn Pro Asn Leu Ile Asp
      260      265      270
Tyr Met Gly Tyr Gly Asn Ala Lys Ile Asp Tyr Arg Arg Gly Arg His
      275      280      285
His Phe Glu Leu Gln Leu Tyr Asp Ile Phe Thr Gln Tyr Trp Arg Tyr
      290      295      300
Asp Arg Trp His Gly Ala Phe Arg Leu Gly Tyr Thr Tyr Arg Ile Asn
      305      310      315      320
Pro Phe Val Gly Ile Tyr Ala Gln Trp Phe Asn Gly Tyr Gly Asp Gly
      325      330      335
Leu Tyr Glu Tyr Asp Val Phe Ser Asn Arg Ile Gly Val Gly Ile Arg
      340      345      350
Leu Asn Pro
      355

```

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

Asn	Pro	Glu	Asn	Gln	Phe	Pro	Gly	Gln	Pro	Val	Ile	Val	Lys	Asp	Tyr	
205					210					215					220	
AAT	GGG	CAA	AAA	GAT	GTG	CGC	TGG	GGG	GGG	TGT	CGT	TCG	GTG	AGC	GCG	724
Asn	Gly	Gln	Lys	Asp	Val	Arg	Trp	Gly	Gly	Cys	Arg	Ser	Val	Ser	Ala	
				225					230					235		
GGG	CAA	CGC	CCT	GTG	TTT	CGT	TTG	GTG	TGG	GAA	AAG	GGA	GGC	CTA	AAA	772
Gly	Gln	Arg	Pro	Val	Phe	Arg	Leu	Val	Trp	Glu	Lys	Gly	Gly	Leu	Lys	
			240					245					250			
ATC	ATG	GTC	GCT	TAT	TGG	CCC	TAT	GTC	CCT	TAT	GAT	CAA	TCC	AAT	CCT	820
Ile	Met	Val	Ala	Tyr	Trp	Pro	Tyr	Val	Pro	Tyr	Asp	Gln	Ser	Asn	Pro	
		255					260					265				
AAT	TTG	ATT	GAT	TAC	ATG	GGG	TAT	GGT	AAC	GCT	AAA	ATT	GAT	TAC	AGG	868
Asn	Leu	Ile	Asp	Tyr	Met	Gly	Tyr	Gly	Asn	Ala	Lys	Ile	Asp	Tyr	Arg	
	270					275					280					
AGA	GGG	CGC	CAC	CAT	TTT	GAA	TTG	CAG	CTT	TAT	GAT	ATT	TTC	ACG	CAA	916
Arg	Gly	Arg	His	His	Phe	Glu	Leu	Gln	Leu	Tyr	Asp	Ile	Phe	Thr	Gln	
	285				290					295					300	
TAC	TGG	CGT	TAT	GAT	CGC	TGG	CAT	GGA	GCT	TTC	CGC	TTA	GGC	TAT	ACC	964
Tyr	Trp	Arg	Tyr	Asp	Arg	Trp	His	Gly	Ala	Phe	Arg	Leu	Gly	Tyr	Thr	
				305					310					315		
TAT	CGC	ATT	AAC	CCT	TTT	GTG	GGG	ATT	TAT	GCG	CAG	TGG	TTT	AAC	GGC	1012
Tyr	Arg	Ile	Asn	Pro	Phe	Val	Gly	Ile	Tyr	Ala	Gln	Trp	Phe	Asn	Gly	
			320					325					330			
TAT	GGC	GAT	GGC	TTG	TAT	GAA	TAC	GAT	GTT	TTT	TCC	AAT	CGT	ATA	GGG	1060
Tyr	Gly	Asp	Gly	Leu	Tyr	Glu	Tyr	Asp	Val	Phe	Ser	Asn	Arg	Ile	Gly	
		335					340					345				
GTA	GGA	ATA	CGC	TTA	AAC	CCT	TAAAAAAGCG	TTCTTTTAYG	CTATAATTAA	GACC						1115
Val	Gly	Ile	Arg	Leu	Asn	Pro										
		350				355										
AAAAA																1120

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

Met	Lys	Ser	Ile	Leu	Leu	Phe	Met	Ile	Phe	Val	Val	Cys	Gln	Leu	Glu
1				5				10						15	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

GAAATAAGGA TGCTTG ATG AAA AGC ATT TTG CTC TTT ATG ATT TTT GTA GTT	52
Met Lys Ser Ile Leu Leu Phe Met Ile Phe Val Val	
1 5 10	
TGT CAG TTA GAA GGC AAA AAA TTT TCA CAA GAT AAT TTT AAG GTG GAT	100
Cys Gln Leu Glu Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp	
15 20 25	
TAT AAC TAC TAT TTG CGC AAA CAG GAT TTG CAC ATC ATT AAA ACG CAA	148
Tyr Asn Tyr Tyr Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln	
30 35 40	
AAC GAT TTG TCC AAT TCT TGG TAT CTC CCT CCA CAA AAA GCC CCC AAA	196
Asn Asp Leu Ser Asn Ser Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys	
45 50 55 60	
GAA CAT TCT TGG GTG GAT TTT GCT AAA AAA TAT TTA AAC ATG ATG GAT	244
Glu His Ser Trp Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp	
65 70 75	
TAT CTA GGC ACT TAT TTT CTG CCT TTT TAT CAT AGT TTC ACC CCC ATT	292
Tyr Leu Gly Thr Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile	
80 85 90	
TTT CAA TGG TAC CAC CCC AAT ATC AAC CCG TAT CAA CGC AAT GAG TTT	340
Phe Gln Trp Tyr His Pro Asn Ile Asn Pro Tyr Gln Arg Asn Glu Phe	
95 100 105	
AAG TTC CAA ATT AGT TTT AGA GTG CCT GTA TTT AGG CAT ATT CTT TGG	388
Lys Phe Gln Ile Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp	
110 115 120	
ACT AAA GGC ACG CTG TAT TTA GCT TAT ACC CAA ACT GAC TGG TTT CAA	436
Thr Lys Gly Thr Leu Tyr Leu Ala Tyr Thr Gln Thr Asp Trp Phe Gln	
125 130 135 140	
ATT TAC AAT GAC CCC CAA TCC GCT CCC ATG CGA ATG ATG AAT TTC ATG	484
Ile Tyr Asn Asp Pro Gln Ser Ala Pro Met Arg Met Met Asn Phe Met	
145 150 155	
CCT GAA CTC ATT TAT GTT TAT CCT ATC AAT TTT AAA CCT TTT GGG GGT	532
Pro Glu Leu Ile Tyr Val Tyr Pro Ile Asn Phe Lys Pro Phe Gly Gly	
160 165 170	
AAA ATA GGG AAT TTT TCT GAA ATT TGG ATA GGT TGG CAG CAC ATT TCT	580
Lys Ile Gly Asn Phe Ser Glu Ile Trp Ile Gly Trp Gln His Ile Ser	
175 180 185	
AAT GGC GTG GGG GGC GCG CAA TGT TAC CAA CCT TTT AAT AAA GAA GGC	628
Asn Gly Val Gly Gly Ala Gln Cys Tyr Gln Pro Phe Asn Lys Glu Gly	
190 195 200	
AAT CCT GAA AAC CAG TTT CCA GGA CAA CCT GTA ATC GTT AAA GAT TAT	676

```

Phe Ser Val Leu Leu Ile Thr Gly Trp Ile Val Ser Arg Gly Ile Lys
145                      150                      155                      160
Glu Gly Ile Glu Lys Leu Asn Leu Val Leu Met Pro Leu Leu Phe Ala
                      165                      170                      175
Thr Phe Phe Gly Leu Leu Phe Tyr Ala Met Ser Met Asp Ser Phe Ser
                      180                      185                      190
Lys Ala Phe His Phe Met Phe Asp Phe Lys Pro Lys Asp Leu Thr Ser
                      195                      200                      205
Gln Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser Ile
                      210                      215                      220
Gly Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr Gln
225                      230                      235                      240
Asn Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu Ile
                      245                      250                      255
Ser Leu Val Ala Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr Gly
                      260                      265                      270
Ala Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro Val
                      275                      280                      285
Val Phe Gly Gln Met Gly Ala Ile Gly Ile Leu Val Ser Ile Leu Phe
                      290                      295                      300
Leu Leu Ala Leu Ala Phe Ala Gly Ile Thr Ser Thr Val Ala Leu Leu
305                      310                      315                      320
Glu Pro Ser Val Met Tyr Leu Thr Glu Arg Tyr Gln Tyr Ser Arg Phe
                      325                      330                      335
Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val Val Gly Val Val
                      340                      345                      350
Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr Leu Thr Phe Phe
                      355                      360                      365
Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser Ser Thr Ile Ile
                      370                      375                      380
Met Pro Leu Gly Gly Met Ala Thr Phe Ile Phe Met Gly Trp Val Leu
385                      390                      395                      400
Lys Lys Glu Lys Leu Arg Leu Leu Ser Val His Phe Leu Gly Pro Lys
                      405                      410                      415
Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr Pro Leu Ile
                      420                      425                      430
Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
                      435                      440

```

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...1081
- (D) OTHER INFORMATION:

Gly Val Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr Leu
 350 355 360 365

ACT TTC TTT GAA AAA AGT CTT TTT GAT TGG TTG GAT TTT GCA TCA AGC 1155
 Thr Phe Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser Ser
 370 375 380

ACC ATT ATC ATG CCT TTA GGC GGG ATG GCA ACC TTT ATT TTT ATG GGT 1203
 Thr Ile Ile Met Pro Leu Gly Gly Met Ala Thr Phe Ile Phe Met Gly
 385 390 395

TGG GTT TTG AAA AAA GAA AAA TTG CGT CTT TTG AGC GTG CAC TTT TTA 1251
 Trp Val Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Val His Phe Leu
 400 405 410

GGC CCT AAA TTG TTT GCA ACT TGG TAT TTC TTG CTT AAA TAT ATC ACC 1299
 Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr
 415 420 425

CCT TTA ATT GTG TTT TCC ATT TGG TTG AGC AAG ATT TAT TAAAATATTT GG 1350
 Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
 430 435 440

CATGGGAAAA TTTTCTAAAT TAGGCT 1376

(2) INFORMATION FOR SEQ ID NO:1340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala Ala Leu Gly
 1 5 10 15

Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr Met Thr Gly
 20 25 30

Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe Leu Ser Leu
 35 40 45

Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu Gly Gln Ser
 50 55 60

Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp Ile Asn Pro
 65 70 75 80

Lys Lys Arg Trp Lys Tyr Ala Gly Leu Leu Val Ser Gly Pro Leu
 85 90 95

Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu Tyr Tyr Leu
 100 105 110

Val Ser Val Ser Phe Asn Leu Pro Asn Asn Ile Gln Glu Ser Glu Gln
 115 120 125

Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser Ile Gly Leu
 130 135 140

130								135								140							
ATA	GGG	CTT	TTT	AGC	GTT	TTA	TTG	ATA	ACC	GGA	TGG	ATT	GTT	TCT	AGG	483							
Ile	Gly	Leu	Phe	Ser	Val	Leu	Leu	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg								
			145							150				155									
GGG	ATT	AAA	GAA	GGC	ATT	GAA	AAG	CTC	AAT	TTG	GTT	TTA	ATG	CCC	TTA	531							
Gly	Ile	Lys	Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu								
		160						165					170										
CTC	TTT	GCT	ACT	TTT	TTT	GGT	TTG	CTT	TTC	TAT	GCG	ATG	AGC	ATG	GAT	579							
Leu	Phe	Ala	Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp								
		175					180					185											
TCT	TTT	TCT	AAA	GCT	TTT	CAT	TTC	ATG	TTT	GAT	TTC	AAA	CCA	AAA	GAT	627							
Ser	Phe	Ser	Lys	Ala	Phe	His	Phe	Met	Phe	Asp	Phe	Lys	Pro	Lys	Asp								
190						195				200					205								
TTG	ACC	TCT	CAA	GTG	TTC	ACT	TAT	TCC	TTG	GGG	CAG	GTT	TTC	TTT	TCC	675							
Leu	Thr	Ser	Gln	Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser								
				210					215					220									
TTA	AGC	ATC	GGT	TTA	GGG	ATC	AAT	ATC	ACT	TAC	GCT	GCG	GTT	ACG	GAT	723							
Leu	Ser	Ile	Gly	Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp								
			225					230					235										
AAA	ACG	CAG	AAT	TTG	CTT	AAA	AGC	ACT	ATT	TGG	GTG	GTT	TTA	TCA	GGA	771							
Lys	Thr	Gln	Asn	Leu	Leu	Lys	Ser	Thr	Ile	Trp	Val	Val	Leu	Ser	Gly								
		240					245					250											
ATT	CTA	ATT	TCT	CTT	GTG	GCA	GGA	CTT	ATG	ATT	TTC	ACT	TTT	GTG	TTT	819							
Ile	Leu	Ile	Ser	Leu	Val	Ala	Gly	Leu	Met	Ile	Phe	Thr	Phe	Val	Phe								
		255					260					265											
GAA	TAT	GGG	GCG	AAT	GTC	TCA	CAA	GGC	ACA	GGG	TTA	ATC	TTC	ACT	TCT	867							
Glu	Tyr	Gly	Ala	Asn	Val	Ser	Gln	Gly	Thr	Gly	Leu	Ile	Phe	Thr	Ser								
270					275					280					285								
TTA	CCG	GTG	GTT	TTT	GGC	CAA	ATG	GGA	GCG	ATA	GGC	ATT	CTT	GTT	TCG	915							
Leu	Pro	Val	Val	Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Ile	Leu	Val	Ser								
				290					295					300									
ATT	CTT	TTC	TTG	CTC	GCG	CTC	GCT	TTT	GCT	GGC	ATC	ACT	TCT	ACG	GTG	963							
Ile	Leu	Phe	Leu	Leu	Ala	Leu	Ala	Phe	Ala	Gly	Ile	Thr	Ser	Thr	Val								
			305					310					315										
GCT	TTA	TTG	GAG	CCA	AGC	GTG	ATG	TAT	CTT	ACC	GAA	AGG	TAT	CAA	TAC	1011							
Ala	Leu	Leu	Glu	Pro	Ser	Val	Met	Tyr	Leu	Thr	Glu	Arg	Tyr	Gln	Tyr								
		320					325					330											
TCT	CGT	TTT	AAG	GTT	ACT	TGG	GGT	CTT	GTA	GCA	CTA	ATT	TTT	GTG	GTA	1059							
Ser	Arg	Phe	Lys	Val	Thr	Trp	Gly	Leu	Val	Ala	Leu	Ile	Phe	Val	Val								
		335					340					345											
GGC	GTG	GTG	TTG	ATT	TTC	TCG	CTC	CAT	AAG	GAT	TAT	AAA	GAT	TAT	CTC	1107							

260

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1338
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

TGGTAGTTAA GA ATG GGT AAT CAT TTT TCT AAA TTA GGA TTT GTT TTA GCC	51
Met Gly Asn His Phe Ser Lys Leu Gly Phe Val Leu Ala	
1 5 10	
GCA TTA GGA AGC GCG ATA GGT TTA GGG CAT ATC TGG CGT TTC CCC TAC	99
Ala Leu Gly Ser Ala Ile Gly Leu Gly His Ile Trp Arg Phe Pro Tyr	
15 20 25	
ATG ACT GGG GTG AGT GGT GGG GGT GCT TTT GTT TTA TTG TTT TTA TTT	147
Met Thr Gly Val Ser Gly Gly Gly Ala Phe Val Leu Leu Phe Leu Phe	
30 35 40 45	
TTA TCT TTA AGC GTT GGC GCG GCG ATG TTT ATC GCT GAA ATG CTA TTA	195
Leu Ser Leu Ser Val Gly Ala Ala Met Phe Ile Ala Glu Met Leu Leu	
50 55 60	
GGA CAA AGC ACT CAA AAA AAT GTA ACA GAA GCT TTT AAA GAG CTT GAC	243
Gly Gln Ser Thr Gln Lys Asn Val Thr Glu Ala Phe Lys Glu Leu Asp	
65 70 75	
ATT AAC CCC AAA AAA CGC TGG AAA TAC GCA GGG CTT TTG CTT GTT TCT	291
Ile Asn Pro Lys Lys Arg Trp Lys Tyr Ala Gly Leu Leu Leu Val Ser	
80 85 90	
GGG CCA TTA ATA CTG ACT TTT TAC GGC ACG ATT TTA GGT TGG GTG CTT	339
Gly Pro Leu Ile Leu Thr Phe Tyr Gly Thr Ile Leu Gly Trp Val Leu	
95 100 105	
TAT TAT TTG GTG AGT GTT AGT TTT AAT TTG CCT AAC AAT ATC CAA GAA	387
Tyr Tyr Leu Val Ser Val Ser Phe Asn Leu Pro Asn Asn Ile Gln Glu	
110 115 120 125	
TCT GAA CAA ATT TTT ACT CAA ACT TTG CAG TCT ATA GGG CTA CAA TCC	435
Ser Glu Gln Ile Phe Thr Gln Thr Leu Gln Ser Ile Gly Leu Gln Ser	

AAT GCC GTG CCG CCT TTA TTG AGT GTA GCG CTC GCG CAG GCG GTC TTT 824
 Asn Ala Val Pro Pro Leu Leu Ser Val Ala Leu Ala Gln Ala Val Phe
 245 250 255

GAC TTT TTA AAG GGG TAAGATGTTT AACAATAATG ACTTTAAGGA TTACAGAAAA T 880
 Asp Phe Leu Lys Gly
 260

880

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

Met Asp Glu Lys Ala Asn Leu Phe Lys Glu Tyr Leu Arg Leu Leu Asp
 1 5 10 15
 Leu Val Lys Pro Lys Ile Phe Val Phe Glu Asn Val Val Gly Leu Met
 20 25 30
 Ser Met Gln Lys Gly Gln Leu Phe Lys Gln Ile Cys Asn Ala Phe Lys
 35 40 45
 Glu Arg Asp Tyr Ile Leu Glu His Ala Ile Leu Asn Ala Leu Asp Tyr
 50 55 60
 Gly Val Pro Gln Met Arg Glu Arg Val Ile Leu Val Gly Val Leu Lys
 65 70 75 80
 Ser Phe Lys Gln Lys Phe Tyr Phe Pro Lys Pro Ile Lys Thr His Phe
 85 90 95
 Ser Leu Lys Asp Ala Leu Gly Asp Leu Pro Pro Ile Gln Ser Gly Glu
 100 105 110
 Asn Gly Asp Ala Leu Gly Tyr Leu Lys Asn Ala Asp Asn Val Phe Leu
 115 120 125
 Glu Phe Val Arg Asn Ser Lys Glu Leu Ser Glu His Ser Ser Pro Lys
 130 135 140
 Asn Asn Glu Lys Leu Ile Lys Ile Met Gln Thr Leu Lys Asp Gly Gln
 145 150 155 160
 Ser Lys Asp Asp Leu Pro Glu Ser Leu Arg Pro Lys Ser Gly Tyr Ile
 165 170 175
 Asn Thr Tyr Ala Lys Met Trp Trp Glu Lys Pro Ala Pro Thr Ile Thr
 180 185 190
 Arg Asn Phe Ser Thr Pro Ser Ser Arg Cys Ile His Pro Arg Asp
 195 200 205
 Ser Arg Ala Leu Ser Ile Arg Glu Gly Ala Arg Leu Gln Ser Phe Pro
 210 215 220
 Asp Asn Tyr Lys Phe Cys Gly Ser Gly Ser Ala Lys Arg Leu Gln Ile
 225 230 235 240
 Gly Asn Ala Val Pro Pro Leu Leu Ser Val Ala Leu Ala Gln Ala Val
 245 250 255
 Phe Asp Phe Leu Lys Gly

GTA AAA CCA AAA ATA TTT GTT TTT GAA AAT GTG GTG GGT TTA ATG TCT	152
Val Lys Pro Lys Ile Phe Val Phe Glu Asn Val Val Gly Leu Met Ser	
20 25 30	
ATG CAA AAA GGG CAA TTA TTC AAA CAA ATT TGT AAC GCT TTT AAA GAG	200
Met Gln Lys Gly Gln Leu Phe Lys Gln Ile Cys Asn Ala Phe Lys Glu	
35 40 45	
AGA GAT TAT ATT TTA GAG CAT GCC ATT TTG AAC GCC CTA GAT TAT GGT	248
Arg Asp Tyr Ile Leu Glu His Ala Ile Leu Asn Ala Leu Asp Tyr Gly	
50 55 60 65	
GTG CCT CAA ATG AGA GAA CGA GTG ATT TTA GTG GGC GTG CTT AAA AGC	296
Val Pro Gln Met Arg Glu Arg Val Ile Leu Val Gly Val Leu Lys Ser	
70 75 80	
TTT AAA CAA AAA TTT TAC TTC CCT AAA CCC ATA AAA ACG CAT TTT TCT	344
Phe Lys Gln Lys Phe Tyr Phe Pro Lys Pro Ile Lys Thr His Phe Ser	
85 90 95	
CTG AAA GAC GCT TTA GGG GAT TTA CCA CCC ATT CAA AGC GGT GAA AAT	392
Leu Lys Asp Ala Leu Gly Asp Leu Pro Pro Ile Gln Ser Gly Glu Asn	
100 105 110	
GGT GAT GCT TTA GGT TAT CTT AAA AAT GCG GAT AAT GTT TTT TTG GAA	440
Gly Asp Ala Leu Gly Tyr Leu Lys Asn Ala Asp Asn Val Phe Leu Glu	
115 120 125	
TTT GTG CGA AAT TCT AAA GAA TTA AGC GAA CAT AGC AGT CCT AAA AAC	488
Phe Val Arg Asn Ser Lys Glu Leu Ser Glu His Ser Ser Pro Lys Asn	
130 135 140 145	
AAT GAA AAA CTG ATA AAA ATC ATG CAA ACG CTA AAA GAC GGA CAG AGT	536
Asn Glu Lys Leu Ile Lys Ile Met Gln Thr Leu Lys Asp Gly Gln Ser	
150 155 160	
AAA GAT GAT TTG CCA GAA AGT CTG CGT CCC AAA AGT GGT TAT ATT AAT	584
Lys Asp Asp Leu Pro Glu Ser Leu Arg Pro Lys Ser Gly Tyr Ile Asn	
165 170 175	
ACC TAT GCC AAA ATG TGG TGG GAA AAA CCA GCC CCC ACC ATT ACA AGA	632
Thr Tyr Ala Lys Met Trp Trp Glu Lys Pro Ala Pro Thr Ile Thr Arg	
180 185 190	
AAT TTT TCT ACC CCA AGC AGT TCT AGG TGT ATC CAT CCA AGA GAC TCT	680
Asn Phe Ser Thr Pro Ser Ser Ser Arg Cys Ile His Pro Arg Asp Ser	
195 200 205	
AGA GCG TTA AGC ATT AGA GAG GGG GCA AGA TTG CAA AGC TTT CCT GAT	728
Arg Ala Leu Ser Ile Arg Glu Gly Ala Arg Leu Gln Ser Phe Pro Asp	
210 215 220 225	
AAT TAT AAA TTC TGT GGG AGT GGT AGC GCT AAA AGA TTG CAA ATT GGC	776
Asn Tyr Lys Phe Cys Gly Ser Gly Ser Ala Lys Arg Leu Gln Ile Gly	
230 235 240	

385		390		395		400									
Leu	Val	Ile	Asp	Thr	Pro	Gln	Asp	Phe	Ser	Gly	Ala	Ile	Ile	Glu	Arg
			405						410					415	
Leu	Gly	Lys	Arg	Lys	Ala	Glu	Met	Lys	Ala	Met	Asn	Pro	Met	Ser	Asp
			420						425					430	
Gly	Tyr	Thr	Arg	Leu	Glu	Phe	Glu	Ile	Pro	Ala	Arg	Gly	Leu	Ile	Gly
		435					440					445			
Tyr	Arg	Ser	Glu	Phe	Leu	Thr	Asp	Thr	Lys	Gly	Glu	Gly	Val	Met	Asn
	450					455					460				
His	Ser	Phe	Leu	Glu	Phe	Arg	Pro	Phe	Ser	Gly	Ser	Val	Glu	Ser	Arg
465					470					475				480	
Lys	Asn	Gly	Ala	Leu	Ile	Ser	Met	Glu	Asn	Gly	Glu	Ala	Thr	Ala	Phe
			485						490					495	
Ser	Leu	Phe	Asn	Ile	Gln	Glu	Arg	Gly	Thr	Leu	Phe	Ile	Asn	Pro	Gln
		500						505					510		
Thr	Lys	Val	Tyr	Val	Gly	Met	Val	Ile	Gly	Glu	His	Ser	Arg	Asp	Asn
		515					520					525			
Asp	Leu	Asp	Val	Asn	Pro	Ile	Lys	Ser	Lys	His	Leu	Thr	Asn	Met	Arg
	530					535					540				
Ala	Ser	Gly	Ser	Asp	Asp	Ala	Ile	Lys	Leu	Thr	Pro	Pro	Arg	Thr	Met
545					550					555				560	
Val	Leu	Glu	Arg	Ala	Leu	Glu	Trp	Ile	Glu	Glu	Asp	Glu	Ile	Leu	Glu
			565					570					575		
Val	Thr	Pro	Leu	Asn	Leu	Arg	Ile	Arg	Lys	Lys	Ile	Leu	Asp	Pro	Asn
		580						585					590		
Met	Arg	Lys	Arg	Ala	Lys	Lys									
		595													

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 880 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 54...839
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

TTCTACTAGG	CGGACCACCA	TGCCAGAGCT	ATTCTACCCT	TGGCAAAAGA	AAA	ATG	56
						Met	
						1	
GAT	GAA	AAA	GCG	AAT	CTG	TTT	AAA
GAA	TAT	TTG	CGG	CTT	TTA	GAT	TTA
Asp	Glu	Lys	Ala	Asn	Leu	Phe	Lys
		5			10		15
							104

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

```

Met Lys Asn Ile Arg Asn Ile Ala Val Ile Ala His Val Asp His Gly
 1           5           10           15
Lys Thr Thr Leu Val Asp Gly Leu Leu Ser Gln Ser Gly Thr Phe Ser
      20           25           30
Glu Arg Glu Lys Val Asp Glu Arg Val Met Asp Ser Asn Asp Leu Glu
      35           40           45
Arg Glu Arg Gly Ile Thr Ile Leu Ser Lys Asn Thr Ala Ile Tyr Tyr
      50           55           60
Lys Asp Thr Lys Ile Asn Ile Ile Asp Thr Pro Gly His Ala Asp Phe
65           70           75           80
Gly Gly Glu Val Glu Arg Val Leu Lys Met Val Asp Gly Val Leu Leu
      85           90           95
Leu Val Asp Ala Gln Glu Gly Val Met Pro Gln Thr Lys Phe Val Val
      100          105          110
Lys Lys Ala Leu Ser Phe Gly Ile Cys Pro Ile Val Val Val Asn Lys
      115          120          125
Ile Asp Lys Pro Ala Ala Glu Pro Asp Arg Val Val Asp Glu Val Phe
      130          135          140
Asp Leu Phe Val Ala Met Gly Ala Ser Asp Lys Gln Leu Asp Phe Pro
145          150          155          160
Val Val Tyr Ala Ala Ala Arg Asp Gly Tyr Ala Met Lys Ser Leu Asp
      165          170          175
Asp Glu Lys Lys Asn Leu Glu Pro Leu Phe Glu Thr Ile Leu Glu His
      180          185          190
Val Pro Ser Pro Ser Gly Ser Val Asp Glu Pro Leu Gln Met Gln Ile
      195          200          205
Phe Thr Leu Asp Tyr Asp Asn Tyr Val Gly Lys Ile Gly Ile Ala Arg
      210          215          220
Val Phe Asn Gly Ser Val Lys Lys Asn Glu Ser Val Leu Leu Met Lys
225          230          235          240
Ser Asp Gly Ser Lys Glu Asn Gly Arg Ile Thr Lys Leu Ile Gly Phe
      245          250          255
Leu Gly Leu Ala Arg Thr Glu Ile Glu Asn Ala Tyr Ala Gly Asp Ile
      260          265          270
Val Ala Ile Ala Gly Phe Asn Ala Met Asp Val Gly Asp Ser Val Val
      275          280          285
Asp Pro Ala Asn Pro Met Pro Leu Asp Pro Met His Leu Glu Glu Pro
      290          295          300
Thr Met Ser Val Tyr Phe Ala Val Asn Asp Ser Pro Leu Ala Gly Leu
305          310          315          320
Glu Gly Lys His Val Thr Ala Asn Lys Leu Lys Asp Arg Leu Leu Lys
      325          330          335
Glu Met Gln Thr Asn Ile Ala Met Lys Cys Glu Glu Met Gly Glu Gly
      340          345          350
Lys Phe Lys Val Ser Gly Arg Gly Glu Leu Gln Ile Thr Ile Leu Ala
      355          360          365
Glu Asn Leu Arg Arg Glu Gly Phe Glu Phe Ser Ile Ser Arg Pro Glu
      370          375          380
Val Ile Ile Lys Glu Glu Asn Gly Val Lys Cys Glu Pro Phe Glu His

```

AAA GCT GAG ATG AAA GCG ATG AAT CCC ATG AGT GAT GGC TAT ACA AGA	1353
Lys Ala Glu Met Lys Ala Met Asn Pro Met Ser Asp Gly Tyr Thr Arg	
425 430 435	
TTA GAA TTT GAA ATT CCT GCA AGA GGG CTT ATC GGT TAT AGG AGC GAG	1401
Leu Glu Phe Glu Ile Pro Ala Arg Gly Leu Ile Gly Tyr Arg Ser Glu	
440 445 450	
TTT TTA ACC GAC ACC AAG GGC GAA GGC GTG ATG AAT CAT AGC TTT TTA	1449
Phe Leu Thr Asp Thr Lys Gly Glu Gly Val Met Asn His Ser Phe Leu	
455 460 465	
GAA TTC CGC CCT TTC AGC GGG AGC GTG GAA TCG CGC AAA AAT GGG GCG	1497
Glu Phe Arg Pro Phe Ser Gly Ser Val Glu Ser Arg Lys Asn Gly Ala	
470 475 480	
CTA ATC AGC ATG GAA AAT GGC GAA GCG ACC GCT TTT TCC CTT TTC AAT	1545
Leu Ile Ser Met Glu Asn Gly Glu Ala Thr Ala Phe Ser Leu Phe Asn	
485 490 495 500	
ATC CAA GAA AGA GGC ACG CTT TTT ATC AAC CCC CAA ACG AAG GTT TAT	1593
Ile Gln Glu Arg Gly Thr Leu Phe Ile Asn Pro Gln Thr Lys Val Tyr	
505 510 515	
GTG GGC ATG GTC ATT GGC GAG CAC AGC CGG GAT AAT GAT TTA GAT GTC	1641
Val Gly Met Val Ile Gly Glu His Ser Arg Asp Asn Asp Leu Asp Val	
520 525 530	
AAT CCT ATT AAA TCC AAG CAT TTA ACC AAC ATG AGA GCG AGC GGG AGC	1689
Asn Pro Ile Lys Ser Lys His Leu Thr Asn Met Arg Ala Ser Gly Ser	
535 540 545	
GAT GAT GCG ATC AAA CTC ACC CCG CCT AGG ACT ATG GTG TTA GAA AGA	1737
Asp Asp Ala Ile Lys Leu Thr Pro Pro Arg Thr Met Val Leu Glu Arg	
550 555 560	
GCG TTA GAA TGG ATT GAA GAA GAT GAG ATT TTG GAA GTT ACC CCC TTG	1785
Ala Leu Glu Trp Ile Glu Glu Asp Glu Ile Leu Glu Val Thr Pro Leu	
565 570 575 580	
AAT TTA AGG ATC AGG AAA AAG ATT TTA GAC CCT AAC ATG AGG AAA AGG	1833
Asn Leu Arg Ile Arg Lys Lys Ile Leu Asp Pro Asn Met Arg Lys Arg	
585 590 595	
GCG AAA AAA TAAATAGAAT TTTTGTGAAT GCATGCCAAT TTATTCAACC AA	1884
Ala Lys Lys	

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

Ser Gly Ser Val Asp Glu Pro Leu Gln Met Gln Ile Phe Thr Leu Asp	
200 205 210	
TAT GAC AAT TAT GTG GGC AAA ATC GGT ATC GCT AGG GTG TTT AAT GGC	729
Tyr Asp Asn Tyr Val Gly Lys Ile Gly Ile Ala Arg Val Phe Asn Gly	
215 220 225	
TCG GTT AAA AAG AAT GAA AGC GTG CTG TTG ATG AAA AGC GAT GGG AGT	777
Ser Val Lys Lys Asn Glu Ser Val Leu Leu Met Lys Ser Asp Gly Ser	
230 235 240	
AAA GAA AAT GGC CGT ATC ACT AAG CTT ATA GGT TTT TTA GGG CTG GCT	825
Lys Glu Asn Gly Arg Ile Thr Lys Leu Ile Gly Phe Leu Gly Leu Ala	
245 250 255 260	
AGG ACT GAG ATT GAA AAC GCT TAT GCG GGC GAT ATT GTA GCG ATT GCC	873
Arg Thr Glu Ile Glu Asn Ala Tyr Ala Gly Asp Ile Val Ala Ile Ala	
265 270 275	
GGG TTT AAT GCA ATG GAT GTG GGC GAT AGC GTC GTT GAT CCT GCT AAC	921
Gly Phe Asn Ala Met Asp Val Gly Asp Ser Val Val Asp Pro Ala Asn	
280 285 290	
CCC ATG CCT TTA GAT CCC ATG CAT TTA GAA GAG CCT ACG ATG AGC GTG	969
Pro Met Pro Leu Asp Pro Met His Leu Glu Glu Pro Thr Met Ser Val	
295 300 305	
TAT TTT GCT GTC AAT GAT TCA CCC TTA GCC GGG TTA GAA GGA AAG CAT	1017
Tyr Phe Ala Val Asn Asp Ser Pro Leu Ala Gly Leu Glu Gly Lys His	
310 315 320	
GTT ACT GCT AAT AAA TTG AAA GAC AGG CTC TTA AAA GAA ATG CAA ACC	1065
Val Thr Ala Asn Lys Leu Lys Asp Arg Leu Leu Lys Glu Met Gln Thr	
325 330 335 340	
AAT ATC GCT ATG AAA TGC GAA GAA ATG GGC GAG GGC AAG TTT AAA GTG	1113
Asn Ile Ala Met Lys Cys Glu Glu Met Gly Glu Gly Lys Phe Lys Val	
345 350 355	
AGT GGG CGT GGG GAA TTG CAA ATC ACT ATT TTA GCT GAA AAC TTG CGC	1161
Ser Gly Arg Gly Glu Leu Gln Ile Thr Ile Leu Ala Glu Asn Leu Arg	
360 365 370	
CGT GAA GGG TTT GAA TTT AGC ATT TCA CGC CCT GAA GTC ATC ATT AAA	1209
Arg Glu Gly Phe Glu Phe Ser Ile Ser Arg Pro Glu Val Ile Ile Lys	
375 380 385	
GAA GAA AAT GGC GTT AAA TGC GAG CCT TTT GAG CAT TTA GTG ATT GAC	1257
Glu Glu Asn Gly Val Lys Cys Glu Pro Phe Glu His Leu Val Ile Asp	
390 395 400	
ACG CCC CAA GAT TTT AGT GGG GCT ATC ATT GAG AGA TTG GGC AAA AGA	1305
Thr Pro Gln Asp Phe Ser Gly Ala Ile Ile Glu Arg Leu Gly Lys Arg	
405 410 415 420	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

TATTGTGTTA TACTTCTAAT TTCAATTTTG CTTGTTAGGA CATTT ATG AAA AAT ATT	57
Met Lys Asn Ile	
1	
AGA AAT ATC GCT GTA ATC GCG CAT GTT GAT CAT GGG AAA ACC ACT CTA	105
Arg Asn Ile Ala Val Ile Ala His Val Asp His Gly Lys Thr Thr Leu	
5 10 15 20	
GTA GAT GGC TTA CTT TCT CAA TCT GGC ACA TTT AGT GAG AGG GAA AAA	153
Val Asp Gly Leu Leu Ser Gln Ser Gly Thr Phe Ser Glu Arg Glu Lys	
25 30 35	
GTG GAT GAA AGG GTG ATG GAT AGC AAT GAT TTG GAA AGA GAA AGA GGG	201
Val Asp Glu Arg Val Met Asp Ser Asn Asp Leu Glu Arg Glu Arg Gly	
40 45 50	
ATT ACT ATC CTG TCT AAA AAC ACC GCT ATT TAT TAC AAA GAC ACT AAA	249
Ile Thr Ile Leu Ser Lys Asn Thr Ala Ile Tyr Tyr Lys Asp Thr Lys	
55 60 65	
ATC AAT ATC ATT GAC ACT CCC GGG CAT GCT GAT TTT GGG GGC GAA GTG	297
Ile Asn Ile Ile Asp Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val	
70 75 80	
GAG CGC GTT TTA AAA ATG GTG GAT GGG GTG TTG CTT TTA GTG GAC GCT	345
Glu Arg Val Leu Lys Met Val Asp Gly Val Leu Leu Leu Val Asp Ala	
85 90 95 100	
CAA GAA GGG GTC ATG CCT CAA ACT AAA TTC GTG GTT AAA AAG GCT TTG	393
Gln Glu Gly Val Met Pro Gln Thr Lys Phe Val Val Lys Lys Ala Leu	
105 110 115	
AGT TTT GGG ATT TGC CCT ATT GTG GTG GTG AAT AAA ATT GAT AAG CCT	441
Ser Phe Gly Ile Cys Pro Ile Val Val Val Asn Lys Ile Asp Lys Pro	
120 125 130	
GCC GCT GAA CCG GAC AGA GTG GTG GAT GAA GTT TTT GAC TTG TTC GTA	489
Ala Ala Glu Pro Asp Arg Val Val Asp Glu Val Phe Asp Leu Phe Val	
135 140 145	
GCC ATG GGG GCT AGC GAT AAG CAA TTG GAT TTC CCT GTG GTG TAT GCC	537
Ala Met Gly Ala Ser Asp Lys Gln Leu Asp Phe Pro Val Val Tyr Ala	
150 155 160	
GCC GCA CGA GAT GGC TAT GCG ATG AAA AGT TTA GAC GAT GAA AAG AAA	585
Ala Ala Arg Asp Gly Tyr Ala Met Lys Ser Leu Asp Asp Glu Lys Lys	
165 170 175 180	
AAT TTA GAG CCT TTG TTT GAA ACG ATT TTA GAG CAT GTG CCA AGC CCT	633
Asn Leu Glu Pro Leu Phe Glu Thr Ile Leu Glu His Val Pro Ser Pro	
185 190 195	
AGC GGG AGC GTT GAT GAG CCT TTG CAA ATG CAA ATT TTC ACG CTT GAT	681

	260		265		270
Glu Met Ala	Leu Lys Phe His Ile Arg Ser Leu Ile Asp Phe Asp Lys				
275		280		285	
Pro Phe Lys	Asn Leu Met Thr Lys Ala Val Gly Leu Ala Leu Lys Lys				
290		295		300	
Thr Pro Asn	Lys Asp Gln Lys Ile Ser Cys Phe Tyr Gln Asn Ser Lys				
305		310		315	
Phe Lys Arg	Ser Pro Ser Ser Phe Phe Asn Asn Pro Lys Lys Ile Phe				
	325		330		335
Asn Ile His	Cys Ser Ser Lys Glu Asn Lys Ile Leu Asp His Leu Phe				
	340		345		350
Ser Leu Pro	His Met Thr Leu Lys Asn Asn Ala His Phe Ala Leu Gly				
	355		360		365
Ile Val Thr	Gly Asn Asn Lys Glu Lys Leu His Pro Lys Gln Glu Lys				
	370		375		380
Asn Thr Ile	Pro Ile Phe Arg Gly Ser Asp Ile Leu Lys Asp Gly Leu				
385		390		395	
Lys Ala Pro	Ser Gln Phe Ile Asn Ala Gly Leu Lys Asp Cys Gln Gln				
	405		410		415
Val Ala Pro	Leu Ser Leu Tyr Gln Ala Arg Glu Lys Ile Val Tyr Lys				
	420		425		430
Phe Ile Ser	Lys Leu Val Phe Phe Tyr Asp Asn Lys Gln Arg Leu				
	435		440		445
Phe Leu Asn	Ser Ala Asn Met Phe Val Leu Lys Glu Asn Phe Pro Ile				
	450		455		460
Asn Ala His	Ala Leu Lys Glu Leu Leu Asn Ser Asp Leu Met Gln Phe				
465		470		475	
Ile Phe Glu	Ser Leu Phe Lys Thr His Lys Ile Leu Arg Lys Asp Leu				
	485		490		495
Glu Cys Leu	Pro Leu Phe Val Gln Phe Ile Asn Asp Asn Phe Asp Glu				
	500		505		510
Lys Phe Tyr	Leu Lys Asn Leu Gly Ile Glu Lys Lys Asp Pro Lys His				
	515		520		525
Phe Thr Ile	Arg Lys Asn His Ala Cys Cys Leu Ser Phe Gly Phe Arg				
	530		535		540
Gly					
545					

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1884 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...1842
- (D) OTHER INFORMATION:

GAC CCT AAA CAT TTC ACC ATC AGG AAA AAT CAT GCA TGT TGC TTG TCT 1633
 Asp Pro Lys His Phe Thr Ile Arg Lys Asn His Ala Cys Cys Leu Ser
 525 530 535 540

TTT GGC TTT AGG GGA TAATCTCATC ACGCTTAGCC TTTTAAAAGA AATCGCTTTC A 1689
 Phe Gly Phe Arg Gly
 545

AACAGCAA 1697

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

Met Pro Ser Asn Ala Leu Leu Ile Glu Glu Ile Thr His Leu Ile Asn
 1 5 10 15
 Val Ser His Ser Ser Val His Asn Trp Ile Lys Thr Asn Leu Leu Glu
 20 25 30
 Lys Leu Glu Ile Asp His Lys Ile Tyr Val Lys Thr Ser Ser Phe Leu
 35 40 45
 Asp Phe Cys Arg Asn His Leu Gly Lys Asn Lys Leu Asn Lys Tyr Ala
 50 55 60
 Asn Lys Ser Leu Lys Gly Val His Asn His Gln Glu Leu Ile Leu Lys
 65 70 75 80
 Tyr Leu Glu Ile Leu Glu Asn Ser Ser Asp Leu Glu Lys Leu Gly Ser
 85 90 95
 Tyr Tyr Glu Glu Glu Leu Ser Asn Ala Thr Arg Asn Leu Glu Gly Ile
 100 105 110
 Tyr Tyr Thr Pro Asn Arg Ile Val Glu Gln Leu Phe Thr Leu Pro Lys
 115 120 125
 Asp Phe Asp Val Ser Gln Ala Ile Phe Cys Asp Pro Ala Val Gly Ser
 130 135 140
 Gly Asn Phe Ile Met His Ala Leu Lys Leu Gly Phe Lys Val Glu Asn
 145 150 155 160
 Ile Tyr Gly Tyr Asp Thr Asp Ala Phe Ala Val Ala Leu Thr Lys Lys
 165 170 175
 Arg Ile Lys Glu Arg Tyr His Leu Asp Cys Leu Asn Ile Val Gln Lys
 180 185 190
 Asp Phe Leu Asn Leu Lys His Thr Pro Gln Phe Asp Cys Ile Phe Thr
 195 200 205
 Asn Pro Pro Trp Gly Lys Lys Tyr Asn Gln Asn Gln Lys Glu Asn Phe
 210 215 220
 Lys Gln Gln Phe Asn Leu Ser Gln Ser Leu Asp Ser Ala Ser Leu Phe
 225 230 235 240
 Phe Ile Ala Ser Leu Asn Cys Leu Lys Glu Asn Ala His Leu Gly Leu
 245 250 255
 Leu Leu Pro Glu Ser Cys Leu Asn Ile Asp Ala Phe Lys Lys Met Arg

Ala	Leu	Lys	Lys	Thr	Pro	Asn	Lys	Asp	Gln	Lys	Ile	Ser	Cys	Phe	Tyr	
				305					310					315		
CAA	AAT	AGC	AAG	TTC	AAA	CGC	TCG	CCC	TCT	TCT	TTT	TTT	AAC	AA	CCT	1009
Gln	Asn	Ser	Lys	Phe	Lys	Arg	Ser	Pro	Ser	Ser	Phe	Phe	Asn	Asn	Pro	
			320					325					330			
AAA	AAG	ATT	TTT	AAT	ATC	CAT	TGC	TCT	AGC	AAA	GAA	AAT	AAA	ATT	TTA	1057
Lys	Lys	Ile	Phe	Asn	Ile	His	Cys	Ser	Ser	Lys	Glu	Asn	Lys	Ile	Leu	
		335					340					345				
GAC	CAC	CTT	TTT	TCC	CTC	CCT	CAT	ATG	ACT	TTA	AAA	AAT	AAC	GCT	CAT	1105
Asp	His	Leu	Phe	Ser	Leu	Pro	His	Met	Thr	Leu	Lys	Asn	Asn	Ala	His	
	350					355					360					
TTT	GCT	TTA	GGG	ATT	GTT	ACA	GGC	AAC	AAT	AAA	GAA	AAA	TTA	CAC	CCC	1153
Phe	Ala	Leu	Gly	Ile	Val	Thr	Gly	Asn	Asn	Lys	Glu	Lys	Leu	His	Pro	
365					370					375					380	
AAA	CAA	GAA	AAA	AAT	ACC	ATT	CCC	ATT	TTT	AGG	GGT	TCA	GAT	ATT	TTA	1201
Lys	Gln	Glu	Lys	Asn	Thr	Ile	Pro	Ile	Phe	Arg	Gly	Ser	Asp	Ile	Leu	
				385					390					395		
AAA	GAC	GGA	TTA	AAA	GCC	CCT	AGC	CAA	TTC	ATT	AAC	GCT	GGT	TTA	AAA	1249
Lys	Asp	Gly	Leu	Lys	Ala	Pro	Ser	Gln	Phe	Ile	Asn	Ala	Gly	Leu	Lys	
		400						405				410				
GAC	TGC	CAG	CAA	GTC	GCC	CCC	TTA	AGC	CTT	TAT	CAA	GCT	AGA	GAA	AAA	1297
Asp	Cys	Gln	Gln	Val	Ala	Pro	Leu	Ser	Leu	Tyr	Gln	Ala	Arg	Glu	Lys	
		415					420					425				
ATC	GTG	TAT	AAA	TTC	ATT	TCT	TCA	AAG	CTT	GTC	TTT	TTT	TAT	GAC	AAT	1345
Ile	Val	Tyr	Lys	Phe	Ile	Ser	Ser	Lys	Leu	Val	Phe	Phe	Tyr	Asp	Asn	
	430					435					440					
AAG	CAA	CGC	CTT	TTT	TTA	AAC	AGC	GCG	AAC	ATG	TTT	GTT	TTA	AAA	GAA	1393
Lys	Gln	Arg	Leu	Phe	Leu	Asn	Ser	Ala	Asn	Met	Phe	Val	Leu	Lys	Glu	
445					450				455					460		
AAT	TTC	CCT	ATC	AAC	GCT	CAT	GCA	TTA	AAA	GAA	TTG	TTA	AAC	AGC	GAT	1441
Asn	Phe	Pro	Ile	Asn	Ala	His	Ala	Leu	Lys	Glu	Leu	Leu	Asn	Ser	Asp	
				465					470					475		
TTA	ATG	CAA	TTC	ATT	TTT	GAA	TCG	CTT	TTT	AAA	ACG	CAT	AAA	ATC	TTA	1489
Leu	Met	Gln	Phe	Ile	Phe	Glu	Ser	Leu	Phe	Lys	Thr	His	Lys	Ile	Leu	
			480					485					490			
AGA	AAA	GAT	TTG	GAA	TGT	TTG	CCC	CTA	TTT	GTG	CAA	TTT	ATT	AAC	GAT	1537
Arg	Lys	Asp	Leu	Glu	Cys	Leu	Pro	Leu	Phe	Val	Gln	Phe	Ile	Asn	Asp	
		495					500					505				
AAT	TTT	GAT	GAA	AAA	TTT	TAT	TTA	AAA	AAT	TTA	GGG	ATA	GAA	AAA	AAA	1585
Asn	Phe	Asp	Glu	Lys	Phe	Tyr	Leu	Lys	Asn	Leu	Gly	Ile	Glu	Lys	Lys	
	510					515					520					

80						85					90					
AAG	TTG	GGT	TCT	TAT	TAT	GAA	GAA	GAG	CTT	TCT	AAC	GCC	ACC	AGA	AAT	337
Lys	Leu	Gly	Ser	Tyr	Tyr	Glu	Glu	Glu	Leu	Ser	Asn	Ala	Thr	Arg	Asn	
		95					100					105				
TTA	GAA	GGC	ATT	TAC	TAC	ACT	CCT	AAC	AGG	ATA	GTA	GAA	CAA	CTT	TTC	385
Leu	Glu	Gly	Ile	Tyr	Tyr	Thr	Pro	Asn	Arg	Ile	Val	Glu	Gln	Leu	Phe	
	110					115					120					
ACC	CTC	CCT	AAA	GAT	TTT	GAT	GTC	TCT	CAA	GCG	ATT	TTT	TGC	GAT	CCG	433
Thr	Leu	Pro	Lys	Asp	Phe	Asp	Val	Ser	Gln	Ala	Ile	Phe	Cys	Asp	Pro	
125					130					135					140	
GCT	GTG	GGG	AGT	GGG	AAT	TTT	ATC	ATG	CAT	GCT	TTA	AAA	CTG	GGT	TTT	481
Ala	Val	Gly	Ser	Gly	Asn	Phe	Ile	Met	His	Ala	Leu	Lys	Leu	Gly	Phe	
				145					150					155		
AAG	GTT	GAA	AAC	ATT	TAT	GGC	TAT	GAT	ACG	GAC	GCT	TTT	GCT	GTC	GCT	529
Lys	Val	Glu	Asn	Ile	Tyr	Gly	Tyr	Asp	Thr	Asp	Ala	Phe	Ala	Val	Ala	
			160					165					170			
TTG	ACT	AAA	AAG	CGT	ATT	AAA	GAG	CGT	TAT	CAT	TTA	GAT	TGC	CTT	AAT	577
Leu	Thr	Lys	Lys	Arg	Ile	Lys	Glu	Arg	Tyr	His	Leu	Asp	Cys	Leu	Asn	
		175					180					185				
ATT	GTG	CAA	AAA	GAT	TTT	TTA	AAT	TTA	AAA	CAC	ACC	CCG	CAA	TTT	GAT	625
Ile	Val	Gln	Lys	Asp	Phe	Leu	Asn	Leu	Lys	His	Thr	Pro	Gln	Phe	Asp	
	190					195					200					
TGC	ATT	TTC	ACT	AAC	CCG	CCA	TGG	GGC	AAG	AAA	TAC	AAT	CAA	AAC	CAA	673
Cys	Ile	Phe	Thr	Asn	Pro	Pro	Trp	Gly	Lys	Lys	Tyr	Asn	Gln	Asn	Gln	
205					210					215					220	
AAA	GAA	AAT	TTT	AAA	CAG	CAA	TTC	AAC	CTC	TCT	CAA	AGC	CTA	GAT	AGC	721
Lys	Glu	Asn	Phe	Lys	Gln	Gln	Phe	Asn	Leu	Ser	Gln	Ser	Leu	Asp	Ser	
				225					230					235		
GCG	TCG	CTC	TTT	TTT	ATA	GCG	AGT	TTG	AAT	TGT	TTA	AAA	GAA	AAC	GCT	769
Ala	Ser	Leu	Phe	Phe	Ile	Ala	Ser	Leu	Asn	Cys	Leu	Lys	Glu	Asn	Ala	
			240					245					250			
CAT	TTG	GGG	TTA	TTA	TTA	CCC	GAA	AGT	TGT	TTG	AAT	ATT	GAT	GCG	TTT	817
His	Leu	Gly	Leu	Leu	Leu	Pro	Glu	Ser	Cys	Leu	Asn	Ile	Asp	Ala	Phe	
		255					260					265				
AAA	AAA	ATG	CGA	GAA	ATG	GCT	TTA	AAG	TTT	CAC	ATT	AGA	AGC	CTG	ATT	865
Lys	Lys	Met	Arg	Glu	Met	Ala	Leu	Lys	Phe	His	Ile	Arg	Ser	Leu	Ile	
	270					275					280					
GAT	TTT	GAC	AAA	CCT	TTT	AAA	AAT	CTA	ATG	ACT	AAG	GCT	GTG	GGT	TTG	913
Asp	Phe	Asp	Lys	Pro	Phe	Lys	Asn	Leu	Met	Thr	Lys	Ala	Val	Gly	Leu	
285					290					295					300	
GCG	CTT	AAA	AAA	ACC	CCT	AAT	AAG	GAT	CAA	AAA	ATC	TCA	TGC	TTT	TAT	961

65		70		75		80									
Pro	Asn	Asn	Ile	Gly	Ser	Val	Val	Gln	Val	Lys	Leu	Pro	Gly	Ile	Ile
		85		90		95									
Gln	Ile	Leu	Ile	Lys	Glu	Lys	Asn	Glu	Asn	Ala	Val	Leu	Phe	Asn	Arg
		100		105		110									
Cys	Asp	Ser	Leu	Glu	Leu	Phe	Gln	Lys	Glu	Asp	Ser	Ile	Ala	Gln	Glu
		115		120		125									
Pro	Lys	Lys	Asp	Glu	Arg	Glu	Ser	Lys	Glu	Trp	Leu	Asp	Ser	Lys	Glu
		130		135		140									
Ala	Leu	Phe	Ser	Asn	Ser	Lys	Asn	Arg	Ala	Ile	Leu	Glu	Asn	Leu	His
145				150		155								160	
Lys	Ser														

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 14...1648
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

TTTAGGGGGG TAA ATG CCT TCA AAC GCT CTT TTG ATT GAA GAA ATC ACT	49
Met Pro Ser Asn Ala Leu Leu Ile Glu Glu Ile Thr	
1 5 10	
CAT TTA ATC AAT GTT TCT CAT AGT AGC GTG CAT AAT TGG ATC AAA ACC	97
His Leu Ile Asn Val Ser His Ser Ser Val His Asn Trp Ile Lys Thr	
15 20 25	
AAT CTT TTA GAG AAA CTA GAA ATT GAT CAT AAA ATT TAT GTG AAA ACG	145
Asn Leu Leu Glu Lys Leu Glu Ile Asp His Lys Ile Tyr Val Lys Thr	
30 35 40	
AGT TCT TTT TTA GAT TTT TGC CGC AAC CAT TTA GGG AAA AAC AAG CTT	193
Ser Ser Phe Leu Asp Phe Cys Arg Asn His Leu Gly Lys Asn Lys Leu	
45 50 55 60	
AAC AAA TAC GCT AAC AAA TCC TTA AAA GGC GTG CAT AAC CAT CAA GAA	241
Asn Lys Tyr Ala Asn Lys Ser Leu Lys Gly Val His Asn His Gln Glu	
65 70 75	
TTG ATT TTA AAA TAC CTA GAA ATA TTA GAA AAT AGC TCT GAT CTA GAA	289
Leu Ile Leu Lys Tyr Leu Glu Ile Leu Glu Asn Ser Ser Asp Leu Glu	

CTC CCT AAA GAA ATT CAT GAA AAA TTC GGC GCG TTA GTG CTA TTT GTT 196
 Leu Pro Lys Glu Ile His Glu Lys Phe Gly Ala Leu Val Leu Phe Val
 45 50 55

TTA GCC GGA TAC ACC TTA GAA AGC TTG ATA ATT GAT ACA AAA AGC GTG 244
 Leu Ala Gly Tyr Thr Leu Glu Ser Leu Ile Ile Asp Thr Lys Ser Val
 60 65 70

CAA TTT GAA GCC GGG TTT GGC CCT AAT AAC ATT GGC AGT GTG GTT CAA 292
 Gln Phe Glu Ala Gly Phe Gly Pro Asn Asn Ile Gly Ser Val Val Gln
 75 80 85

GTA AAA CTT CCT GGC ATC ATT CAA ATC CTT ATC AAA GAA AAA AAT GAA 340
 Val Lys Leu Pro Gly Ile Ile Gln Ile Leu Ile Lys Glu Lys Asn Glu
 90 95 100 105

AAT GCC GTT TTA TTC AAT CGT TGC GAT TCG CTT GAA TTG TTT CAA AAA 388
 Asn Ala Val Leu Phe Asn Arg Cys Asp Ser Leu Glu Leu Phe Gln Lys
 110 115 120

GAA GAT TCA ATC GCG CAA GAG CCA AAA AAA GAC GAG CGG GAG TCT AAA 436
 Glu Asp Ser Ile Ala Gln Glu Pro Lys Lys Asp Glu Arg Glu Ser Lys
 125 130 135

GAA TGG CTG GAT TCT AAA GAG GCT CTT TTT TCC AAT TCC AAA AAC CGC 484
 Glu Trp Leu Asp Ser Lys Glu Ala Leu Phe Ser Asn Ser Lys Asn Arg
 140 145 150

GCG ATT TTA GAA AAT CTG CAC AAA AGC TAAAGGAATC ATTGATGAGC GTTTTGA 538
 Ala Ile Leu Glu Asn Leu His Lys Ser
 155 160

AATTGCATGT AAAAGTCTTT CGTTTTGAAA CCAATA 574

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

Met Gln Arg Glu Leu Arg Leu Leu Asn Asn Lys His Cys Met Glu Tyr
 1 5 10 15
 Leu Gln Phe Leu Ser Lys Asn His Leu Ser Phe Asn Leu Leu Cys Glu
 20 25 30
 Arg Asp Ala Ile Asp Phe Ser Pro Lys Leu Pro Lys Glu Ile His Glu
 35 40 45
 Lys Phe Gly Ala Leu Val Leu Phe Val Leu Ala Gly Tyr Thr Leu Glu
 50 55 60
 Ser Leu Ile Ile Asp Thr Lys Ser Val Gln Phe Glu Ala Gly Phe Gly

```

Lys Ile Glu Phe Lys Glu Arg Lys Glu Leu Arg Phe Lys Glu Gln Glu
865                870                875                880
Glu Ile Thr Thr Lys Gln Lys Gln Ala Lys Glu Ile Leu Glu Lys Ile
                885                890                895
Pro Asp Gln Gln Asp Lys Glu Ile Gln Lys Phe Tyr Lys Asp Phe Ser
                900                905                910
Lys Leu Leu Gln Thr Pro Thr Thr Ser Gln Asn Phe Glu Glu Ile Ser
                915                920                925
His Ser Tyr Asp Ala Ile Ile Ser Gln Leu Lys Gln His Lys Glu Gln
                930                935                940
Thr Thr His Leu Leu Asn Lys Tyr Asp Asn Asp Leu Ser Tyr Ala Ile
945                950                955                960
Thr Asn Lys Arg Leu His Lys His Leu Met Glu Gln Asn Ile Ser Asn
                965                970                975
Ser Ala Gly Ile Phe Thr Leu Leu Ser Ala Leu Lys Lys Ala Ile Asp
                980                985                990
Ala Arg Ile Phe Lys Arg Gln Glu Ile Leu Asn Glu Glu Tyr Tyr Leu
                995                1000                1005
Lys Asn Ala Ile Lys Ala Glu Leu Asn Asn Ala Phe Lys Lys Asp Pro
1010                1015                1020
Ser Leu Lys Asp Leu Glu Lys Glu Lys Glu Leu Ile Ile Gln Thr Leu
025                1030                1035                1040
Phe Asn Glu Leu Thr Gln Asn His His Gln Gly Asn Pro His Ala
                1045                1050                1055

```

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...511
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

```

TAGAAGAATT TGAAAGGTTG CTCGC ATG CAA AGA GAA TTA AGG CTT TTA AAT      52
                Met Gln Arg Glu Leu Arg Leu Leu Asn
                1                5

AAC AAG CAT TGC ATG GAA TAC TTG CAA TTT CTG TCC AAA AAC CAT TTG      100
Asn Lys His Cys Met Glu Tyr Leu Gln Phe Leu Ser Lys Asn His Leu
10                15                20                25

AGT TTT AAC CTT TTG TGC GAA AGA GAT GCG ATT GAT TTT TCC CCC AAG      148
Ser Phe Asn Leu Leu Cys Glu Arg Asp Ala Ile Asp Phe Ser Pro Lys
                30                35                40

```

-1957-

Met 1	Pro	Tyr	Asn	Glu 5	Ile	Thr	Arg	Val	Gln 10	Ile	Pro	Ala	Leu	Met 15	His
Leu	Ala	Lys	Leu	Gly 20	Tyr	Asp	Phe	Ile 25	Pro	Thr	Asn	Ser	Lys 30	Glu	Asn
Lys	Pro	Asn	Leu	Asp 35	Thr	Ala	Thr 40	Asn	Ile	Leu	Thr	Asn 45	Ser	Phe	Thr
Lys	Ser	Phe	Glu	Arg 50	Leu	Asn 55	Pro	Thr	Lys	Asn 60	Ala	Gln	Glu	Thr	Leu
Ala 65	Glu	Met	Lys	Lys 70	Arg	Leu	Asn	Cys	Asp 75	Asp	Leu	Gly	Lys	Ser 80	Phe
Tyr	Glu	Tyr	Leu	Leu 85	Lys	Ser	Glu	Asn 90	Gln	Ile	Ile	Asp	Phe 95	Asp	Asn
Pro	Asn	Asn	Asn 100	Leu	Tyr	Glu	Met 105	Met	Thr	Glu	Leu	Pro	Tyr 110	Lys	Ser
Phe	Arg	Pro	Asp 115	Thr	Thr	Leu	Phe 120	Ile	Asn	Gly	Leu	Pro	Leu 125	Val	Asn
Ile	Glu 130	Val	Lys	Gln 135	Pro	Tyr	Ala 135	Lys	Lys	Gly 140	Ile	Lys	Glu	Glu	Arg
Asp 145	Arg	His	Ile	Lys 150	Arg	Tyr	Glu 150	Asn	Pro	Glu 155	Asn	Lys	Val	Phe 160	Tyr
Asn	Leu	Ala	Gln 165	Ile	Trp	Leu	Phe 170	Ser	Asp 170	Asn	Leu	Pro	Tyr 175	Asp	Glu
Asn	Lys	Pro	Asp 180	Gln	Gly	Ala	Phe 185	Tyr	Ser	Ala	Ser	Tyr	Ser 190	Pro	Ile
Phe	Gln 195	Arg	Phe	Val 200	Glu	Ala	His 200	Arg	Leu	Asp	Ile	Xaa 205	Pro	Xaa	Pro
Xaa	Gln 210	Lys	Asn	Asp 215	Gln	Asn	His 215	Gln	Asn	Asp 220	Gln	Asn	His	Arg	Ser
Leu 225	Glu	Glu	Ile	Gln 230	Lys	Ser	Val 235	Leu	Asn	Glu 235	Phe	Asn	Leu	Lys	Asp 240
Thr	Asp	Thr	Pro	Lys 245	Ser	Pro	Lys	Asp 250	Thr	Pro	Thr	Asn	Ser 255	Leu	Leu
Thr	Ser	Phe	Cys 260	Ser	Pro	Lys	Arg 265	Leu	Cys	Phe	Ile	Leu	Lys 270	Tyr	Gly
Ile	Ser 275	Phe	Leu	Lys 280	Glu	Lys	Ser 280	Glu	Phe	Lys	Lys	His 285	Val	Trp	Arg
Tyr	Ala 290	Gln	Met	Phe 295	Ala	Ser	Leu 295	Asn	Val	Leu	Lys	Glu	Leu	Gln	Lys
His 305	Tyr	Gly	Thr	Asn 310	Gln	Asn	Leu 315	Lys	Asp	Pro	Leu	Lys	Gly	Ile	Ile 320
Trp	His	Thr	Gln 325	Gly	Ser	Gly	Lys 330	Thr	Ala	Leu	Thr	Tyr	His 335	Leu	Thr
Lys	Leu	Ile	Arg 340	Asp	Phe	Phe	Ser 345	Arg	Ser	Asn	Leu	Asn	Lys 350	Lys	Thr
Lys	Phe 355	Tyr	Phe	Ile	Val	Asp	Arg 360	Leu	Asp	Leu	Leu	Glu	Gln	Ala	Lys
Asn	Glu 370	Phe	Leu	Lys	Arg	Gly 375	Leu	Cys	Val	His	Glu	Ala	Glu	Asn	Lys
Glu 385	Asp	Leu	Ser	Gln 390	Lys	Leu	Lys 395	Ser	Ser	Ser	Val	Phe	Glu	Gly	Ser 400
Gln	Gly	Asn	Asp 405	Glu	Ile	Ile	Val 410	Val	Asn	Ile	Gln	Lys	Phe 415	Lys	Ala
Pro	Asn	Glu	Glu	Lys	Ser	Pro	Asn	Glu	Asp	Pro	Ser	Asn	Ser	Ala	Pro

GAG ATT TTA GAA AAA ATC CCG GAT CAA CAA GAT AAA GAA ATC CAA AAG	2739
Glu Ile Leu Glu Lys Ile Pro Asp Gln Gln Asp Lys Glu Ile Gln Lys	
895 900 905	
TTT TAC AAA GAC TTT TCA AAA TTA CTC CAA ACG CCC ACA ACA AGC CAG	2787
Phe Tyr Lys Asp Phe Ser Lys Leu Leu Gln Thr Pro Thr Thr Ser Gln	
910 915 920	
AAT TTT GAG GAA ATT TCT CAT TCC TAT GAT GCG ATC ATT TCA CAA CTC	2835
Asn Phe Glu Glu Ile Ser His Ser Tyr Asp Ala Ile Ile Ser Gln Leu	
925 930 935	
AAA CAA CAC AAA GAA CAA ACC ACC CAC TTA TTA AAC AAA TAC GAT AAT	2883
Lys Gln His Lys Glu Gln Thr Thr His Leu Leu Asn Lys Tyr Asp Asn	
940 945 950	
GAT TTG TCT TAT GCG ATC ACG AAC AAA CGC CTT CAT AAG CAC CTT ATG	2931
Asp Leu Ser Tyr Ala Ile Thr Asn Lys Arg Leu His Lys His Leu Met	
955 960 965 970	
GAA CAA AAC ATT TCT AAC TCA GCG GGA ATT TTC ACG CTT TTA AGC GCC	2979
Glu Gln Asn Ile Ser Asn Ser Ala Gly Ile Phe Thr Leu Leu Ser Ala	
975 980 985	
TTA AAA AAA GCT ATT GAT GCG CGT ATT TTT AAG CGT CAA GAA ATC TTA	3027
Leu Lys Lys Ala Ile Asp Ala Arg Ile Phe Lys Arg Gln Glu Ile Leu	
990 995 1000	
AAC GAA GAG TAT TAC CTA AAA AAT GCC ATA AAA GCA GAA TTA AAT AAC	3075
Asn Glu Glu Tyr Tyr Leu Lys Asn Ala Ile Lys Ala Glu Leu Asn Asn	
1005 1010 1015	
GCT TTC AAA AAA GAC CCC TCC TTA AAA GAT TTA GAA AAA GAA AAA GAA	3123
Ala Phe Lys Lys Asp Pro Ser Leu Lys Asp Leu Glu Lys Glu Lys Glu	
1020 1025 1030	
CTT ATC ATT CAA ACC CTT TTT AAC GAA CTC ACA CAA AAC CAC CAT CAA	3171
Leu Ile Ile Gln Thr Leu Phe Asn Glu Leu Thr Gln Asn His His Gln	
1035 1040 1045 1050	
GGA AAT CCG CAT GCC TAATAACGCT TTATTGCAAA TCAAACAAGA CACCCT	3222
Gly Asn Pro His Ala	
1055	

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

GGC TTT GAT TTA CCC AGT CTC AAA CGC CTT TAT ATC CAC AGA GAA TTA	2067
Gly Phe Asp Leu Pro Ser Leu Lys Arg Leu Tyr Ile His Arg Glu Leu	
670 675 680	
AAA GAT CAC AAT TTG CTC CAA GCC CTA GCC AGA GTG AAT CGC TCC TAT	2115
Lys Asp His Asn Leu Leu Gln Ala Leu Ala Arg Val Asn Arg Ser Tyr	
685 690 695	
AAA AAC ATG TCT TTT GGC TAC CTT ATA GAT TTT GTA GGC ATT CAA GAA	2163
Lys Asn Met Ser Phe Gly Tyr Leu Ile Asp Phe Val Gly Ile Gln Glu	
700 705 710	
AAT TTT GAC AAA ACG ACT GAT GAT TAC TTG AAA GAA TTA AAC CGA TTC	2211
Asn Phe Asp Lys Thr Thr Asp Asp Tyr Leu Lys Glu Leu Asn Arg Phe	
715 720 725 730	
AAT CAA AGC GGT GCC AAT AGC GAT TCT CAT ATC AAA GAC ATG TTT GCG	2259
Asn Gln Ser Gly Ala Asn Ser Asp Ser His Ile Lys Asp Met Phe Ala	
735 740 745	
GAT CGT AAG ACT TTA GAA GAA GAC ATT AAA AAC GCC TAT GAT GAT CTT	2307
Asp Arg Lys Thr Leu Glu Glu Asp Ile Lys Asn Ala Tyr Asp Asp Leu	
750 755 760	
TTT GAT TAC CCC ATT GAC GAT ATA GAG GGC ATG ACT AGC GCC ATT GTC	2355
Phe Asp Tyr Pro Ile Asp Asp Ile Glu Gly Met Thr Ser Ala Ile Val	
765 770 775	
AGC ATG AGC GCA ATG AAC GAG CTT GTA AAA GTC TCA CGC GCC ATT AAC	2403
Ser Met Ser Ala Met Asn Glu Leu Val Lys Val Ser Arg Ala Ile Asn	
780 785 790	
ACG CTC AAA GAG CGC TAC AAT TTA ATC CGC ACT TCT AAT GAT AAA AAA	2451
Thr Leu Lys Glu Arg Tyr Asn Leu Ile Arg Thr Ser Asn Asp Lys Lys	
795 800 805 810	
ATC CTT TCA CTA AAA GAA AAA ATT GAT ATT GAA AAG ATC CAT AAA ATC	2499
Ile Leu Ser Leu Lys Glu Lys Ile Asp Ile Glu Lys Ile His Lys Ile	
815 820 825	
TCT TCA ATG CTT CAT CAA AAA GCC AAA CAC CTC CAT GCG TTA AAG AAT	2547
Ser Ser Met Leu His Gln Lys Ala Lys His Leu His Ala Leu Lys Asn	
830 835 840	
ATC AAT GAG CCT AAA AAC CCA AAC GAT TTA ATG ATT TTA GAA GAC CTC	2595
Ile Asn Glu Pro Lys Asn Pro Asn Asp Leu Met Ile Leu Glu Asp Leu	
845 850 855	
ATC GCT CTT TTA GAC TTT AAA ATA GAG TTT AAA GAA CGC AAA GAA TTA	2643
Ile Ala Leu Leu Asp Phe Lys Ile Glu Phe Lys Glu Arg Lys Glu Leu	
860 865 870	
CGC TTT AAA GAA CAA GAA GAG ATT ACC ACC AAA CAA AAG CAA GCT AAA	2691
Arg Phe Lys Glu Gln Glu Glu Ile Thr Thr Lys Gln Lys Gln Ala Lys	
875 880 885 890	

GAA TCC ATT CAA AAC AGC CGC AAT TTA CAA AGG GTG TTT ATC ATA GAT	1395
Glu Ser Ile Gln Asn Ser Arg Asn Leu Gln Arg Val Phe Ile Ile Asp	
445 450 455	
GAA GCC CAC AGG AGC TAC GAT CCT AAA GGT TGC TTT TAC GCT AAT TTG	1443
Glu Ala His Arg Ser Tyr Asp Pro Lys Gly Cys Phe Tyr Ala Asn Leu	
460 465 470	
ATA GAA TGC GAC AAG ACA GCA ATT AAA ATC GCC CTC ACA GGC ACG CCC	1491
Ile Glu Cys Asp Lys Thr Ala Ile Lys Ile Ala Leu Thr Gly Thr Pro	
475 480 485 490	
CTA TTA GAA GAC AAC GCG CAA GAT AAA GCC ACT AAA AAC ACT TTT GGC	1539
Leu Leu Glu Asp Asn Ala Gln Asp Lys Ala Thr Lys Asn Thr Phe Gly	
495 500 505	
AAC TAC TTG CAC ACC TAT TCT TAT ACA GAA TCC ATT AAA GAC AGA CAC	1587
Asn Tyr Leu His Thr Tyr Ser Tyr Thr Glu Ser Ile Lys Asp Arg His	
510 515 520	
ACC CTA AAA CTC CAG TTA GAA AGC ATT GAA ACG AGC TAT AAA GAA AAA	1635
Thr Leu Lys Leu Gln Leu Glu Ser Ile Glu Thr Ser Tyr Lys Glu Lys	
525 530 535	
TTA CAA GAA ATC TAT CGC CTT TTA CAA GAA AGC ATC ACT ATT GAA GAC	1683
Leu Gln Glu Ile Tyr Arg Leu Leu Gln Glu Ser Ile Thr Ile Glu Asp	
540 545 550	
ACA GAA GTT AAA AAA GAA ACG ATT TTT AAC GAT GAA AAA TAC ATT AAC	1731
Thr Glu Val Lys Lys Glu Thr Ile Phe Asn Asp Glu Lys Tyr Ile Asn	
555 560 565 570	
GCC ATG CTC TAT TAT ATC ATT AGA GAT TTA TTG GAT TTT AGG CGT TTG	1779
Ala Met Leu Tyr Tyr Ile Ile Arg Asp Leu Leu Asp Phe Arg Arg Leu	
575 580 585	
AAT GAT AAT GAA CGC TTA AAG GCT ATG GTG GTT TGT TTT TCT AGC AAG	1827
Asn Asp Asn Glu Arg Leu Lys Ala Met Val Val Cys Phe Ser Ser Lys	
590 595 600	
CAA GCC AGA TTA GCT GAT TGT CTT TTT AAT GAA GTC CAA GAA AAA GTC	1875
Gln Ala Arg Leu Ala Asp Cys Leu Phe Asn Glu Val Gln Glu Lys Val	
605 610 615	
TTA CAA GAA AAC CCC AAC CTA AGG ATT TTA AAC AAA CTC AAA TCC AGC	1923
Leu Gln Glu Asn Pro Asn Leu Arg Ile Leu Asn Lys Leu Lys Ser Ser	
620 625 630	
CTG ATT TTG CAT GAT GAA CAA GAA GTC AAA GAA AAG GTT CAT TCT TTC	1971
Leu Ile Leu His Asp Glu Gln Glu Val Lys Glu Lys Val His Ser Phe	
635 640 645 650	
AAA CAT GAA GAT ACC GAT ATA GTC TTT GTG TTT AAC ATG CTT TTA ACC	2019
Lys His Glu Asp Thr Asp Ile Val Phe Val Phe Asn Met Leu Leu Thr	
-- 655 660 665	

GAT CAA AAT CAT CGA TCG CTT GAA GAA ATT CAA AAA AGC GTC TTA AAC	723
Asp Gln Asn His Arg Ser Leu Glu Glu Ile Gln Lys Ser Val Leu Asn	
220 225 230	
GAA TTT AAC CTT AAA GAC ACC GAC ACC CCA AAA AGC CCT AAA GAC ACC	771
Glu Phe Asn Leu Lys Asp Thr Asp Thr Pro Lys Ser Pro Lys Asp Thr	
235 240 245 250	
CCC ACA AAC TCC CTT TTA ACT TCG TTT TGC TCT CCA AAA AGG CTT TGC	819
Pro Thr Asn Ser Leu Leu Thr Ser Phe Cys Ser Pro Lys Arg Leu Cys	
255 260 265	
TTT ATC CTA AAA TAC GGC ATC AGT TTC TTA AAA GAA AAA TCA GAG TTT	867
Phe Ile Leu Lys Tyr Gly Ile Ser Phe Leu Lys Glu Lys Ser Glu Phe	
270 275 280	
AAA AAA CAC GTT TGG CGT TAT GCG CAG ATG TTT GCG AGC TTG AAC GTT	915
Lys Lys His Val Trp Arg Tyr Ala Gln Met Phe Ala Ser Leu Asn Val	
285 290 295	
TTA AAA GAA TTG CAA AAG CAT TAT GGA ACA AAC CAA AAC CTA AAA GAT	963
Leu Lys Glu Leu Gln Lys His Tyr Gly Thr Asn Gln Asn Leu Lys Asp	
300 305 310	
CCC CTA AAA GGC ATC ATC TGG CAC ACG CAA GGC AGC GGT AAA ACC GCC	1011
Pro Leu Lys Gly Ile Ile Trp His Thr Gln Gly Ser Gly Lys Thr Ala	
315 320 325 330	
TTA ACC TAC CAC TTA ACC AAA CTC ATC AGA GAC TTT TTT AGC CGA TCC	1059
Leu Thr Tyr His Leu Thr Lys Leu Ile Arg Asp Phe Phe Ser Arg Ser	
335 340 345	
AAC CTA AAC AAA AAG ACT AAA TTT TAT TTT ATT GTG GAC AGG TTG GAT	1107
Asn Leu Asn Lys Lys Thr Lys Phe Tyr Phe Ile Val Asp Arg Leu Asp	
350 355 360	
TTA TTG GAG CAA GCC AAA AAC GAG TTT TTA AAA AGA GGC CTT TGT GTG	1155
Leu Leu Glu Gln Ala Lys Asn Glu Phe Leu Lys Arg Gly Leu Cys Val	
365 370 375	
CAT GAG GCA GAA AAT AAA GAG GAT TTG AGC CAA AAA TTA AAA AGC TCT	1203
His Glu Ala Glu Asn Lys Glu Asp Leu Ser Gln Lys Leu Lys Ser Ser	
380 385 390	
AGC GTT TTT GAA GGC TCT CAA GGG AAT GAT GAA ATC ATC GTT GTG AAT	1251
Ser Val Phe Glu Gly Ser Gln Gly Asn Asp Glu Ile Ile Val Val Asn	
395 400 405 410	
ATC CAA AAA TTC AAA GCC CCC AAT GAA GAA AAA TCC CCC AAT GAA GAC	1299
Ile Gln Lys Phe Lys Ala Pro Asn Glu Glu Lys Ser Pro Asn Glu Asp	
415 420 425	
CCC TCT AAT AGC GCT CCT AAA GAA ATC ATT TCT AAA ACA GAA TTA CAA	1347
Pro Ser Asn Ser Ala Pro Lys Glu Ile Ile Ser Lys Thr Glu Leu Gln	
430 435 440	

CCTTAAATCT AAGGGGTGTG C															ATG	CCA	TAC	AAT	GAA	ATC	ACA	AGG	GTT	CAA	51
															Met	Pro	Tyr	Asn	Glu	Ile	Thr	Arg	Val	Gln	
															1				5					10	
ATC	CCT	GCC	TTA	ATG	CAT	TTA	GCC	AAG	TTG	GGC	TAT	GAT	TTT	ATC	CCC	99									
Ile	Pro	Ala	Leu	Met	His	Leu	Ala	Lys	Leu	Gly	Tyr	Asp	Phe	Ile	Pro										
															15		20				25				
ACT	AAT	TCT	AAA	GAA	AAT	AAG	CCC	AAC	CTA	GAC	ACC	GCC	ACC	AAC	ATT	147									
Thr	Asn	Ser	Lys	Glu	Asn	Lys	Pro	Asn	Leu	Asp	Thr	Ala	Thr	Asn	Ile										
															30		35				40				
TTA	ACC	AAT	AGT	TTC	ACT	AAA	TCC	TTT	GAG	CGG	TTA	AAC	CCC	ACT	AAA	195									
Leu	Thr	Asn	Ser	Phe	Thr	Lys	Ser	Phe	Glu	Arg	Leu	Asn	Pro	Thr	Lys										
															45		50				55				
AAC	GCA	CAA	GAA	ACG	CTT	GCT	GAA	ATG	AAA	AAA	CGC	TTG	AAT	TGC	GAT	243									
Asn	Ala	Gln	Glu	Thr	Leu	Ala	Glu	Met	Lys	Lys	Arg	Leu	Asn	Cys	Asp										
															60		65				70				
GAT	TTG	GGC	AAA	AGC	TTT	TAT	GAA	TAC	TTG	CTC	AAA	AGC	GAG	AAT	CAA	291									
Asp	Leu	Gly	Lys	Ser	Phe	Tyr	Glu	Tyr	Leu	Leu	Lys	Ser	Glu	Asn	Gln										
															75		80				85		90		
ATC	ATA	GAC	TTT	GAT	AAC	CCT	AAC	AAC	AAT	CTT	TAT	GAA	ATG	ATG	ACT	339									
Ile	Ile	Asp	Phe	Asp	Asn	Pro	Asn	Asn	Asn	Leu	Tyr	Glu	Met	Met	Thr										
															95		100				105				
GAA	TTA	CCC	TAC	AAA	TCT	TTT	AGG	CCT	GAC	ACC	ACC	CTT	TTT	ATC	AAT	387									
Glu	Leu	Pro	Tyr	Lys	Ser	Phe	Arg	Pro	Asp	Thr	Thr	Leu	Phe	Ile	Asn										
															110		115				120				
GGC	TTG	CCT	TTG	GTG	AAT	ATA	GAA	GTT	AAA	CAG	CCT	TAC	GCC	AAA	AAA	435									
Gly	Leu	Pro	Leu	Val	Asn	Ile	Glu	Val	Lys	Gln	Pro	Tyr	Ala	Lys	Lys										
															125		130				135				
GGC	ATT	AAA	GAA	GAA	AGA	GAT	CGC	CAC	ATC	AAA	CGC	TAT	GAA	AAC	CCT	483									
Gly	Ile	Lys	Glu	Glu	Arg	Asp	Arg	His	Ile	Lys	Arg	Tyr	Glu	Asn	Pro										
															140		145				150				
GAA	AAC	AAA	GTT	TTT	TAT	AAT	CTC	GCG	CAA	ATC	TGG	CTT	TTT	AGC	GAT	531									
Glu	Asn	Lys	Val	Phe	Tyr	Asn	Leu	Ala	Gln	Ile	Trp	Leu	Phe	Ser	Asp										
															155		160				165		170		
AAC	TTA	CCC	TAT	GAT	GAA	AAC	AAA	CCC	GAT	CAA	GGC	GCG	TTT	TAT	AGC	579									
Asn	Leu	Pro	Tyr	Asp	Glu	Asn	Lys	Pro	Asp	Gln	Gly	Ala	Phe	Tyr	Ser										
															175		180				185				
GCT	TCT	TAT	TCG	CCC	ATT	TTC	CAA	CGC	TTT	GTT	GAA	GCT	CAT	AGG	CTA	627									
Ala	Ser	Tyr	Ser	Pro	Ile	Phe	Gln	Arg	Phe	Val	Glu	Ala	His	Arg	Leu										
															190		195				200				
GAT	ATT	WCC	CCC	SSN	CCC	CSC	CAA	AAA	AAT	GAT	CAA	AAT	CAT	CAA	AAC	675									
Asp	Ile	Xaa	Pro	Xaa	Pro	Xaa	Gln	Lys	Asn	Asp	Gln	Asn	His	Gln	Asn										
															205		210				215				

AGCCTTTGTG TGTTCCTTTG TAAA

563

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

```

Met Ser Asn Leu Gln Glu Leu Arg Glu His Leu Lys Glu Leu Glu Asn
 1           5           10           15
Ser Phe Glu Ile Gly Ser Phe Thr Lys Glu Asn Ile Lys Glu Tyr Ala
          20           25           30
Lys Cys Phe Phe Met Ser Leu Ser Met Phe Leu Glu Glu Gln Glu Lys
          35           40           45
Asn Gln Gln Glu Glu Phe Leu Glu Gln Asp Thr Lys Glu Asn Gln Glu
          50           55           60
Glu Leu Ile Lys Asn Ile Gln Thr Ser Ile Ala Lys Asn Gln Glu Leu
        65           70           75           80
Glu Lys Ile Ser Phe Glu Lys Trp Glu Asn Lys Ile Gln Glu Arg Val
          85           90           95
Leu Pro Lys Leu Lys Arg Ile Val Thr His Lys Leu Gln Glu Ser Ile
          100          105          110
Thr Ser Ser Ile Asn Thr Gln Leu Glu Ser Phe Lys Lys Asp Glu Leu
          115          120          125
Asp Leu Ser Ser Val Phe Glu Ile Gln Arg Lys Asn Thr Gln Ile Ala
          130          135          140
Tyr Arg Leu Ala Ile Gly Gly Leu Ile Gly Ile Ile Ala Leu Ser Ser
        145          150          155          160
Gln Ile

```

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...3186
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 24...509

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

CAACTCTTTT TTAAGGGGGA CAC ATG TCT AAT TTG CAA GAA CTT AGA GAG CAT	53
Met Ser Asn Leu Gln Glu Leu Arg Glu His	
1 5 10	
TTA AAA GAA TTA GAA AAT TCC TTT GAA ATA GGC TCT TTT ACT AAA GAA	101
Leu Lys Glu Leu Glu Asn Ser Phe Glu Ile Gly Ser Phe Thr Lys Glu	
15 20 25	
AAT ATT AAA GAA TAC GCT AAA TGC TTT TTT ATG AGT TTA AGC ATG TTT	149
Asn Ile Lys Glu Tyr Ala Lys Cys Phe Phe Met Ser Leu Ser Met Phe	
30 35 40	
TTA GAA GAA CAA GAA AAA AAC CAA CAA GAA GAG TTT TTA GAA CAA GAT	197
Leu Glu Glu Gln Glu Lys Asn Gln Gln Glu Glu Phe Leu Glu Gln Asp	
45 50 55	
ACC AAA GAA AAT CAA GAA GAG CTC ATT AAA AAC ATT CAA ACA AGC ATT	245
Thr Lys Glu Asn Gln Glu Glu Leu Ile Lys Asn Ile Gln Thr Ser Ile	
60 65 70	
GCT AAA AAC CAA GAG TTA GAA AAA ATC TCT TTT GAA AAA TGG GAG AAT	293
Ala Lys Asn Gln Glu Leu Glu Lys Ile Ser Phe Glu Lys Trp Glu Asn	
75 80 85 90	
AAA ATT CAA GAA AGG GTT TTG CCT AAG TTA AAA CGC ATT GTT ACG CAT	341
Lys Ile Gln Glu Arg Val Leu Pro Lys Leu Lys Arg Ile Val Thr His	
95 100 105	
AAG TTG CAA GAA AGT ATC ACA TCT AGC ATA AAC ACG CAA TTA GAG AGT	389
Lys Leu Gln Glu Ser Ile Thr Ser Ser Ile Asn Thr Gln Leu Glu Ser	
110 115 120	
TTT AAA AAA GAT GAG TTA GAT TTA TCT AGC GTG TTT GAA ATC CAA AGA	437
Phe Lys Lys Asp Glu Leu Asp Leu Ser Ser Val Phe Glu Ile Gln Arg	
125 130 135	
AAG AAC ACT CAA ATA GCG TAT AGA TTA GCT ATA GGG GGG CTT ATA GGT	485
Lys Asn Thr Gln Ile Ala Tyr Arg Leu Ala Ile Gly Gly Leu Ile Gly	
140 145 150	
ATC ATT GCT TTA AGC TCG CAA ATT TGATTATTAA CTCTATACTT CACGCTTTTT	539
Ile Ile Ala Leu Ser Ser Gln Ile	
155 160	

```

Tyr Leu Met Met Ser Ala Leu Lys Tyr Ser Asn Ile Asp Ile Leu Ala
145                      150                      155                      160
Leu Asp Arg Leu Asn Gly Leu Tyr Ser Phe Thr Lys Tyr Phe Asp Gly
                      165                      170                      175
Ile Tyr Asn Gln Gly Glu Asn Phe His Ile Asn Pro Phe Ser Leu Glu
                      180                      185                      190
Asp Ser Ala Thr Asn Arg Ala Phe Leu Leu His Phe Tyr Ala Gln Met
                      195                      200                      205
Ala Lys Val Asp Ser Tyr Asp Asp His Lys Asp Lys Val Glu Asp Arg
210                      215                      220
Thr Ala Leu Leu Asn Ala Ile Asp Thr Met Tyr Arg Asn Tyr Asn Asp
225                      230                      235                      240
Glu Val Lys Gln Ala Lys Phe Ser Asn Gln Glu Leu Pro Leu Pro Phe
                      245                      250                      255
Asp Leu Lys Glu Phe Val Asn Ala Ile Ala Lys Thr Asn Thr Asp Ile
260                      265                      270
Leu Asp Ser Ser Phe Glu Asp Tyr Leu Lys Ser Ser Leu Phe Ser Ser
275                      280                      285
Arg Met Asp Ser Leu Asp Phe Lys Thr Arg Ile Ser Thr Ile Asn Thr
290                      295                      300
Asp Ser Ile Leu His Asn Asp Asp Asp Ala Gly Leu Leu Ala Tyr Tyr
305                      310                      315                      320
Val Phe His Lys Met Ile Asp Arg Ala Leu Lys Ile Asn Arg Gly Phe
                      325                      330                      335
Leu Cys Phe Ile Asp Glu Phe Lys Ser Tyr Ala Gln Asn Glu Met Met
340                      345                      350
Asn Lys Lys Ile Asn Glu Ile Ile Thr Gln Ala Arg Lys Ala Asn Gly
355                      360                      365
Val Ile Val Leu Ala Leu Gln Asp Ile Asn Gln Leu Ser Glu Val Arg
370                      375                      380
Asn Ala Gln Ser Phe Ile Lys Asn Met Gly Gln Leu Ile Leu Tyr Pro
385                      390                      395                      400
Gln Arg Asn Ile Asp Thr Lys Asp Leu Asn Asp Lys Phe Gly Ile Arg
405                      410                      415
Leu Ser Asp Thr Glu Lys His Phe Leu Glu Asn Thr Ala Val Asn Glu
420                      425                      430
Tyr Lys Val Leu Leu Lys Asn Met Asn Asp Gly Ser Ser Asn Ile Ile
435                      440                      445
Asp Val Ser Leu Ser Ser Leu Gly Asn Tyr Leu Gln Ile Phe Ser Ser
450                      455                      460
Asn Ser Ser Met Val Glu His Ile Asp Asn Leu Ile Lys His Tyr Pro
465                      470                      475                      480
Lys Thr Trp Arg Glu Val Phe Val Ser Asn Lys His Glu Asn Phe Asp
485                      490                      495
Asp Lys Lys His Leu Glu Lys Val Leu Lys
500                      505

```

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

CAT TTT TTA GAA AAC ACC GCC GTT AAT GAA TAC AAA GTC TTA CTC AAA	1352
His Phe Leu Glu Asn Thr Ala Val Asn Glu Tyr Lys Val Leu Leu Lys	
425 430 435	
AAC ATG AAT GAT GGC TCA TCT AAC ATT ATA GAT GTG AGC CTA AGT TCT	1400
Asn Met Asn Asp Gly Ser Ser Asn Ile Ile Asp Val Ser Leu Ser Ser	
440 445 450	
TTG GGT AAT TAC CTA CAA ATC TTT AGC TCT AAT TCT AGC ATG GTA GAA	1448
Leu Gly Asn Tyr Leu Gln Ile Phe Ser Ser Asn Ser Ser Met Val Glu	
455 460 465 470	
CAC ATT GAT AAT CTC ATT AAG CAT TAC CCT AAA ACT TGG CGA GAA GTC	1496
His Ile Asp Asn Leu Ile Lys His Tyr Pro Lys Thr Trp Arg Glu Val	
475 480 485	
TTT GTG AGT AAC AAA CAC GAA AAT TTT GAT GAC AAA AAA CAC TTA GAA	1544
Phe Val Ser Asn Lys His Glu Asn Phe Asp Asp Lys Lys His Leu Glu	
490 495 500	
AAG GTG CTT AAA TGAAAAACAT CATGCGTTTA GTTTTTGTGA TAGTGGCTAT GT	1598
Lys Val Leu Lys	
505	

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

Met	Gln	Glu	Cys	Ala	Leu	Asn	Leu	Val	Ile	Arg	Ala	Lys	Ser	Lys	Ala
1				5				10						15	
Lys	Leu	Asp	Lys	Ser	Leu	Lys	Glu	Ile	Leu	Ser	Leu	Leu	Asn	Asn	Ala
			20					25						30	
Gly	Leu	Gly	Ser	Val	Thr	Glu	Thr	Ile	Gly	Leu	Lys	Pro	Ser	Tyr	Phe
		35					40					45			
Ser	Phe	Phe	Pro	Asn	Asn	Ala	Asn	Ile	Asn	Pro	Arg	Met	Arg	His	Gln
		50				55					60				
Thr	Ser	Gln	Val	Ile	Ala	Ser	Leu	Ile	Leu	Phe	Glu	Lys	Asn	Asn	Thr
65					70					75					80
Gly	Phe	Arg	Ala	Asn	Ser	Trp	Gly	Asp	Met	Pro	Leu	Ser	Val	Phe	Lys
			85					90						95	
Asn	Leu	Asp	His	Ser	Pro	Tyr	Leu	Phe	Asn	Phe	His	Asn	Gln	Glu	Val
			100					105					110		
Lys	His	Lys	Gly	Val	Leu	Ala	His	Asn	Val	Ala	Arg	Val	Val	Gly	His
		115					120					125			
Thr	Met	Ile	Ile	Gly	Ala	Thr	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Ile	Ser
		130				135						140			

Ala Phe Leu Leu His Phe Tyr Ala Gln Met Ala Lys Val Asp Ser Tyr	
200 205 210	
GAT GAC CAT AAG GAT AAA GTA GAA GAT AGA ACA GCC CTT TTA AAT GCT	728
Asp Asp His Lys Asp Lys Val Glu Asp Arg Thr Ala Leu Leu Asn Ala	
215 220 225 230	
ATT GAT ACG ATG TAT AGA AAT TAT AAC GAT GAA GTC AAA CAA GCC AAA	776
Ile Asp Thr Met Tyr Arg Asn Tyr Asn Asp Glu Val Lys Gln Ala Lys	
235 240 245	
TTT AGC AAC CAA GAA TTA CCC CTT CCT TTT GAT TTA AAA GAG TTT GTC	824
Phe Ser Asn Gln Glu Leu Pro Leu Pro Phe Asp Leu Lys Glu Phe Val	
250 255 260	
AAT GCC ATT GCT AAA ACC AAT ACA GAC ATT TTA GAT AGT AGT TTT GAA	872
Asn Ala Ile Ala Lys Thr Asn Thr Asp Ile Leu Asp Ser Ser Phe Glu	
265 270 275	
GAC TAT TTA AAA TCT TCC TTA TTT TCT AGC CGA ATG GAT AGT CTA GAT	920
Asp Tyr Leu Lys Ser Ser Leu Phe Ser Ser Arg Met Asp Ser Leu Asp	
280 285 290	
TTT AAA ACT CGT ATT AGC ACC ATA AAT ACC GAT AGC ATT TTA CAT AAT	968
Phe Lys Thr Arg Ile Ser Thr Ile Asn Thr Asp Ser Ile Leu His Asn	
295 300 305 310	
GAT GAT GAC GCT GGG CTT TTA GCC TAC TAT GTC TTT CAT AAG ATG ATT	1016
Asp Asp Asp Ala Gly Leu Leu Ala Tyr Tyr Val Phe His Lys Met Ile	
315 320 325	
GAC AGA GCC TTA AAA ATC AAT CGT GGG TTT TTA TGC TTT ATT GAT GAG	1064
Asp Arg Ala Leu Lys Ile Asn Arg Gly Phe Leu Cys Phe Ile Asp Glu	
330 335 340	
TTT AAG TCT TAC GCT CAA AAT GAA ATG ATG AAT AAA AAA ATC AAT GAA	1112
Phe Lys Ser Tyr Ala Gln Asn Glu Met Met Asn Lys Lys Ile Asn Glu	
345 350 355	
ATC ATT ACT CAA GCT AGA AAG GCT AAT GGG GTG ATT GTT CTA GCC TTA	1160
Ile Ile Thr Gln Ala Arg Lys Ala Asn Gly Val Ile Val Leu Ala Leu	
360 365 370	
CAA GAC ATT AAC CAA CTA AGC GAA GTG AGA AAC GCT CAA AGC TTT ATA	1208
Gln Asp Ile Asn Gln Leu Ser Glu Val Arg Asn Ala Gln Ser Phe Ile	
375 380 385 390	
AAA AAT ATG GGG CAA TTG ATT TTG TAT CCC CAA AGA AAT ATT GAT ACC	1256
Lys Asn Met Gly Gln Leu Ile Leu Tyr Pro Gln Arg Asn Ile Asp Thr	
395 400 405	
AAA GAT TTA AAC GAT AAA TTT GGC ATT AGA CTA AGC GAT ACA GAA AAA	1304
Lys Asp Leu Asn Asp Lys Phe Gly Ile Arg Leu Ser Asp Thr Glu Lys	
410 415 420	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

ATAATTATAT AGAATTAGTG CAAGCCAATC GTTTGAGC ATG CAA GAG TGT GCT TTA	56
Met Gln Glu Cys Ala Leu	
1 5	
AAC TTA GTT ATA AGG GCT AAA AGT AAA GCT AAA TTA GAC AAG TCT TTA	104
Asn Leu Val Ile Arg Ala Lys Ser Lys Ala Lys Leu Asp Lys Ser Leu	
10 15 20	
AAA GAG ATT TTA TCC TTG CTT AAT AAT GCT GGA CTA GGC AGT GTT ACA	152
Lys Glu Ile Leu Ser Leu Leu Asn Asn Ala Gly Leu Gly Ser Val Thr	
25 30 35	
GAA ACT ATA GGG CTA AAA CCA TCT TAT TTT TCA TTC TTC CCA AAT AAC	200
Glu Thr Ile Gly Leu Lys Pro Ser Tyr Phe Ser Phe Phe Pro Asn Asn	
40 45 50	
GCC AAT ATC AAC CCT AGA ATG AGA CAT CAA ACT TCC CAA GTC ATA GCA	248
Ala Asn Ile Asn Pro Arg Met Arg His Gln Thr Ser Gln Val Ile Ala	
55 60 65 70	
TCT TTG ATT TTG TTT GAG AAA AAT AAT ACA GGT TTT AGA GCA AAT TCT	296
Ser Leu Ile Leu Phe Glu Lys Asn Asn Thr Gly Phe Arg Ala Asn Ser	
75 80 85	
TGG GGG GAT ATG CCC TTA TCT GTG TTT AAG AAC CTA GAC CAT AGC CCT	344
Trp Gly Asp Met Pro Leu Ser Val Phe Lys Asn Leu Asp His Ser Pro	
90 95 100	
TAT TTG TTT AAT TTT CAT AAT CAA GAA GTC AAA CAT AAG GGC GTG TTA	392
Tyr Leu Phe Asn Phe His Asn Gln Glu Val Lys His Lys Gly Val Leu	
105 110 115	
GCC CAC AAT GTC GCA CGA GTA GTG GGA CAT ACC ATG ATT ATA GGA GCA	440
Ala His Asn Val Ala Arg Val Val Gly His Thr Met Ile Ile Gly Ala	
120 125 130	
ACA GGT GCT GGT AAA ACC ACA CTC ATT AGC TAT TTG ATG ATG AGT GCC	488
Thr Gly Ala Gly Lys Thr Thr Leu Ile Ser Tyr Leu Met Met Ser Ala	
135 140 145 150	
TTA AAA TAT TCT AAC ATT GAT ATT TTA GCT CTT GAT AGA CTA AAT GGT	536
Leu Lys Tyr Ser Asn Ile Asp Ile Leu Ala Leu Asp Arg Leu Asn Gly	
155 160 165	
TTG TAT TCC TTT ACC AAG TAT TTT GAT GGG ATT TAT AAT CAA GGC GAA	584
Leu Tyr Ser Phe Thr Lys Tyr Phe Asp Gly Ile Tyr Asn Gln Gly Glu	
170 175 180	
AAC TTT CAT ATT AAC CCT TTT TCA TTA GAA GAT AGC GCA ACT AAT AGA	632
Asn Phe His Ile Asn Pro Phe Ser Leu Glu Asp Ser Ala Thr Asn Arg	
185 190 195	
GCC TTT TTA TTG CAT TTT TAT GCC CAA ATG GCA AAA GTG GAT AGT TAT	680

```

Met Leu Glu Ser Ala Leu Lys Tyr Cys Lys Glu Lys Ala Ile Asp Leu
 1           5           10           15
Leu Val Gly Phe Val Pro Lys Thr Tyr Ser Met Ala Gln Glu Cys Asn
          20           25           30
Ile Leu Gly Leu Tyr Asp Asp Ala Phe Ile Ile Thr Lys Gln Glu Asn
      35           40           45
Leu Val Gly Ile Ile Ser Leu Gln Gly Leu Ser Tyr Ser Asn Leu Met
      50           55           60
Gln Lys Asp Leu Glu Gly Tyr Phe Asp Ala Arg Gln Asn Val Leu Asn
65           70           75           80
Thr Ile Ser Lys Asp Ile Gln Leu Arg Ile Val Ala Lys Arg Arg Lys
          85           90           95
Glu Phe Ile Asn Gln Ser Pro Asn Ile Asp Asn Ile Tyr Ala Lys Ala
          100          105          110
Ile Ile Thr Gln Phe Glu Ser Lys Gly Ile Tyr Lys Thr Glu Tyr Phe
          115          120          125
Leu Val Phe Glu Thr Ile Thr Ser Asn Val Lys Ser Phe Phe Glu Lys
          130          135          140
Lys Lys Leu Glu Met Thr Thr Ser Ile Asn Glu Glu Leu Glu Glu Ser
145          150          155          160
Ser Lys Glu Asp Lys Gln Glu Asn Glu Asn Xaa Ser Asn Glu Thr His
          165          170          175
Ser Asn Thr Ser Ser Lys Lys Asp Lys Lys Asn Lys Phe Lys Lys Lys
          180          185          190
Ile Thr Phe Ser Thr Lys Ser Lys Arg Ala Leu Leu Ile Gln Thr Ile
          195          200          205
Glu Arg Val Lys Asn Ala Leu Lys Glu Phe Lys Pro Thr Leu Leu Asn
          210          215          220
Ser Lys Glu Val Leu Asn Phe Tyr Ala Glu Tyr Ile Asn Gly Lys Tyr
225          230          235          240
Ile Ala Phe Asn Pro Lys Leu Lys Arg Leu Ser Asp Thr Ile Leu His
          245          250          255
Leu Met Cys Ile Leu Arg Lys Ile Thr Leu Ser Leu Asn Phe Lys Ile
          260          265          270
Lys Thr Pro Phe Val Arg Val Trp Gly Leu Arg Leu Met Arg Ala Lys
          275          280          285
Lys Phe Leu Arg Ser Leu Tyr Leu Leu Phe Tyr Thr Pro Lys Leu Asn
          290          295          300

```

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...1556
- (D) OTHER INFORMATION:

135	140	145	150	
ACT TCA ATT AAT GAA GAG TTA GAA GAA AGC TCT AAA GAA GAT AAA CAA				534
Thr Ser Ile Asn Glu Glu Leu Glu Glu Ser Ser Lys Glu Asp Lys Gln				
	155	160	165	
GAG AAT GAA AAT MGC TCC AAT GAA ACT CAT TCA AAC ACA AGC TCT AAA				582
Glu Asn Glu Asn Xaa Ser Asn Glu Thr His Ser Asn Thr Ser Ser Lys				
	170	175	180	
AAA GAC AAG AAA AAC AAG TTC AAA AAA AAG ATA ACC TTT AGC ACC AAA				630
Lys Asp Lys Lys Asn Lys Phe Lys Lys Lys Ile Thr Phe Ser Thr Lys				
	185	190	195	
AGT AAA AGA GCC TTA CTC ATT CAA ACC ATA GAA AGA GTA AAA AAC GCT				678
Ser Lys Arg Ala Leu Leu Ile Gln Thr Ile Glu Arg Val Lys Asn Ala				
	200	205	210	
CTT AAA GAA TTT AAA CCC ACT TTA CTA AAT TCT AAA GAA GTA TTA AAT				726
Leu Lys Glu Phe Lys Pro Thr Leu Leu Asn Ser Lys Glu Val Leu Asn				
	215	220	225	230
TTC TAC GCA GAA TAC ATC AAT GGC AAA TAC ATC GCC TTT AAT CCT AAA				774
Phe Tyr Ala Glu Tyr Ile Asn Gly Lys Tyr Ile Ala Phe Asn Pro Lys				
	235	240	245	
TTA AAG CGA TTA AGC GAT ACT ATA TTG CAT CTA ATG TGC ATT TTA AGA				822
Leu Lys Arg Leu Ser Asp Thr Ile Leu His Leu Met Cys Ile Leu Arg				
	250	255	260	
AAG ATT ACT TTG TCA TTG AAT TTC AAA ATC AAA ACA CCT TTT GTG CGT				870
Lys Ile Thr Leu Ser Leu Asn Phe Lys Ile Lys Thr Pro Phe Val Arg				
	265	270	275	
GTG TGG GGA TTA AGG CTT ATG AGA GCG AAG AAA TTT CTT CGC TCC CTA				918
Val Trp Gly Leu Arg Leu Met Arg Ala Lys Lys Phe Leu Arg Ser Leu				
	280	285	290	
TAT CTA CTC TTT TAC ACA CCC AAA TTG AAC TAGATTAAAT CTTTCATATC CGC				971
Tyr Leu Leu Phe Tyr Thr Pro Lys Leu Asn				
	295	300		
TCTTTAGGGC AATTGAAAG CTG				995

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...948
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

TAAAAACACC CCTAAAAGAA AAAGAAAGTC TTCTTA ATG TTA GAA AGC GCC CTT	54
Met Leu Glu Ser Ala Leu	
1 5	
AAA TAT TGC AAG GAA AAA GCC ATA GAC CTT TTA GTA GGG TTT GTG CCA	102
Lys Tyr Cys Lys Glu Lys Ala Ile Asp Leu Leu Val Gly Phe Val Pro	
10 15 20	
AAA ACC TAT TCT ATG GCA CAA GAG TGC AAT ATT TTA GGC TTG TAT GAT	150
Lys Thr Tyr Ser Met Ala Gln Glu Cys Asn Ile Leu Gly Leu Tyr Asp	
25 30 35	
GAT GCT TTC ATT ATT ACC AAA CAA GAA AAT CTA GTA GGC ATT ATA TCC	198
Asp Ala Phe Ile Ile Thr Lys Gln Glu Asn Leu Val Gly Ile Ile Ser	
40 45 50	
TTA CAA GGA CTA AGC TAT TCT AAT TTA ATG CAA AAA GAC TTA GAG GGC	246
Leu Gln Gly Leu Ser Tyr Ser Asn Leu Met Gln Lys Asp Leu Glu Gly	
55 60 65 70	
TAT TTT GAT GCT AGA CAA AAT GTT CTC AAC ACC ATT AGT AAA GAC ATT	294
Tyr Phe Asp Ala Arg Gln Asn Val Leu Asn Thr Ile Ser Lys Asp Ile	
75 80 85	
CAA TTA AGA ATT GTG GCT AAA AGG CGT AAG GAA TTT ATC AAT CAA AGT	342
Gln Leu Arg Ile Val Ala Lys Arg Arg Lys Glu Phe Ile Asn Gln Ser	
90 95 100	
CCA AAT ATT GAC AAT ATT TAT GCC AAA GCT ATT ATC ACA CAA TTT GAA	390
Pro Asn Ile Asp Asn Ile Tyr Ala Lys Ala Ile Ile Thr Gln Phe Glu	
105 110 115	
AGC AAG GGA ATC TAT AAA ACA GAG TAT TTT TTA GTG TTT GAA ACT ATC	438
Ser Lys Gly Ile Tyr Lys Thr Glu Tyr Phe Leu Val Phe Glu Thr Ile	
120 125 130	
ACT TCT AAT GTC AAG TCT TTC TTT GAA AAA AAG AAA TTG GAA ATG ACT	486
Thr Ser Asn Val Lys Ser Phe Phe Glu Lys Lys Lys Leu Glu Met Thr	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

```

CTGGTTTATG AGTATTTTTT AAAAGAAGTC CCC ATG CAA TTA GTT GGT ATT TCA      54
                        Met Gln Leu Val Gly Ile Ser
                          1                5

GTT TCT AAT CTC AAA GAA ATC AGC TCC AAA GAA AAA TTT CTT TGG CTC      102
Val Ser Asn Leu Lys Glu Ile Ser Ser Lys Glu Lys Phe Leu Trp Leu
    10                15                20

AAT GCT AAG AGT TTT TTA CTC TCA GGA TTT GTG CCT TTT ATT ATG ATA      150
Asn Ala Lys Ser Phe Leu Leu Ser Gly Phe Val Pro Phe Ile Met Ile
    25                30                35

CCT TGG CTA GAT ATA TTG AAC TCT TTT GTG CTT TAT GTG TGC TTT CTC      198
Pro Trp Leu Asp Ile Leu Asn Ser Phe Val Leu Tyr Val Cys Phe Leu
    40                45                50                55

TTA ATT TTT AGC ATA GCG GAG TTC TTT GAT GAA GAT ATA AGT GAC ATT      246
Leu Ile Phe Ser Ile Ala Glu Phe Phe Asp Glu Asp Ile Ser Asp Ile
                60                65                70

TTA ATC GCT CAT TCC AAA ATT AAA ACC AAA GCT AAT TCA TTT TAC GCT T      295
Leu Ile Ala His Ser Lys Ile Lys Thr Lys Ala Asn Ser Phe Tyr Ala
                75                80                85

AAAAGGAAAA AATATGCAAA AAGAAGTCTT AGTAGAAAA      334

```

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

```

Met Gln Leu Val Gly Ile Ser Val Ser Asn Leu Lys Glu Ile Ser Ser
  1                5                10                15
Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Phe Leu Leu Ser Gly
    20                25                30
Phe Val Pro Phe Ile Met Ile Pro Trp Leu Asp Ile Leu Asn Ser Phe
    35                40                45
Val Leu Tyr Val Cys Phe Leu Leu Ile Phe Ser Ile Ala Glu Phe Phe
    50                55                60
Asp Glu Asp Ile Ser Asp Ile Leu Ile Ala His Ser Lys Ile Lys Thr
    65                70                75                80
Lys Ala Asn Ser Phe Tyr Ala
                85

```

(2) INFORMATION FOR SEQ ID NO:1323:

AAC AAT CTT ACA AAA TAT TAT CCA AGT TCT GTG TGATTAAAAA AGAAAGAAAT 488
 Asn Asn Leu Thr Lys Tyr Tyr Pro Ser Ser Val
 140 145 150

ATCGCATGAA AAAATTAAGT CATTTTAGAA AGCTTATCGC CTT 531

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met	Ile	Lys	Leu	Ile	Leu	His	Lys	Lys	Ser	Ile	Gln	Ile	Asp	Glu	Thr	1	5	10	15
Leu	Leu	Asn	Val	Lys	Glu	His	Leu	Glu	Lys	Phe	Tyr	Ser	Asn	Lys	Glu	20	25	30	
Gln	Glu	Thr	Ile	Ala	Gln	Thr	Leu	Glu	Asn	Glu	Thr	Glu	Ile	Ser	Cys	35	40	45	
Ser	Tyr	Phe	Trp	Asp	Lys	Asp	Phe	Leu	Leu	Leu	Glu	Gln	Leu	Leu	Glu	50	55	60	
Asn	Xaa	Leu	Gly	His	Phe	Thr	Phe	Glu	Ser	Glu	Phe	Ala	Leu	Leu	Lys	65	70	75	80
Asp	Lys	Glu	Thr	Leu	Asn	Leu	Ser	Gln	Ile	Lys	Gln	Ile	Gly	Val	Leu	85	90	95	
Lys	Val	Leu	Thr	Tyr	Xaa	Met	Ile	Gln	Thr	Leu	Lys	Asn	Gln	Ile	Ile	100	105	110	
His	Leu	Ala	Gln	Val	Val	Asn	Glu	Glu	Asn	Leu	Glu	Lys	Asp	Glu	Glu	115	120	125	
Leu	Val	Val	Tyr	His	Leu	Asn	Phe	Thr	Ser	Arg	Asn	Asn	Leu	Thr	Lys	130	135	140	
Tyr	Tyr	Pro	Ser	Ser	Val											145	150		

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...294
- (D) OTHER INFORMATION:

(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...468
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

ATTTACTAAA GGAAACAA ATG ATT AAA CTA ATC TTA CAC AAG AAG TCC ATA	51
Met Ile Lys Leu Ile Leu His Lys Lys Ser Ile	
1 5 10	
CAA ATT GAT GAA ACA TTG CTG AAT GTA AAA GAG CAT TTA GAA AAG TTT	99
Gln Ile Asp Glu Thr Leu Leu Asn Val Lys Glu His Leu Glu Lys Phe	
15 20 25	
TAT TCA AAT AAA GAA CAA GAG ACA ATC GCT CAA ACT TTA GAG AAT GAA	147
Tyr Ser Asn Lys Glu Gln Glu Thr Ile Ala Gln Thr Leu Glu Asn Glu	
30 35 40	
ACA GAA ATT TCT TGT AGC TAT TTT TGG GAC AAA GAC TTC TTG TTG TTA	195
Thr Glu Ile Ser Cys Ser Tyr Phe Trp Asp Lys Asp Phe Leu Leu Leu	
45 50 55	
GAG CAA CTT TTA GAA AAT RAT TTA GGT CAT TTT ACC TTT GAG AGC GAG	243
Glu Gln Leu Leu Glu Asn Xaa Leu Gly His Phe Thr Phe Glu Ser Glu	
60 65 70 75	
TTT GCC CTA CTA AAA GAT AAA GAG ACT TTA AAC CTA TCT CAA ATC AAA	291
Phe Ala Leu Leu Lys Asp Lys Glu Thr Leu Asn Leu Ser Gln Ile Lys	
80 85 90	
CAA ATC GGT GTC TTA AAG GTT CTT ACC TAT GAR ATG ATA CAA ACC TTA	339
Gln Ile Gly Val Leu Lys Val Leu Thr Tyr Xaa Met Ile Gln Thr Leu	
95 100 105	
AAA AAT CAA ATC ATT CAT TTA GCA CAA GTT GTC AAT GAA GAA AAT TTA	387
Lys Asn Gln Ile Ile His Leu Ala Gln Val Val Asn Glu Glu Asn Leu	
110 115 120	
GAA AAA GAT GAA GAA CTT GTT GTC TAC CAC CTA AAT TTC ACG TCA CGC	435
Glu Lys Asp Glu Glu Leu Val Val Tyr His Leu Asn Phe Thr Ser Arg	
125 130 135	

Lys Tyr Asn Phe Asp Phe Asp Val Ile Phe Tyr Ser Phe Gly Glu Gln
 185 190 195
 TTA ATG CCT ATT CTT ACT AGA ATG TTA GTT TCT GTC TCT AAG TCT CAT 678
 Leu Met Pro Ile Leu Thr Arg Met Leu Val Ser Val Ser Lys Ser His
 200 205 210
 AGA AAG AGA CTT GAA AAC TAT GGC AAA GAC ATT AAA ACC TAATTTAGAT AA 729
 Arg Lys Arg Leu Glu Asn Tyr Gly Lys Asp Ile Lys Thr
 215 220 225
 AGATGAGTTA AACACA 745

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

Met Gly Gln Lys Arg Met Asn Lys Ser Asn Lys Leu Val Ile Ile Asn
 1 5 10 15
 Arg Ala Ile Pro Gly Gly Gly Lys Thr Ser Leu Ile Lys Gln Ile Glu
 20 25 30
 Glu Leu Ala Lys Ser Leu Gly His Ser Ile Ser Val His Ser Thr Asp
 35 40 45
 Glu Tyr Phe Ile Gln Thr Asp Glu Glu Gly Ile Arg His Tyr Val Val
 50 55 60
 Asp Lys Lys Lys Leu Asn Glu Tyr His Gln Asn Asn Gln Glu Ala Phe
 65 70 75 80
 Lys Gln Ala Leu Glu Asn Arg Ile Asp Ile Val Val Cys Asp Asn Thr
 85 90 95
 Asn Phe Glu Ser Trp Gln Ser Lys Pro Tyr Thr Asp Met Ala Arg Glu
 100 105 110
 Phe Gly Tyr Lys Ile Leu Leu Ile Asp Phe Lys Asn Arg His Leu Glu
 115 120 125
 Thr Pro Met Asp Tyr Gly Trp Asp Val Ala Gln Cys Ile Lys Lys Pro
 130 135 140
 Arg Gly Ile Ala Lys His Tyr Asp Tyr Asp Phe Tyr Leu Glu Arg Val
 145 150 155 160
 Leu Val Glu Pro Gln Asp Tyr Glu Lys Gln Asn Arg Glu Leu Ser Leu
 165 170 175
 Lys Ala Leu Glu Phe Leu Lys Tyr Asn Phe Asp Phe Asp Val Ile Phe
 180 185 190
 Tyr Ser Phe Gly Glu Gln Leu Met Pro Ile Leu Thr Arg Met Leu Val
 195 200 205
 Ser Val Ser Lys Ser His Arg Lys Arg Leu Glu Asn Tyr Gly Lys Asp
 210 215 220
 Ile Lys Thr
 225

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

TAAGGGGGGA TTTGGAAGGT GTTGGAATTG AAATTA	ATG GGA CAG AAG AGG ATG	54
	Met Gly Gln Lys Arg Met	
	1 5	
AAT AAA TCA AAC AAA TTA GTC ATT ATC AAT CGC GCC ATT CCA GGT GGG	102	
Asn Lys Ser Asn Lys Leu Val Ile Ile Asn Arg Ala Ile Pro Gly Gly		
10 15 20		
GGC AAG ACC TCT TTG ATC AAA CAG ATT GAA GAG TTG GCA AAA AGC TTG	150	
Gly Lys Thr Ser Leu Ile Lys Gln Ile Glu Glu Leu Ala Lys Ser Leu		
25 30 35		
GGG CAT TCT ATT AGC GTT CAT TCT ACC GAT GAA TAT TTC ATC CAA ACA	198	
Gly His Ser Ile Ser Val His Ser Thr Asp Glu Tyr Phe Ile Gln Thr		
40 45 50		
GAT GAA GAG GGT ATC AGG CAT TAT GTT GTT GAT AAA AAG AAA CTC AAT	246	
Asp Glu Glu Gly Ile Arg His Tyr Val Val Asp Lys Lys Lys Leu Asn		
55 60 65 70		
GAA TAC CAC CAA AAC AAT CAA GAA GCC TTC AAA CAA GCT TTA GAA AAT	294	
Glu Tyr His Gln Asn Asn Gln Glu Ala Phe Lys Gln Ala Leu Glu Asn		
75 80 85		
CGT ATA GAT ATT GTA GTG TGC GAT AAC ACC AAT TTT GAA TCG TGG CAA	342	
Arg Ile Asp Ile Val Val Cys Asp Asn Thr Asn Phe Glu Ser Trp Gln		
90 95 100		
AGC AAA CCA TAT ACA GAT ATG GCT AGA GAA TTT GGC TAT AAA ATT TTG	390	
Ser Lys Pro Tyr Thr Asp Met Ala Arg Glu Phe Gly Tyr Lys Ile Leu		
105 110 115		
TTG ATT GAT TTT AAG AAT AGA CAC TTA GAA ACC CCC ATG GAT TAT GGA	438	
Leu Ile Asp Phe Lys Asn Arg His Leu Glu Thr Pro Met Asp Tyr Gly		
120 125 130		
TGG GAT GTT GCG CAA TGC ATC AAG AAG CCA CGA GGT ATT GCA AAG CAT	486	
Trp Asp Val Ala Gln Cys Ile Lys Lys Pro Arg Gly Ile Ala Lys His		
135 140 145 150		
TAT GAC TAT GAT TTT TAT TTG GAG AGG GTT TTG GTT GAG CCA CAG GAT	534	
Tyr Asp Tyr Asp Phe Tyr Leu Glu Arg Val Leu Val Glu Pro Gln Asp		
155 160 165		
TAT GAG AAA CAA AAT AGA GAG TTG AGC TTA AAA GCC TTA GAA TTT TTG	582	
Tyr Glu Lys Gln Asn Arg Glu Leu Ser Leu Lys Ala Leu Glu Phe Leu		
170 175 180		
AAA TAC AAT TTT GAT TTT GAT GTG ATT TTT TAT TCT TTT GGG GAG CAA	630	

		35					40					45				
Leu	Lys	Gln	Leu	Glu	Asn	Lys	Glu	Asn	Leu	Lys	Ala	Asp	Asn	Asn	Thr	
	50					55					60					
Glu	Phe	Lys	Glu	Glu	Asn	Gln	Asp	Thr	Lys	Glu	Asn	Gln	Pro	Asn	Asp	
65					70					75					80	
Leu	Phe	Ser	Leu	Pro	Leu	Pro	Thr	Gln	Thr	Thr	Ile	Asn	Gly	Ile	Lys	
				85					90					95		
Glu	Phe	Val	Glu	Glu	Pro	Val	Ile	Glu	Thr	Glu	Lys	Lys	Glu	Thr	Ser	
			100					105					110			
Gln	Asn	Glu	Pro	Ile	Gln	Glu	Lys	Lys	Glu	Arg	Ile	Phe	Lys	Asn	Phe	
		115					120					125				
Phe	Ser	Arg	Ile	Gly	Phe	Asp	Lys	Ser	Ile	Ala	Pro	Thr	Met	Leu	Phe	
	130					135					140					
Glu	Glu	Val	Arg	Asp	Ala	Ser	Val	Ile	Tyr	His	Leu	Glu	Lys	Lys	Leu	
145					150					155					160	
Gly	Asp	Tyr	Ile	Phe	Tyr	Val	Ala	Cys	Phe	Phe	Phe	Gly	Thr	Thr	Ala	
			165						170						175	
Leu	Leu	Ile	Ile	Leu	Leu	Thr	Ile	Leu	Leu	Pro	Leu	Lys	Gln	Lys	Glu	
			180					185					190			
Pro	Tyr	Leu	Val	Gln	Phe	Ser	Asn	Asn	Lys	Glu	Asn	Phe	Ala	Leu	Val	
		195					200					205				
Gln	Lys	Ala	Asp	Ser	Ser	Ile	Thr	Ala	Asn	Lys	Ala	Leu	Ile	Arg	Ser	
	210					215					220					
Leu	Val	Gly	Ala	Tyr	Val	Leu	Asn	Arg	Glu	Ser	Ile	Thr	His	Ile	Glu	
225					230					235					240	
Gln	His	Glu	Lys	Met	Arg	Gln	Asn	Thr	Ile	Lys	Glu	Gln	Ser	Ser	Asn	
				245					250					255		
Glu	Val	Trp	Tyr	Glu	Phe	Glu	Lys	Leu	Ile	Ala	His	Tyr	Asp	Ser	Ile	
			260					265					270			
Tyr	Thr	Asn	Pro	Leu	Leu	Thr	Arg	Lys	Val	Lys	Ile	Ala	Asn	Ile	Tyr	
	275						280					285				
Leu	Asp	Lys	Asp	Leu	Ala	Tyr	Ile	Asp	Ile	Glu	Val	Ser	Leu	Tyr	His	
	290					295					300					
Ser	Gly	Glu	Leu	Glu	Ser	Leu	Lys	Arg	Tyr	Lys	Val	Val	Met	Ser	Phe	
305					310					315					320	
Glu	Phe	Lys	Lys	Gln	Glu	Ile	Asn	Phe	Asp	Ser	Met	Ser	Leu	Asn	Pro	
				325					330					335		
Thr	Gly	Phe	Met	Val	Thr	Ser	Tyr	Asp	Val	Thr	Glu	Ile	Ala	Ile	Val	
			340					345					350			
Asn	Tyr	Pro	Thr	Ala	Lys	Ala	Ile	Gly	Leu	Phe	Leu	Ala	Ser			
		355					360					365				

(2) INFORMATION FOR SEO ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 37...717

ACT CAT ATT GAG CAA CAT GAA AAA ATG CGT CAA AAC ACC ATT AAA GAG	771
Thr His Ile Glu Gln His Glu Lys Met Arg Gln Asn Thr Ile Lys Glu	
240 245 250	
CAA AGT TCC AAT GAA GTA TGG TAT GAA TTT GAA AAA CTC ATC GCT CAT	819
Gln Ser Ser Asn Glu Val Trp Tyr Glu Phe Glu Lys Leu Ile Ala His	
255 260 265	
TAT GAC AGC ATT TAC ACT AAT CCT TTA CTC ACA AGA AAA GTA AAG ATT	867
Tyr Asp Ser Ile Tyr Thr Asn Pro Leu Leu Thr Arg Lys Val Lys Ile	
270 275 280	
GCA AAT ATT TAC TTA GAT AAA GAT TTA GCC TAT ATT GAC ATT GAA GTG	915
Ala Asn Ile Tyr Leu Asp Lys Asp Leu Ala Tyr Ile Asp Ile Glu Val	
285 290 295 300	
AGC TTG TAT CAT AGT GGA GAA TTA GAG AGC TTG AAG CGC TAT AAA GTG	963
Ser Leu Tyr His Ser Gly Glu Leu Glu Ser Leu Lys Arg Tyr Lys Val	
305 310 315	
GTG ATG AGT TTT GAA TTT AAA AAA CAA GAA ATC AAT TTT GAC TCC ATG	1011
Val Met Ser Phe Glu Phe Lys Lys Gln Glu Ile Asn Phe Asp Ser Met	
320 325 330	
TCT TTA AAT CCT ACA GGC TTT ATG GTT ACA AGT TAT GAT GTA ACT GAA	1059
Ser Leu Asn Pro Thr Gly Phe Met Val Thr Ser Tyr Asp Val Thr Glu	
335 340 345	
ATT GCG ATT GTG AAT TAC CCA ACC GCT AAA GCG ATT GGG CTT TTT CTT	1107
Ile Ala Ile Val Asn Tyr Pro Thr Ala Lys Ala Ile Gly Leu Phe Leu	
350 355 360	
GCT TCA TAGCTCCATA ACTAGCTAGA TCCAATATGT TTCCATATTT AGAACTAACC CC	1165
Ala Ser	
365	
GTTAGAGGAA GCTCCACAAG	1185

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

Met Ser Lys Arg Ser Glu Val Leu Glu Gln Phe His Gly Gly Leu Lys	
1 5 10 15	
Asn Leu Glu Leu Gln Thr Lys Arg Arg Met Gly Leu Trp Gly Asp Pro	
20 25 30	
Lys Glu Asn Glu Glu Gln Thr Leu Phe Leu Glu Glu Ile Glu Asn Glu	

GGC	GGT	TTA	AAA	AAT	TTA	GAA	TTA	CAA	ACT	AAA	AGA	CGC	ATG	GGT	TTG	99
Gly	Gly	Leu	Lys	Asn	Leu	Glu	Leu	Gln	Thr	Lys	Arg	Arg	Met	Gly	Leu	
		15					20					25				
TGG	GGC	GAT	CCA	AAA	GAG	AAT	GAA	GAA	CAA	ACT	TTG	TTT	TTA	GAA	GAA	147
Trp	Gly	Asp	Pro	Lys	Glu	Asn	Glu	Glu	Gln	Thr	Leu	Phe	Leu	Glu	Glu	
	30					35					40					
ATT	GAA	AAT	GAA	TTA	AAG	CAA	TTA	GAA	AAC	AAA	GAA	AAT	CTT	AAA	GCA	195
Ile	Glu	Asn	Glu	Leu	Lys	Gln	Leu	Glu	Asn	Lys	Glu	Asn	Leu	Lys	Ala	
45					50				55					60		
GAC	AAC	AAC	ACA	GAA	TTT	AAA	GAA	GAA	AAT	CAA	GAC	ACT	AAA	GAA	AAC	243
Asp	Asn	Asn	Thr	Glu	Phe	Lys	Glu	Glu	Asn	Gln	Asp	Thr	Lys	Glu	Asn	
				65					70					75		
CAG	CCT	AAC	GAT	TTG	TTT	TCT	TTG	CCA	TTG	CCC	ACT	CAA	ACC	ACC	ATC	291
Gln	Pro	Asn	Asp	Leu	Phe	Ser	Leu	Pro	Leu	Pro	Thr	Gln	Thr	Thr	Ile	
			80					85					90			
AAT	GGA	ATT	AAA	GAA	TTT	GTA	GAA	GAG	CCT	GTG	ATA	GAA	ACA	GAG	AAA	339
Asn	Gly	Ile	Lys	Glu	Phe	Val	Glu	Glu	Pro	Val	Ile	Glu	Thr	Glu	Lys	
		95					100					105				
AAA	GAA	ACA	TCC	CAA	AAT	GAG	CCA	ATC	CAA	GAA	AAA	AAA	GAA	AGA	ATT	387
Lys	Glu	Thr	Ser	Gln	Asn	Glu	Pro	Ile	Gln	Glu	Lys	Lys	Glu	Arg	Ile	
	110					115					120					
TTT	AAA	AAC	TTT	TTC	TCC	AGA	ATA	GGC	TTT	GAT	AAA	AGT	ATT	GCC	CCT	435
Phe	Lys	Asn	Phe	Phe	Ser	Arg	Ile	Gly	Phe	Asp	Lys	Ser	Ile	Ala	Pro	
125					130					135				140		
ACA	ATG	CTT	TTT	GAA	GAA	GTG	AGA	GAT	GCA	AGC	GTT	ATC	TAT	CAT	TTA	483
Thr	Met	Leu	Phe	Glu	Glu	Val	Arg	Asp	Ala	Ser	Val	Ile	Tyr	His	Leu	
				145					150					155		
GAG	AAA	AAA	TTA	GGC	GAT	TAT	ATC	TTT	TAT	GTA	GCG	TGT	TTC	TTC	TTT	531
Glu	Lys	Lys	Leu	Gly	Asp	Tyr	Ile	Phe	Tyr	Val	Ala	Cys	Phe	Phe	Phe	
			160					165					170			
GGC	ACA	ACG	GCA	TTG	CTT	ATT	ATC	TTA	CTG	ACT	ATT	CTG	TTG	CCC	TTA	579
Gly	Thr	Thr	Ala	Leu	Leu	Ile	Ile	Leu	Leu	Thr	Ile	Leu	Leu	Pro	Leu	
			175				180					185				
AAA	CAA	AAA	GAG	CCG	TAT	TTA	GTG	CAA	TTT	TCT	AAC	AAT	AAA	GAA	AAT	627
Lys	Gln	Lys	Glu	Pro	Tyr	Leu	Val	Gln	Phe	Ser	Asn	Asn	Lys	Glu	Asn	
	190					195					200					
TTT	GCT	TTA	GTT	CAA	AAG	GCA	GAT	AGC	AGC	ATT	ACA	GCC	AAT	AAA	GCT	675
Phe	Ala	Leu	Val	Gln	Lys	Ala	Asp	Ser	Ser	Ile	Thr	Ala	Asn	Lys	Ala	
205					210					215				220		
CTT	ATT	CGT	TCA	TTA	GTG	GGA	GCG	TAT	GTG	CTA	AAC	AGG	GAA	AGC	ATT	723
Leu	Ile	Arg	Ser	Leu	Val	Gly	Ala	Tyr	Val	Leu	Asn	Arg	Glu	Ser	Ile	
				225					230					235		

Cys Val Leu Pro Tyr Glu Tyr Glu Asn Lys Glu Asp Lys Glu Asn Ser
 145 150 155 160
 Glu Glu Ile Leu Lys Glu Asp Phe Arg Leu Leu Asn Thr Lys Gly Gly
 165 170 175
 Leu Ser Val Lys Arg Ala Leu Ile Asn Asn Arg His Ser Tyr Glu Ala
 180 185 190
 Ile Lys Leu Arg Pro Ile Lys Gln Glu Leu Val Pro Gly Leu Cys Leu
 195 200 205
 Phe Phe Gln Gly Ser Leu Glu Phe Asn Asp Lys Thr Thr Lys Thr Met
 210 215 220
 Arg Thr Ser Leu Leu Asp Gln Ile Gln Gln Asp Asp Lys Ser Tyr Leu
 225 230 235 240
 Lys Ile Trp Glu Lys Tyr Leu Ile Lys Ser Ala Gln Lys Ser Phe Asn
 245 250 255
 Glu Ala Lys Glu Val Gly Val Leu Glu Ile Glu Ser Val Ser Lys Glu
 260 265 270
 Gly Gly Asn Leu Arg Ile Arg Phe Lys Pro Ala Leu Gly Lys Asn Lys
 275 280 285
 Met Glu Ile Leu Lys Lys Ser Gln Phe Lys Lys Gly Ser Asp Leu Gly
 290 295 300
 Val Leu Glu Asp Leu Asp Pro Gln Asn Glu Glu Asn Leu Ile Asn Leu
 305 310 315 320
 Ile Ser Glu Gln Lys Lys Gln Ile Ser Lys Asn Asn Ser Gln Ser Ile
 325 330 335
 Met Ile Glu Asp Ile Ser Gly Asp Asp Phe Ile Ile Asp Tyr Asp Leu
 340 345 350
 Ser Ile Lys Glu Gly Asp Ala Phe His Leu Asn Tyr Met Gly Asp Leu
 355 360 365
 Asn Thr Leu Lys Lys Gln Tyr Ser Ala Leu Asp Lys Thr Lys Lys Gly
 370 375 380
 Leu Lys Arg Gln Ser
 385

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...1113
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

TCCATAGGCT AGTTG ATG TCA AAA AGA AGC GAA GTT TTA GAA CAA TTT CAT 51
 Met Ser Lys Arg Ser Glu Val Leu Glu Gln Phe His
 1 5 10

```

Lys Lys Gly Ser Asp Leu Gly Val Leu Glu Asp Leu Asp Pro Gln Asn
    300                      305                      310

GAA GAA AAT TTA ATC AAT CTT ATT TCT GAA CAA AAG AAA CAA ATT TCT      1013
Glu Glu Asn Leu Ile Asn Leu Ile Ser Glu Gln Lys Lys Gln Ile Ser
    315                      320                      325

AAA AAC AAC AGC CAA TCA ATA ATG ATT GAA GAC ATT AGT GGG GAT GAT      1061
Lys Asn Asn Ser Gln Ser Ile Met Ile Glu Asp Ile Ser Gly Asp Asp
    330                      335                      340                      345

TTT ATT ATA GAT TAC GAT CTT TCC ATA AAA GAG GGC GAT GCT TTT CAT      1109
Phe Ile Ile Asp Tyr Asp Leu Ser Ile Lys Glu Gly Asp Ala Phe His
    350                      355                      360

TTA AAT TAT ATG GGG GAT CTA AAT ACG CTT AAA AAA CAA TAT AGC GCA      1157
Leu Asn Tyr Met Gly Asp Leu Asn Thr Leu Lys Lys Gln Tyr Ser Ala
    365                      370                      375

TTA GAT AAG ACA AAG AAA GGT TTG AAG CGC CAA TCC TAATTTAGGA TTAATT      1209
Leu Asp Lys Thr Lys Lys Gly Leu Lys Arg Gln Ser
    380                      385

TTAAACATTA AAGAGGATAA AGAGAATAGT GATAGCGATA ATGATACTGC A      1260

```

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

```

Met Leu Ser Phe Ile Lys Glu Asp Ser Ile Ile Lys Ala Tyr Asn Leu
 1           5           10           15
Asn Thr Ala Lys Leu Glu Pro Lys Asp Arg Glu Lys Leu Gly Leu Leu
    20           25           30
Lys Ile Glu Lys Asn Lys Ile Tyr Phe His Leu Asp Glu Lys Arg Tyr
    35           40           45
Leu Lys Leu Glu Ile Ile Gly Lys Thr Lys Glu Lys Glu Ile Lys Asn
    50           55           60
Ala Phe Cys Ser Asn Ala Phe Leu Ala Ala Gln Val Leu Asn Leu Asn
    65           70           75           80
Gln Glu Arg Gln Val Leu Glu Leu Lys Cys His Phe Phe Lys His Pro
    85           90           95
Ile Lys Ile Leu Pro Glu Pro Leu Asn Ile Asn Phe Lys Asp Thr Ile
    100          105          110
Ile Lys Lys Leu Leu Lys Asp Met Gly Lys Asp Lys Lys Ile Glu Asp
    115          120          125
Phe Lys Glu Thr Cys Ile Leu Lys Ile Ala Gly Phe Thr Tyr Phe Val
    130          135          140

```

75	80	85	
TGC CAT TTC TTC AAG CAC CCT ATA AAA ATT CTT CCT GAA CCA TTA AAC			341
Cys His Phe Phe Lys His Pro Ile Lys Ile Leu Pro Glu Pro Leu Asn			
90	95	100	105
ATT AAT TTC AAA GAC ACA ATC ATA AAA AAG TTA CTA AAA GAT ATG GGC			389
Ile Asn Phe Lys Asp Thr Ile Ile Lys Lys Leu Leu Lys Asp Met Gly			
	110	115	120
AAA GAT AAA AAA ATA GAA GAT TTT AAA GAA ACT TGT ATT TTA AAA ATA			437
Lys Asp Lys Lys Ile Glu Asp Phe Lys Glu Thr Cys Ile Leu Lys Ile			
	125	130	135
GCT GGT TTT ACT TAT TTT GTG TGC GTA TTG CCT TAT GAA TAT GAG AAT			485
Ala Gly Phe Thr Tyr Phe Val Cys Val Leu Pro Tyr Glu Tyr Glu Asn			
	140	145	150
AAA GAG GAT AAA GAG AAT AGT GAA GAG ATT TTA AAA GAA GAT TTC AGG			533
Lys Glu Asp Lys Glu Asn Ser Glu Glu Ile Leu Lys Glu Asp Phe Arg			
	155	160	165
CTG TTA AAT ACC AAG GGG GGA TTA AGC GTT AAG CGT GCT TTG ATA AAT			581
Leu Leu Asn Thr Lys Gly Gly Leu Ser Val Lys Arg Ala Leu Ile Asn			
	170	175	180
AAC AGG CAT TCT TAT GAA GCG ATA AAA TTA AGA CCC ATT AAA CAA GAG			629
Asn Arg His Ser Tyr Glu Ala Ile Lys Leu Arg Pro Ile Lys Gln Glu			
	190	195	200
TTA GTG CCT GGT TTG TGT TTG TTT TTT CAA GGT TCA TTA GAA TTT AAT			677
Leu Val Pro Gly Leu Cys Leu Phe Phe Gln Gly Ser Leu Glu Phe Asn			
	205	210	215
GAT AAA ACC ACA AAA ACC ATG CGA ACG AGC CTT TTA GAC CAG ATC CAG			725
Asp Lys Thr Thr Lys Thr Met Arg Thr Ser Leu Leu Asp Gln Ile Gln			
	220	225	230
CAA GAT GAC AAA TCT TAT TTA AAA ATT TGG GAA AAA TAT CTC ATC AAA			773
Gln Asp Asp Lys Ser Tyr Leu Lys Ile Trp Glu Lys Tyr Leu Ile Lys			
	235	240	245
AGC GCT CAA AAA AGT TTT AAT GAG GCA AAA GAA GTG GGG GTT TTA GAG			821
Ser Ala Gln Lys Ser Phe Asn Glu Ala Lys Glu Val Gly Val Leu Glu			
	250	255	260
ATT GAA AGC GTG AGT AAA GAA GGA GGG AAT TTA AGA ATT CGT TTT AAG			869
Ile Glu Ser Val Ser Lys Glu Gly Gly Asn Leu Arg Ile Arg Phe Lys			
	270	275	280
CCA GCT TTA GGC AAG AAT AAA ATG GAA ATC TTA AAG AAA TCA CAA TTT			917
Pro Ala Leu Gly Lys Asn Lys Met Glu Ile Leu Lys Lys Ser Gln Phe			
	285	290	295
AAA AAG GGG AGT GAT TTA GGG GTT TTA GAG GAT TTA GAC CCA CAA AAT			965

(2) INFORMATION FOR SEO ID NO:1313:

(A) LENGTH: 1260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 27...1193
(D) OTHER INFORMATION:

AATGGTTTTT	TAATTAAGGT	TCAAAA	ATG	CTG	AGT	TTT	ATC	AAA	GAA	GAT	AGC					53
			Met	Leu	Ser	Phe	Ile	Lys	Glu	Asp	Ser					
			1					5								
ATC	ATC	AAG	GCT	TAT	AAC	CTC	AAT	ACC	GCA	AAA	CTA	GAG	CCA	AAA	GAT	101
Ile	Ile	Lys	Ala	Tyr	Asn	Leu	Asn	Thr	Ala	Lys	Leu	Glu	Pro	Lys	Asp	
10					15					20					25	
AGA	GAA	AAA	TTG	GGA	TTA	TTA	AAG	ATT	GAA	AAA	AAT	AAA	ATA	TAT	TTT	149
Arg	Glu	Lys	Leu	Gly	Leu	Leu	Lys	Ile	Glu	Lys	Asn	Lys	Ile	Tyr	Phe	
				30					35					40		
CAT	CTA	GAT	GAA	AAG	CGT	TAT	TTG	AAA	TTA	GAG	ATC	ATA	GGC	AAA	ACC	197
His	Leu	Asp	Glu	Lys	Arg	Tyr	Leu	Lys	Leu	Glu	Ile	Ile	Gly	Lys	Thr	
			45					50					55			
AAA	GAA	AAA	GAA	ATT	AAA	AAC	GCT	TTT	TGC	AGT	AAT	GCT	TTT	CTT	GCA	245
Lys	Glu	Lys	Glu	Ile	Lys	Asn	Ala	Phe	Cys	Ser	Asn	Ala	Phe	Leu	Ala	
		60					65					70				
GCT	CAA	GTC	CTA	AAT	TTA	AAC	CAA	GAA	AGA	CAA	GTT	TTA	GAA	TTG	AAG	293
Ala	Gln	Val	Leu	Asn	Leu	Asn	Gln	Glu	Arg	Gln	Val	Leu	Glu	Leu	Lys	

ATA GAG AGC TTA GAA AAA GCT AGC TTG CAA GTG TTA GAA TGT GAA AAT	103
Ile Glu Ser Leu Glu Lys Ala Ser Leu Gln Val Leu Glu Cys Glu Asn	
5 10 15 20	
TGT TCA ATG ACT TAT TAT GAT AGA GAT TAT AAT AGA GAA TGT GAG ATT	151
Cys Ser Met Thr Tyr Tyr Asp Arg Asp Tyr Asn Arg Glu Cys Glu Ile	
25 30 35	
TGC CCT TAT TGC GAT GCT AAA AAA CCT GTC AGA CTT GTA GCA ACA AGT	199
Cys Pro Tyr Cys Asp Ala Lys Lys Pro Val Arg Leu Val Ala Thr Ser	
40 45 50	
TAT TAC CAA AAG AGC GAA GTT TTT TAT TTT GTC TCG AAT TTT ACA GAC	247
Tyr Tyr Gln Lys Ser Glu Val Phe Tyr Phe Val Ser Asn Phe Thr Asp	
55 60 65	
CCT ATT TTT TTA CCG ACA ACC TTA TTT AAG GGG ATT GAA GTG GTT AAA	295
Pro Ile Phe Leu Pro Thr Thr Leu Phe Lys Gly Ile Glu Val Val Lys	
70 75 80	
AGC GAA TGG GAG TTT GCA GAG ATT GCT AAT AAT ATA TTG ATT TTT CAT	343
Ser Glu Trp Glu Phe Ala Glu Ile Ala Asn Asn Ile Leu Ile Phe His	
85 90 95 100	
CAT GAC ATA CAA CAA GAA AAG ATT CTC ATT AAT AAT AAA AGA TTG GAT	391
His Asp Ile Gln Gln Glu Lys Ile Leu Ile Asn Asn Lys Arg Leu Asp	
105 110 115	
CAC TAT AGG ATA GAA ATA GAT TTA GAA AAA GAA TTG ACT ATT TCA TAC	439
His Tyr Arg Ile Glu Ile Asp Leu Glu Lys Glu Leu Thr Ile Ser Tyr	
120 125 130	
AAT GGT TTT TTA ATT AAG GTT CAA AAA TGC TGAGTTTTAT CAAAGAAGAT AGC	492
Asn Gly Phe Leu Ile Lys Val Gln Lys Cys	
135 140	
ATCATCAAGG CTTATAA	509

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

Met Pro Leu Phe Ile Glu Ser Leu Glu Lys Ala Ser Leu Gln Val Leu	
1 5 10 15	
Glu Cys Glu Asn Cys Ser Met Thr Tyr Tyr Asp Arg Asp Tyr Asn Arg	
20 25 30	
Glu Cys Glu Ile Cys Pro Tyr Cys Asp Ala Lys Lys Pro Val Arg Leu	

50		55		60	
Ser Phe Lys Pro Ile Glu	Ser His Phe Pro Met	Ser Ile Pro Leu Val			
65	70	75	80		
Thr Leu Lys Glu Lys Gln Gly Tyr Val	Met Lys Met Ala Glu Gly Tyr				
	85	90	95		
Glu Pro Leu Lys Thr Phe Leu Lys Lys Pro	Ser Ile Leu Glu Asn Glu				
	100	105	110		
Glu Lys Asp Gly Ile Phe Arg Ile Asn Asn Ala	Ile Gln Glu Leu Cys				
	115	120	125		
Lys Asp Asn His Tyr Met Thr Leu Ser Leu Ser	Tyr Tyr Ser Gln Thr				
	130	135	140		
Gln Gly Leu Arg Ser Arg Leu Lys Ile Leu Thr	His Leu Ala Lys Leu				
	145	150	155	160	
Leu Phe Arg Leu Gln Ser Lys Gly Leu Val Tyr	Gly Asp Leu Asn Leu				
	165	170	175		
Asn Asn Val Phe Tyr Lys Asp Asn Ser Ala Phe	Leu Ile Asp Ala Asp				
	180	185	190		
Asn Val Arg Tyr Glu Ser Glu Lys Ala Leu Cys	Val Ile Phe Thr Pro				
	195	200	205		
Asn Tyr Gly Ala Leu Glu Ile Ser Gln Thr Ser	Lys Asn Ser Asp Thr				
	210	215	220		
Thr Asn Tyr Asn Thr Met Leu Ser Asp Thr Phe	Ser Phe Ala Ile Ile				
	225	230	235	240	
Thr Tyr Glu Leu Leu Asn Met Val His Pro Phe	Asp Gly Asn Lys Ala				
	245	250	255		
Asp Asp Ser Val Glu Asn Phe Ile Glu Leu Pro	Trp Ile Glu Asp Arg				
	260	265	270		
Lys Asp Asp Ser Asn Arg Ser Cys Gly Leu Leu	Pro Phe Phe Leu Thr				
	275	280	285		
Arg Asp Leu Lys Asn Leu Leu Ala					
	290	295			

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...469
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

ATGCTTTGAA GAAGGCAAAA AAGATCCTTT GAAACGCCCT ACT ATG CCC TTA TTT	55
Met Pro Leu Phe	
1	

160	165	170	
GAC TTG AAT TTA AAC AAT GTT TTT TAT AAA GAC AAT TCA GCG TTT TTA			579
Asp Leu Asn Leu Asn Asn Val Phe Tyr Lys Asp Asn Ser Ala Phe Leu			
175	180	185	
ATT GAT GCG GAT AAT GTG CGT TAT GAG AGC GAA AAA GCC CTG TGT GTT			627
Ile Asp Ala Asp Asn Val Arg Tyr Glu Ser Glu Lys Ala Leu Cys Val			
190	195	200	
ATT TTT ACG CCT AAC TAT GGG GCT TTA GAG ATT AGC CAA ACC TCT AAA			675
Ile Phe Thr Pro Asn Tyr Gly Ala Leu Glu Ile Ser Gln Thr Ser Lys			
205	210	215	220
AAT AGC GAT ACA ACC AAT TAC AAC ACC ATG CTT AGC GAT ACC TTT TCT			723
Asn Ser Asp Thr Thr Asn Tyr Asn Thr Met Leu Ser Asp Thr Phe Ser			
225	230	235	
TTT GCT ATC ATA ACT TAT GAA CTT TTA AAT ATG GTT CAT CCT TTT GAT			771
Phe Ala Ile Ile Thr Tyr Glu Leu Leu Asn Met Val His Pro Phe Asp			
240	245	250	
GGG AAT AAG GCA GAT GAT AGT GTA GAA AAT TTT ATA GAA TTG CCT TGG			819
Gly Asn Lys Ala Asp Asp Ser Val Glu Asn Phe Ile Glu Leu Pro Trp			
255	260	265	
ATT GAA GAT AGA AAG GAT GAT AGC AAT CGT TCT TGT GGC TTA CTG CCT			867
Ile Glu Asp Arg Lys Asp Asp Ser Asn Arg Ser Cys Gly Leu Leu Pro			
270	275	280	
TTT TTC TTA ACA AGG GAT TTA AAA AAT TTA TTA GCG TAATGCTTTG AAGAAG			919
Phe Phe Leu Thr Arg Asp Leu Lys Asn Leu Leu Ala			
285	290	295	
GCAAAAAAGA TCCTTTGAAA CGCCCTAC			947

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

Met	Glu	Leu	Glu	Glu	Ile	Val	Asp	Ser	Glu	Arg	Asn	Ile	His	Lys	Thr
1				5					10					15	
Ile	Glu	Val	Leu	Gly	Lys	Gly	Gly	Gln	Gly	Ile	Val	Tyr	Arg	Cys	Leu
			20					25					30		
Asp	Lys	Asp	Val	Ala	Ile	Lys	Val	Val	Leu	Arg	Asp	Gly	Asp	Phe	Ile
		35					40					45			
Lys	Asp	Lys	Glu	Ser	Leu	Lys	Gln	Tyr	Glu	Lys	Ser	Val	Leu	Asn	Leu

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 16...903

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

TAGAAAAGGT AGTTT ATG GAG TTA GAA GAA ATT GTT GAT AGT GAG AGG AAT	51
Met Glu Leu Glu Glu Ile Val Asp Ser Glu Arg Asn	
1 5 10	
ATC CAT AAG ACT ATA GAA GTT TTA GGA AAA GGC GGA CAG GGT ATA GTG	99
Ile His Lys Thr Ile Glu Val Leu Gly Lys Gly Gly Gln Gly Ile Val	
15 20 25	
TAT CGC TGT TTG GAT AAG GAT GTG GCT ATT AAG GTA GTA TTG AGG GAT	147
Tyr Arg Cys Leu Asp Lys Asp Val Ala Ile Lys Val Val Leu Arg Asp	
30 35 40	
GGA GAT TTT ATT AAA GAC AAA GAA TCC CTC AAA CAA TAT GAA AAA AGC	195
Gly Asp Phe Ile Lys Asp Lys Glu Ser Leu Lys Gln Tyr Glu Lys Ser	
45 50 55 60	
GTT CTA AAC TTA TCT TTT AAG CCG ATA GAG AGT CAT TTC CCT ATG TCA	243
Val Leu Asn Leu Ser Phe Lys Pro Ile Glu Ser His Phe Pro Met Ser	
65 70 75	
ATT CCA CTG GTA ACT TTG AAA GAA AAA CAA GGC TAT GTG ATG AAA ATG	291
Ile Pro Leu Val Thr Leu Lys Glu Lys Gln Gly Tyr Val Met Lys Met	
80 85 90	
GCT GAG GGC TAT GAA CCA CTA AAA ACT TTT TTA AAG AAG CCC AGC ATT	339
Ala Glu Gly Tyr Glu Pro Leu Lys Thr Phe Leu Lys Lys Pro Ser Ile	
95 100 105	
TTA GAA AAC GAA GAA AAA GAT GGG ATT TTT AGG ATC AAT AAT GCC ATT	387
Leu Glu Asn Glu Glu Lys Asp Gly Ile Phe Arg Ile Asn Asn Ala Ile	
110 115 120	
CAA GAA CTT TGC AAA GAT AAC CAT TAT ATG ACT TTA AGT TTA AGT TAT	435
Gln Glu Leu Cys Lys Asp Asn His Tyr Met Thr Leu Ser Leu Ser Tyr	
125 130 135 140	
TAC TCA CAA ACA CAA GGA TTG AGA TCA CGA TTA AAA ATA CTC ACC CAT	483
Tyr Ser Gln Thr Gln Gly Leu Arg Ser Arg Leu Lys Ile Leu Thr His	
145 150 155	
TTA GCA AAA CTT CTA TTC AGA TTG CAA AGT AAG GGT TTG GTG TAT GGG	531
Leu Ala Lys Leu Leu Phe Arg Leu Gln Ser Lys Gly Leu Val Tyr Gly	

```

Thr Ser Met Thr Ala Phe Arg Phe Phe Glu Ala Leu Lys Lys Arg Gly
      20                      25                      30
His Val Met Arg Val Val Ala Pro His Val Asp Asn Leu Gly Ser Glu
      35                      40                      45
Glu Glu Gly Tyr Tyr Asn Leu Lys Glu Arg Tyr Ile Pro Leu Val Thr
      50                      55                      60
Glu Ile Ser His Lys Gln His Ile Leu Phe Ala Lys Pro Asp Glu Lys
      65                      70                      75                      80
Ile Leu Arg Lys Ala Phe Lys Gly Ala Asp Met Ile His Thr Tyr Leu
      85                      90                      95
Pro Phe Leu Leu Glu Lys Thr Ala Val Lys Ile Ala Arg Glu Met Gln
      100                     105                     110
Val Pro Tyr Ile Gly Ser Phe His Leu Gln Pro Glu His Ile Ser Tyr
      115                     120                     125
Asn Met Lys Leu Gly Trp Phe Ser Trp Phe Asn Met Met Leu Phe Ser
      130                     135                     140
Trp Phe Lys Ser Ser His Tyr Arg Tyr Ile His His Ile His Cys Pro
      145                     150                     155                     160
Ser Lys Phe Ile Val Glu Glu Leu Glu Lys Tyr Asn Tyr Gly Gly Lys
      165                     170                     175
Lys Tyr Ala Ile Ser Asn Gly Phe Asp Pro Met Phe Arg Phe Glu His
      180                     185                     190
Pro Gln Lys Ser Leu Phe Asp Thr Thr Pro Phe Lys Ile Ala Met Val
      195                     200                     205
Gly Arg Tyr Ser Asn Glu Lys Asn Gln Ser Val Leu Ile Lys Ala Val
      210                     215                     220
Ala Leu Ser Lys Tyr Lys Gln Asp Ile Val Leu Leu Lys Gly Lys
      225                     230                     235                     240
Gly Pro Asp Glu Lys Lys Ile Lys Leu Leu Ala Gln Lys Leu Gly Val
      245                     250                     255
Lys Ala Glu Phe Gly Phe Val Asn Ser Asn Glu Leu Leu Glu Ile Leu
      260                     265                     270
Lys Thr Cys Thr Leu Tyr Val His Ala Ala Asn Val Glu Ser Glu Ala
      275                     280                     285
Ile Ala Cys Leu Glu Ala Ile Ser Val Gly Ile Val Pro Val Ile Ala
      290                     295                     300
Asn Ser Pro Leu Ser Ala Thr Arg Gln Phe Ala Leu Asp Glu Arg Ser
      305                     310                     315                     320
Leu Phe Glu Pro Asn Asn Ala Lys Asp Leu Ser Ala Lys Ile Asp Trp
      325                     330                     335
Trp Leu Glu Asn Lys Leu Glu Arg Glu Arg Met Gln Asn Glu Tyr Ala
      340                     345                     350
Lys Ser Ala Leu Asn Tyr Thr Leu Glu Asn Ser Val Ile Gln Ile Glu
      355                     360                     365
Lys Val Tyr Glu Glu Ala Ile Arg Asp Phe Lys Asn Asn Pro His Leu
      370                     375                     380
Phe Lys Thr Leu Ser
      385

```

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

```

Ile Val Leu Leu Leu Lys Gly Lys Gly Pro Asp Glu Lys Lys Ile Lys
      235                      240                      245

CTT TTA GCC CAA AAA CTA GGC GTA AAA GCG GAG TTT GGG TTT GTC AAT      822
Leu Leu Ala Gln Lys Leu Gly Val Lys Ala Glu Phe Gly Phe Val Asn
      250                      255                      260

TCC AAT GAA TTG TTA GAG ATC TTA AAA ACT TGC ACC CTT TAT GTG CAT      870
Ser Asn Glu Leu Leu Glu Ile Leu Lys Thr Cys Thr Leu Tyr Val His
      265                      270                      275                      280

GCA GCC AAT GTG GAA AGC GAA GCG ATT GCG TGC TTA GAG GCC ATT AGC      918
Ala Ala Asn Val Glu Ser Glu Ala Ile Ala Cys Leu Glu Ala Ile Ser
      285                      290                      295

GTG GGG ATT GTG CCT GTT ATC GCT AAT AGC CCT TTA AGC GCG ACC AGG      966
Val Gly Ile Val Pro Val Ile Ala Asn Ser Pro Leu Ser Ala Thr Arg
      300                      305                      310

CAA TTT GCG CTA GAT GAA CGA TCG CTA TTT GAA CCT AAT AAC GCT AAA      1014
Gln Phe Ala Leu Asp Glu Arg Ser Leu Phe Glu Pro Asn Asn Ala Lys
      315                      320                      325

GAT TTG AGC GCT AAA ATA GAT TGG TGG TTA GAA AAC AAG CTT GAA AGA      1062
Asp Leu Ser Ala Lys Ile Asp Trp Trp Leu Glu Asn Lys Leu Glu Arg
      330                      335                      340

GAA AGG ATG CAA AAC GAA TAC GCT AAA AGC GCT TTA AAT TAC ACT TTA      1110
Glu Arg Met Gln Asn Glu Tyr Ala Lys Ser Ala Leu Asn Tyr Thr Leu
      345                      350                      355                      360

GAA AAT TCA GTC ATT CAA ATT GAA AAA GTT TAT GAA GAA GCG ATC AGA      1158
Glu Asn Ser Val Ile Gln Ile Glu Lys Val Tyr Glu Glu Ala Ile Arg
      365                      370                      375

GAT TTT AAA AAT AAC CCC CAT CTC TTT AAA ACC TTA TCA TAATGAAAGG AT      1209
Asp Phe Lys Asn Asn Pro His Leu Phe Lys Thr Leu Ser
      380                      385

AAAAAATGCA AGAAG      1224

```

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

```

Met Val Ile Val Leu Val Val Asp Ser Phe Lys Asp Thr Ser Asn Gly
  1              5              10              15

```

10	15	20	
TTT GAA GCG CTG AAA AAA AGA GGG CAT GTG ATG AGA GTG GTC GCC CCT			150
Phe Glu Ala Leu Lys Lys Arg Gly His Val Met Arg Val Val Ala Pro			
25	30	35	40
CAT GTG GAT AAT TTA GGG AGT GAA GAA GAG GGG TAT TAC AAC CTT AAA			198
His Val Asp Asn Leu Gly Ser Glu Glu Glu Gly Tyr Tyr Asn Leu Lys			
45	50		55
GAG CGC TAC ATC CCC CTA GTT ACA GAA ATT TCA CAC AAA CAA CAC ATC			246
Glu Arg Tyr Ile Pro Leu Val Thr Glu Ile Ser His Lys Gln His Ile			
60	65		70
CTT TTT GCT AAA CCC GAT GAA AAA ATC TTA AGA AAG GCT TTT AAG GGA			294
Leu Phe Ala Lys Pro Asp Glu Lys Ile Leu Arg Lys Ala Phe Lys Gly			
75	80		85
GCG GAT ATG ATC CAT ACT TAT TTG CCT TTT TTG CTA GAA AAA ACA GCC			342
Ala Asp Met Ile His Thr Tyr Leu Pro Phe Leu Leu Glu Lys Thr Ala			
90	95		100
GTA AAA ATC GCG CGA GAA ATG CAA GTG CCT TAT ATT GGC TCT TTC CAT			390
Val Lys Ile Ala Arg Glu Met Gln Val Pro Tyr Ile Gly Ser Phe His			
105	110	115	120
TTA CAG CCA GAG CAT ATT TCT TAT AAC ATG AAA TTG GGG TGG TTT TCT			438
Leu Gln Pro Glu His Ile Ser Tyr Asn Met Lys Leu Gly Trp Phe Ser			
125	130		135
TGG TTC AAC ATG ATG CTT TTT TCG TGG TTT AAA TCT TCG CAT TAC CGC			486
Trp Phe Asn Met Met Leu Phe Ser Trp Phe Lys Ser Ser His Tyr Arg			
140	145		150
TAT ATC CAC CAT ATC CAT TGC CCG TCA AAA TTC ATT GTA GAA GAA TTA			534
Tyr Ile His His Ile His Cys Pro Ser Lys Phe Ile Val Glu Glu Leu			
155	160		165
GAA AAA TAC AAC TAT GGA GGG AAA AAA TAC GCT ATT TCT AAC GGC TTT			582
Glu Lys Tyr Asn Tyr Gly Gly Lys Lys Tyr Ala Ile Ser Asn Gly Phe			
170	175		180
GAT CCC ATG TTT AGA TTT GAA CAC CCG CAA AAA AGC CTT TTT GAC ACC			630
Asp Pro Met Phe Arg Phe Glu His Pro Gln Lys Ser Leu Phe Asp Thr			
185	190	195	200
ACA CCC TTT AAA ATC GCT ATG GTA GGA CGC TAT TCT AAT GAA AAA AAT			678
Thr Pro Phe Lys Ile Ala Met Val Gly Arg Tyr Ser Asn Glu Lys Asn			
205	210		215
CAA AGC GTT TTA ATC AAA GCG GTT GCT TTA AGC AAA TAC AAA CAA GAT			726
Gln Ser Val Leu Ile Lys Ala Val Ala Leu Ser Lys Tyr Lys Gln Asp			
220	225		230
ATT GTA TTA TTG CTC AAA GGC AAA GGG CCT GAT GAG AAA AAA ATC AAA			774


```

      35              40              45
Lys Asn Ala Thr Pro Leu Lys Asp Lys Val Val Ala Asp Val Gly Cys
      50              55              60
Asn Asn Gly Tyr Tyr Leu Phe Lys Met Leu Glu His Gly Pro Lys Ser
65              70              75              80
Leu Val Gly Phe Asp Pro Gly Val Leu Val Lys Lys Gln Phe Glu Phe
      85              90              95
Leu Ala Pro Phe Phe Asp Lys Glu Lys Lys Ile Ile Tyr Glu Ser Leu
      100             105             110
Gly Val Glu Asp Leu His Glu Lys Tyr Pro Asn Ala Phe Asp Val Ile
      115             120             125
Phe Cys Leu Gly Val Leu Tyr His Arg Lys Ser Pro Leu Glu Ala Leu
      130             135             140
Lys Ala Leu Tyr His Ala Leu Lys Ile Lys Gly Glu Leu Val Leu Asp
145             150             155             160
Thr Leu Ile Ile Asp Ser Pro Leu Asp Ile Ala Leu Cys Pro Lys Lys
      165             170             175
Thr Tyr Ala Lys Met Lys Asn Val Tyr Phe Ile Pro Ser Val Ser Ala
      180             185             190
Leu Lys Gly Trp Cys Glu Arg Val Gly Phe Glu Asn Phe Glu Ile Leu
      195             200             205
Ser Val Leu Lys Thr Thr Pro Lys Glu Gln Arg Lys Thr Asp Phe Ile
      210             215             220
Leu Gly Gln Ser Leu Glu Asp Phe Leu Asp Lys Thr Asp Pro Ser Lys
225             230             235             240
Thr Leu Glu Gly Tyr Asp Ala Pro Leu Arg Gly Tyr Phe Lys Met Leu
      245             250             255
Lys Pro Ser Lys Arg
      260

```

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1197
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

```

TTAAATTCAA TTTTAAAGAA GAGTAGTTAA  ATG GTT ATT GTT TTA GTC GTG GAT    54
                               Met Val Ile Val Leu Val Val Asp
                               1                      5

AGT TTT AAA GAC ACC AGT AAT GGC ACT TCT ATG ACA GCG TTT CGT TTT    102
Ser Phe Lys Asp Thr Ser Asn Gly Thr Ser Met Thr Ala Phe Arg Phe

```

CCT AAC GCT TTT GAT GTC ATT TTT TGC TTA GGG GTG CTA TAC CAC AGA	436
Pro Asn Ala Phe Asp Val Ile Phe Cys Leu Gly Val Leu Tyr His Arg	
125 130 135	
AAA AGC CCG CTA GAG GCT TTA AAA GCC TTG TAT CAC GCT TTG AAA ATA	484
Lys Ser Pro Leu Glu Ala Leu Lys Ala Leu Tyr His Ala Leu Lys Ile	
140 145 150	
AAA GGG GAG CTG GTG TTG GAT ACC TTA ATC ATT GAT TCG CCC TTA GAC	532
Lys Gly Glu Leu Val Leu Asp Thr Leu Ile Ile Asp Ser Pro Leu Asp	
155 160 165	
ATC GCC CTT TGC CCT AAA AAA ACT TAT GCT AAA ATG AAA AAT GTT TAT	580
Ile Ala Leu Cys Pro Lys Lys Thr Tyr Ala Lys Met Lys Asn Val Tyr	
170 175 180 185	
TTT ATC CCC AGT GTT AGC GCG TTA AAA GGG TGG TGC GAA AGG GTA GGG	628
Phe Ile Pro Ser Val Ser Ala Leu Lys Gly Trp Cys Glu Arg Val Gly	
190 195 200	
TTT GAA AAT TTT GAG ATT CTT AGC GTT TTA AAG ACC ACG CCT AAA GAA	676
Phe Glu Asn Phe Glu Ile Leu Ser Val Leu Lys Thr Thr Pro Lys Glu	
205 210 215	
CAG CGT AAA ACG GAT TTT ATT TTG GGG CAG AGT TTG GAA GAT TTT TTG	724
Gln Arg Lys Thr Asp Phe Ile Leu Gly Gln Ser Leu Glu Asp Phe Leu	
220 225 230	
GAT AAA ACA GAT CCC TCT AAA ACT TTA GAG GGG TAT GAC GCC CCT TTA	772
Asp Lys Thr Asp Pro Ser Lys Thr Leu Glu Gly Tyr Asp Ala Pro Leu	
235 240 245	
AGG GGG TAT TTT AAA ATG CTT AAA CCA AGC AAG CGT TAAATAAAGG ATTAAG	824
Arg Gly Tyr Phe Lys Met Leu Lys Pro Ser Lys Arg	
250 255 260	
ATAGTGCAAG	834

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

Met	Leu	Ile	Cys	Asn	Asp	Lys	Ser	Asn	Pro	Lys	Thr	Leu	Leu	Glu	Glu
1				5					10					15	
Ile	Met	Ala	Leu	Arg	Pro	Trp	Arg	Lys	Gly	Pro	Phe	Glu	Ile	Ser	Gln
			20					25				30			
Ile	Lys	Ile	Asp	Ser	Glu	Trp	Asp	Ser	Ser	Ile	Lys	Trp	Asp	Leu	Val

	485		490		495
Ile Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu					
	500		505		

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...808
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

AAAAACCCCC	ACGCTATGGT	AAATC	ATG	CTC	ATT	TGT	AAC	GAT	AAA	TCC	AAT	52
	Met	Leu	Ile	Cys	Asn	Asp	Lys	Ser	Asn			
	1			5								
CCA AAA ACC CTT TTA GAA GAA ATC ATG GCG TTA AGG CCA TGG CGT AAA												100
Pro Lys Thr Leu Leu Glu Glu Ile Met Ala Leu Arg Pro Trp Arg Lys												
10		15		20				25				
GGC CCT TTT GAA ATT TCT CAA ATC AAG ATT GAT AGC GAA TGG GAT AGC												148
Gly Pro Phe Glu Ile Ser Gln Ile Lys Ile Asp Ser Glu Trp Asp Ser												
	30		35					40				
TCC ATT AAA TGG GAT CTA GTT AAA AAC GCC ACT CCT TTA AAA GAT AAG												196
Ser Ile Lys Trp Asp Leu Val Lys Asn Ala Thr Pro Leu Lys Asp Lys												
	45		50					55				
GTT GTG GCT GAT GTG GGT TGC AAT AAC GGC TAT TAC TTG TTT AAA ATG												244
Val Val Ala Asp Val Gly Cys Asn Asn Gly Tyr Tyr Leu Phe Lys Met												
	60		65					70				
CTA GAA CAT GGG CCT AAA AGT TTG GTG GGG TTT GAT CCG GGC GTT TTA												292
Leu Glu His Gly Pro Lys Ser Leu Val Gly Phe Asp Pro Gly Val Leu												
	75		80					85				
GTC AAA AAA CAA TTT GAA TTT TTA GCC CCC TTT TTT GAT AAA GAA AAA												340
Val Lys Lys Gln Phe Glu Phe Leu Ala Pro Phe Phe Asp Lys Glu Lys												
	90		95				100					105
AAA ATC ATT TAT GAG TCT TTG GGG GTA GAG GAT TTG CAT GAA AAA TAC												388
Lys Ile Ile Tyr Glu Ser Leu Gly Val Glu Asp Leu His Glu Lys Tyr												
	110						115					120

```

Ser Gly Gly Pro Ala Ser Val Tyr Ala Lys Asp Ala Tyr Lys Pro Ser
  50                      55                      60
Gly Lys Ile Phe Asp Leu Asn Val Pro Ile Leu Gly Ile Cys Tyr Gly
  65                      70                      75                      80
Met Gln Tyr Leu Val Asp Phe Phe Gly Gly Val Val Val Gly Ala Asn
                      85                      90                      95
Glu Gln Glu Phe Gly Lys Ala Val Leu Glu Ile Thr Gln Asn Ser Val
                      100                      105                      110
Ile Phe Glu Gly Val Lys Ile Lys Ser Leu Val Trp Met Ser His Met
                      115                      120                      125
Asp Lys Val Ile Glu Leu Pro Lys Gly Phe Thr Thr Leu Ala Lys Ser
                      130                      135                      140
Pro Asn Ser Pro His Cys Ala Ile Glu Asn Gly Lys Ile Phe Gly Leu
  145                      150                      155                      160
Gln Phe His Pro Glu Val Val Gln Ser Glu Glu Gly Gly Lys Ile Leu
                      165                      170                      175
Glu Asn Phe Ala Leu Leu Val Cys Gly Cys Glu Lys Thr Trp Gly Met
                      180                      185                      190
Gln His Phe Ala Gln Arg Glu Ile Ala Arg Leu Lys Glu Lys Ile Ala
                      195                      200                      205
Asn Ala Lys Val Leu Cys Ala Val Ser Gly Gly Val Asp Ser Thr Val
  210                      215                      220
Val Ala Thr Leu Leu His Arg Ala Ile Lys Asp Asn Leu Ile Ala Val
  225                      230                      235                      240
Phe Val Asp His Gly Leu Leu Arg Lys Asn Glu Lys Glu Arg Val Gln
                      245                      250                      255
Ala Met Phe Lys Asp Leu Lys Ile Pro Leu Asn Thr Ile Asp Ala Lys
                      260                      265                      270
Glu Val Phe Leu Ser Lys Leu Lys Gly Val Ser Glu Pro Glu Leu Lys
                      275                      280                      285
Arg Lys Ile Ile Gly Glu Thr Phe Ile Glu Val Phe Glu Lys Glu Ala
  290                      295                      300
Lys Lys His His Leu Lys Gly Lys Ile Glu Phe Leu Ala Gln Gly Thr
  305                      310                      315                      320
Leu Tyr Pro Asp Val Ile Glu Ser Val Ser Val Lys Gly Pro Ser Lys
                      325                      330                      335
Val Ile Lys Thr His His Asn Val Gly Gly Leu Pro Glu Trp Met Asp
                      340                      345                      350
Phe Lys Leu Ile Glu Pro Leu Arg Glu Leu Phe Lys Asp Glu Val Arg
                      355                      360                      365
Leu Leu Gly Lys Glu Leu Gly Val Ser Gln Asp Phe Leu Met Arg His
  370                      375                      380
Pro Phe Pro Gly Pro Gly Leu Ala Val Arg Ile Leu Gly Glu Ile Ser
  385                      390                      395                      400
Glu Ser Lys Ile Lys Arg Leu Gln Glu Ala Asp Phe Ile Phe Ile Glu
                      405                      410                      415
Glu Leu Lys Lys Ala Asn Leu Tyr Asp Lys Val Trp Gln Ala Phe Cys
                      420                      425                      430
Val Leu Leu Asn Val Asn Ser Val Gly Val Met Gly Asp Asn Arg Thr
                      435                      440                      445
Tyr Glu Asn Ala Ile Cys Leu Arg Ala Val Asn Ala Ser Asp Gly Met
  450                      455                      460
Thr Ala Ser Phe Ser Phe Leu Glu His Ser Phe Leu Glu Lys Val Ser
  465                      470                      475                      480
Asn Arg Ile Thr Asn Glu Val Ser Gly Ile Asn Arg Val Val Tyr Asp

```

CAG GAT TTT TTA ATG CGC CAC CCT TTT CCA GGG CCT GGG CTT GCT GTA	1203
Gln Asp Phe Leu Met Arg His Pro Phe Pro Gly Pro Gly Leu Ala Val	
380 385 390	
AGG ATT TTA GGC GAA ATC AGT GAG AGT AAG ATC AAA CGC TTG CAA GAA	1251
Arg Ile Leu Gly Glu Ile Ser Glu Ser Lys Ile Lys Arg Leu Gln Glu	
395 400 405	
GCG GAT TTT ATT TTT ATA GAG GAA CTT AAA AAA GCC AAT TTG TAT GAC	1299
Ala Asp Phe Ile Phe Ile Glu Glu Leu Lys Lys Ala Asn Leu Tyr Asp	
410 415 420 425	
AAG GTT TGG CAA GCT TTT TGC GTG CTG TTG AAT GTC AAT TCT GTG GGG	1347
Lys Val Trp Gln Ala Phe Cys Val Leu Leu Asn Val Asn Ser Val Gly	
430 435 440	
GTT ATG GGG GAT AAC CGC ACT TAT GAA AAC GCT ATT TGC TTA AGA GCG	1395
Val Met Gly Asp Asn Arg Thr Tyr Glu Asn Ala Ile Cys Leu Arg Ala	
445 450 455	
GTA AAT GCG AGC GAT GGC ATG ACG GCG AGC TTT TCA TTT TTA GAG CAT	1443
Val Asn Ala Ser Asp Gly Met Thr Ala Ser Phe Ser Phe Leu Glu His	
460 465 470	
TCT TTT TTA GAA AAG GTT TCT AAC CGT ATC ACT AAT GAA GTG AGC GGT	1491
Ser Phe Leu Glu Lys Val Ser Asn Arg Ile Thr Asn Glu Val Ser Gly	
475 480 485	
ATC AAT AGG GTG GTG TAT GAC ATT ACC TCT AAA CCA CCA GGA ACG ATT	1539
Ile Asn Arg Val Val Tyr Asp Ile Thr Ser Lys Pro Pro Gly Thr Ile	
490 495 500 505	
GAA TGG GAA TGATTATCTT AAAAAATAGC ACTA	1572
Glu Trp Glu	

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

Met Ile Leu Val Leu Asp Phe Gly Ser Gln Tyr Thr Gln Leu Ile Ala	
1 5 10 15	
Arg Arg Leu Arg Glu Arg Gly Ile Tyr Thr Glu Ile Val Pro Phe Phe	
20 25 30	
Glu Ser Ile Glu Asn Ile Gln Lys Lys Ala Pro Lys Gly Leu Ile Leu	
35 40 45	

AAC GGC AAG ATT TTT GGC TTG CAA TTC CAC CCA GAA GTC GTT CAA AGC	531
Asn Gly Lys Ile Phe Gly Leu Gln Phe His Pro Glu Val Val Gln Ser	
155 160 165	
GAA GAA GGG GGT AAG ATT TTA GAA AAT TTT GCC CTT TTA GTT TGC GGC	579
Glu Glu Gly Gly Lys Ile Leu Glu Asn Phe Ala Leu Leu Val Cys Gly	
170 175 180 185	
TGT GAA AAA ACT TGG GGG ATG CAG CAT TTC GCT CAA AGA GAA ATC GCA	627
Cys Glu Lys Thr Trp Gly Met Gln His Phe Ala Gln Arg Glu Ile Ala	
190 195 200	
CGA TTG AAA GAA AAA ATC GCT AAC GCT AAG GTT TTG TGC GCG GTG AGT	675
Arg Leu Lys Glu Lys Ile Ala Asn Ala Lys Val Leu Cys Ala Val Ser	
205 210 215	
GGG GGC GTG GAT TCT ACG GTG GTC GCT ACG CTG TTG CAC AGA GCC ATT	723
Gly Gly Val Asp Ser Thr Val Val Ala Thr Leu Leu His Arg Ala Ile	
220 225 230	
AAG GAT AAT TTG ATC GCT GTT TTT GTG GAT CAT GGC TTG TTG CGT AAA	771
Lys Asp Asn Leu Ile Ala Val Phe Val Asp His Gly Leu Leu Arg Lys	
235 240 245	
AAT GAA AAA GAA AGG GTG CAA GCG ATG TTT AAG GAC TTG AAA ATC CCT	819
Asn Glu Lys Glu Arg Val Gln Ala Met Phe Lys Asp Leu Lys Ile Pro	
250 255 260 265	
TTA AAC ACG ATA GAC GCT AAA GAA GTC TTT TTG TCT AAA TTA AAG GGC	867
Leu Asn Thr Ile Asp Ala Lys Glu Val Phe Leu Ser Lys Leu Lys Gly	
270 275 280	
GTG AGC GAG CCT GAA TTG AAG CGA AAA ATC ATC GGC GAG ACC TTT ATT	915
Val Ser Glu Pro Glu Leu Lys Arg Lys Ile Ile Gly Glu Thr Phe Ile	
285 290 295	
GAA GTG TTT GAA AAA GAA GCC AAA AAG CAC CAT TTA AAA GGC AAA ATT	963
Glu Val Phe Glu Lys Glu Ala Lys Lys His His Leu Lys Gly Lys Ile	
300 305 310	
GAA TTT TTA GCC CAA GGC ACT TTA TAC CCT GAT GTG ATT GAA TCC GTG	1011
Glu Phe Leu Ala Gln Gly Thr Leu Tyr Pro Asp Val Ile Glu Ser Val	
315 320 325	
AGC GTT AAA GGG CCT TCA AAA GTG ATC AAA ACC CAT CAT AAT GTG GGC	1059
Ser Val Lys Gly Pro Ser Lys Val Ile Lys Thr His His Asn Val Gly	
330 335 340 345	
GGA CTG CCT GAA TGG ATG GAT TTT AAA CTC ATA GAG CCT TTA AGG GAG	1107
Gly Leu Pro Glu Trp Met Asp Phe Lys Leu Ile Glu Pro Leu Arg Glu	
350 355 360	
TTG TTT AAA GAT GAG GTG CGC TTA CTG GGT AAA GAA TTG GGC GTT AGT	1155
Leu Phe Lys Asp Glu Val Arg Leu Leu Gly Lys Glu Leu Gly Val Ser	
365 370 375	

(A) LENGTH: 1572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 25...1548
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

TCTCACAAAA ATAAAGAATG AGCG ATG ATT TTA GTA TTA GAT TTT GGG AGT	51
Met Ile Leu Val Leu Asp Phe Gly Ser	
1 5	
CAA TAC ACA CAG CTG ATT GCT AGA AGA TTG AGA GAG AGA GGG ATT TAT	99
Gln Tyr Thr Gln Leu Ile Ala Arg Arg Leu Arg Glu Arg Gly Ile Tyr	
10 15 20 25	
ACA GAA ATA GTC CCT TTT TTT GAA AGC ATA GAA AAC ATT CAA AAA AAA	147
Thr Glu Ile Val Pro Phe Phe Glu Ser Ile Glu Asn Ile Gln Lys Lys	
30 35 40	
GCC CCC AAA GGT TTG ATT TTG AGT GGG GGG CCA GCG AGC GTG TAT GCT	195
Ala Pro Lys Gly Leu Ile Leu Ser Gly Gly Pro Ala Ser Val Tyr Ala	
45 50 55	
AAA GAC GCT TAC AAG CCT AGT GGG AAA ATC TTT GAT TTG AAT GTG CCG	243
Lys Asp Ala Tyr Lys Pro Ser Gly Lys Ile Phe Asp Leu Asn Val Pro	
60 65 70	
ATT TTA GGG ATT TGC TAC GGC ATG CAG TAT TTG GTG GAT TTT TTT GGG	291
Ile Leu Gly Ile Cys Tyr Gly Met Gln Tyr Leu Val Asp Phe Phe Gly	
75 80 85	
GGG GTA GTG GTT GGT GCG AAT GAG CAA GAA TTT GGT AAG GCT GTT TTA	339
Gly Val Val Val Gly Ala Asn Glu Gln Glu Phe Gly Lys Ala Val Leu	
90 95 100 105	
GAA ATC ACT CAA AAT TCT GTG ATT TTT GAA GGC GTG AAG ATT AAA AGC	387
Glu Ile Thr Gln Asn Ser Val Ile Phe Glu Gly Val Lys Ile Lys Ser	
110 115 120	
CTT GTG TGG ATG AGC CAT ATG GAT AAA GTC ATA GAA CTG CCT AAA GGC	435
Leu Val Trp Met Ser His Met Asp Lys Val Ile Glu Leu Pro Lys Gly	
125 130 135	
TTT ACT ACC CTT GCA AAA AGC CCT AAT TCC CCC CAT TGC GCG ATT GAA	483
Phe Thr Thr Leu Ala Lys Ser Pro Asn Ser Pro His Cys Ala Ile Glu	
140 145 150	

```

Leu Tyr Ala Phe Ser Leu Ile Asp Ser Gln Tyr Cys Ser Lys Gly Gly
      110              115              120

AAT TAC AGA TAC GAA CTA GAA AAA TTA GAA CGC TGG TTT GTG CAA AAA    437
Asn Tyr Arg Tyr Glu Leu Glu Lys Leu Glu Arg Trp Phe Val Gln Lys
      125              130              135

GCA CCT GAG TTG GCT GAA AGC TAT AGG GTG AAT TAC AAA AAT CAA TAC    485
Ala Pro Glu Leu Ala Glu Ser Tyr Arg Val Asn Tyr Lys Asn Gln Tyr
      140              145              150

AAT AAA ACA CAG ATC TCA CAA AAA TAAAGAATGA GCGATGATTT TAGTATTAGA    539
Asn Lys Thr Gln Ile Ser Gln Lys
155              160

T                                                                    540

```

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

```

Met Asn Ile Phe Gln Thr Ser Leu Lys Cys Cys Val Gly Leu Val Leu
 1           5           10           15
Ser Val Gly Val Leu Leu Gly Asp Ser Lys Ala Phe Lys Val Arg Val
      20           25           30
Asp Lys Ser Leu Thr Pro Pro Phe Leu Asn Val Leu Ser Leu Ala Phe
      35           40           45
Lys Gln Asp Met Lys Lys Glu Val Ile Phe Val Ile Thr Lys Ser Asn
      50           55           60
Lys Leu Ser Lys Lys Val Leu Cys Asp Phe Asp Ala Phe Leu Leu Pro
      65           70           75           80
Glu Thr Leu Met Ser Gly Met Pro Lys Lys Ala Leu Phe His Lys Glu
      85           90           95
Phe Leu Phe Gln Ser Lys Glu Asn Lys Thr Leu Tyr Ala Phe Ser Leu
      100          105          110
Ile Asp Ser Gln Tyr Cys Ser Lys Gly Gly Asn Tyr Arg Tyr Glu Leu
      115          120          125
Glu Lys Leu Glu Arg Trp Phe Val Gln Lys Ala Pro Glu Leu Ala Glu
      130          135          140
Ser Tyr Arg Val Asn Tyr Lys Asn Gln Tyr Asn Lys Thr Gln Ile Ser
      145          150          155          160
Gln Lys

```

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:


```

Leu Leu Ile Leu Ser Leu Leu Pro Leu Ala Leu Trp Lys Glu Met Ile
                        485                        490                        495
Leu Leu Leu Glu Gly Val Ile Leu Arg Met Trp Phe Met Pro Cys Val
                        500                        505                        510
Arg Trp

```

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...509
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

```

ATTGACGCTT ATAAGGATAA AAG ATG AAT ATT TTT CAA ACG AGT TTG AAA TGT      53
                        Met Asn Ile Phe Gln Thr Ser Leu Lys Cys
                        1                        5                        10

TGC GTG GGG TTG GTT TTG TCT GTG GGG GTC TTA TTA GGG GAT TCT AAA      101
Cys Val Gly Leu Val Leu Ser Val Gly Val Leu Leu Gly Asp Ser Lys
                        15                        20                        25

GCT TTT AAG GTT AGG GTG GAT AAA AGT TTA ACC CCG CCT TTT TTG AAT      149
Ala Phe Lys Val Arg Val Asp Lys Ser Leu Thr Pro Pro Phe Leu Asn
                        30                        35                        40

GTG CTT TCA TTA GCT TTT AAA CAA GAC ATG AAA AAA GAG GTC ATT TTT      197
Val Leu Ser Leu Ala Phe Lys Gln Asp Met Lys Lys Glu Val Ile Phe
                        45                        50                        55

GTG ATT ACC AAA AGC AAT AAG TTG AGT AAA AAA GTG CTT TGT GAT TTT      245
Val Ile Thr Lys Ser Asn Lys Leu Ser Lys Lys Val Leu Cys Asp Phe
                        60                        65                        70

GAC GCT TTT TTA TTG CCT GAG ACT CTG ATG AGC GGC ATG CCT AAA AAA      293
Asp Ala Phe Leu Leu Pro Glu Thr Leu Met Ser Gly Met Pro Lys Lys
                        75                        80                        85                        90

GCA CTA TTC CAT AAA GAG TTT TTA TTC CAA TCT AAA GAA AAT AAA ACG      341
Ala Leu Phe His Lys Glu Phe Leu Phe Gln Ser Lys Glu Asn Lys Thr
                        95                        100                        105

CTC TAT GCG TTT TCG CTG ATT GAT TCT CAA TAT TGC TCA AAA GGT GGA      389

```

		35					40					45				
Asn	Gly	Val	Ile	Lys	Asp	Ile	Val	Pro	Gln	Lys	Ser	Asp	Tyr	Asn	Pro	
	50					55					60					
Thr	Met	Met	Leu	Lys	Ala	Met	Val	Asp	Arg	Val	Tyr	Ser	Asp	Ser	Arg	
65					70					75					80	
Val	Lys	Tyr	Pro	Cys	Val	Arg	Lys	Ser	Phe	Leu	Glu	Asn	Lys	Lys	Asn	
				85					90					95		
His	Lys	Glu	Leu	Arg	Gly	Arg	Glu	Glu	Phe	Val	Arg	Val	Ser	Trp	Asp	
			100					105					110			
Val	Ala	Leu	Asp	Leu	Ala	Ala	Lys	Lys	Leu	Lys	Glu	Ile	Pro	Lys	Glu	
		115					120					125				
Asn	Ile	Tyr	Asn	Ala	Ser	Tyr	Gly	Gly	Trp	Gly	His	Ala	Gly	Ser	Leu	
	130					135					140					
His	Arg	Cys	His	His	Leu	Ala	Trp	Arg	Phe	Phe	Asn	Thr	Thr	Leu	Gly	
145					150					155					160	
Gly	Ala	Ile	Gly	Thr	Asp	Gly	Glu	Tyr	Ser	Asn	Gly	Ala	Ala	Ala	Arg	
				165					170					175		
Ile	Asn	Pro	Met	Ile	Val	Gly	Asp	Met	Glu	Val	Tyr	Ser	Gln	Gln	Thr	
			180					185					190			
Thr	His	Glu	Glu	Met	Ile	Lys	Asn	Cys	Lys	Val	Tyr	Val	Met	Trp	Gly	
		195					200					205				
Ala	Asp	Leu	Leu	Lys	Cys	Asn	Arg	Ile	Asp	Tyr	Phe	Val	Pro	Asn	His	
	210					215					220					
Val	Asn	Asp	Ser	Tyr	Tyr	Pro	Lys	Tyr	Lys	Arg	Ala	Gly	Ile	Lys	Phe	
225					230					235					240	
Ile	Ser	Ile	Asp	Pro	Ile	Tyr	Thr	Glu	Thr	Ala	Gln	Ala	Phe	Ser	Ala	
				245					250					255		
Glu	Trp	Ile	Pro	Ile	Arg	Pro	Asn	Thr	Asp	Val	Ala	Leu	Met	Leu	Gly	
			260					265					270			
Met	Met	His	Tyr	Leu	Tyr	Thr	Ser	Asn	Gln	Tyr	Asp	Lys	Ala	Phe	Ile	
		275					280					285				
Ala	Lys	Tyr	Thr	Asp	Gly	Phe	Asp	Lys	Phe	Leu	Pro	Tyr	Leu	Leu	Gly	
	290					295					300					
Glu	Ser	Asp	Asn	Ala	Pro	Lys	Thr	Leu	Glu	Trp	Ala	Ser	Gln	Ile	Thr	
305					310					315					320	
Gly	Val	Ser	Ala	Glu	Lys	Ile	Lys	Glu	Leu	Ala	Asp	Leu	Phe	Val	Ser	
				325					330					335		
Lys	Arg	Thr	Phe	Leu	Ala	Gly	Asn	Trp	Ala	Met	Gln	Arg	Ala	Gln	Tyr	
			340					345					350			
Gly	Glu	Gln	Pro	Asp	Trp	Ala	Leu	Ile	Val	Leu	Ala	Ser	Met	Ile	Gly	
		355					360					365				

TCG GGT GGG GGC TTT GGC TTT TCT ATG CAT TAT GGA GGG AAC GCT CAA	1206
Ser Gly Gly Gly Phe Gly Phe Ser Met His Tyr Gly Gly Asn Ala Gln	
375 380 385	
GCA AGC TCA GGG GCA AGA ATT GTT CCT ATG ATT TCA CAA GGG CAT AAT	1254
Ala Ser Ser Gly Ala Arg Ile Val Pro Met Ile Ser Gln Gly His Asn	
390 395 400	
TCT GTA AAA AGC GTT ATT CCA GCA TCT AGG GTT TCT GAA GCG ATT TTA	1302
Ser Val Lys Ser Val Ile Pro Ala Ser Arg Val Ser Glu Ala Ile Leu	
405 410 415 420	
AAT CCG GAT AAA GAA ATT GAT TTT ATG GGC AAA AAA CTC AAA TTG CCT	1350
Asn Pro Asp Lys Glu Ile Asp Phe Met Gly Lys Lys Leu Lys Leu Pro	
425 430 435	
AAA ATC AAA ATG ATT TAT AAT TGT GGG GCG GAT TTA TTA GGG CAT GAA	1398
Lys Ile Lys Met Ile Tyr Asn Cys Gly Ala Asp Leu Leu Gly His Glu	
440 445 450	
ACT GAT ACA AAC GAG CTG ATT CGC GCT TTA AGG ACC TTA GAT TGC GTG	1446
Thr Asp Thr Asn Glu Leu Ile Arg Ala Leu Arg Thr Leu Asp Cys Val	
455 460 465	
ATC GTG CAT GAG CCT TGG TGG CGC CTA CGG CAA AAT TTG CTG ATA TTG	1494
Ile Val His Glu Pro Trp Trp Arg Leu Arg Gln Asn Leu Leu Ile Leu	
470 475 480	
TCT TTG CTT CCA CTA GCA CTG TGG AAA GAG ATG ATA TTG CTT TTG GAG	1542
Ser Leu Leu Pro Leu Ala Leu Trp Lys Glu Met Ile Leu Leu Leu Glu	
485 490 495 500	
GGA GTT ATT CTA AGA ATG TGG TTT ATG CCA TGC GTA AGG TGG TAGAGCCTG	1593
Gly Val Ile Leu Arg Met Trp Phe Met Pro Cys Val Arg Trp	
505 510	
TTTATGAATC TAAAGACGAT TATGAGATTT TCAGACAGCT TGC	1636

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

Met	Ser	Ile	Ser	Arg	Arg	Ser	Ile	Leu	Thr	Lys	Ile	Pro	Ile	Ala	Leu
1				5				10						15	
Ala	Ser	Ala	Asn	Val	Leu	Lys	Ala	Val	Gly	Val	Phe	Glu	Lys	Val	Glu
			20					25					30		
Ser	Ile	Pro	His	Ala	Thr	His	Phe	Gly	Pro	Phe	Ile	Ala	Lys	Val	Gln

His	Leu	Ala	Trp	Arg	Phe	Phe	Asn	Thr	Thr	Leu	Gly	Gly	Ala	Ile	Gly		
150							155				160						
ACT	GAT	GGG	GAA	TAT	AGT	AAT	GGC	GCG	GCC	GCA	AGA	ATA	AAC	CCT	ATG	582	
Thr	Asp	Gly	Glu	Tyr	Ser	Asn	Gly	Ala	Ala	Ala	Arg	Ile	Asn	Pro	Met		
165						170				175					180		
ATT	GTA	GGG	GAT	ATG	GAA	GTT	TAT	TCG	CAA	CAA	ACC	ACG	CAT	GAA	GAG	630	
Ile	Val	Gly	Asp	Met	Glu	Val	Tyr	Ser	Gln	Gln	Thr	Thr	His	Glu	Glu		
				185					190					195			
ATG	ATT	AAA	AAT	TGT	AAG	GTG	TAT	GTC	ATG	TGG	GGG	GCG	GAT	TTA	CTC	678	
Met	Ile	Lys	Asn	Cys	Lys	Val	Tyr	Val	Met	Trp	Gly	Ala	Asp	Leu	Leu		
			200					205					210				
AAG	TGC	AAC	CGC	ATT	GAT	TAT	TTT	GTG	CCA	AAC	CAT	GTC	AAT	GAC	AGC	726	
Lys	Cys	Asn	Arg	Ile	Asp	Tyr	Phe	Val	Pro	Asn	His	Val	Asn	Asp	Ser		
		215					220					225					
TAC	TAC	CCC	AAG	TAT	AAA	AGA	GCT	GGT	ATT	AAA	TTC	ATT	AGT	ATC	GAT	774	
Tyr	Tyr	Pro	Lys	Tyr	Lys	Arg	Ala	Gly	Ile	Lys	Phe	Ile	Ser	Ile	Asp		
		230				235					240						
CCC	ATT	TAT	ACC	GAA	ACC	GCT	CAA	GCC	TTT	AGT	GCT	GAA	TGG	ATA	CCC	822	
Pro	Ile	Tyr	Thr	Glu	Thr	Ala	Gln	Ala	Phe	Ser	Ala	Glu	Trp	Ile	Pro		
245					250				255						260		
ATT	CGC	CCT	AAC	ACT	GAT	GTA	GCG	TTA	ATG	CTA	GGC	ATG	ATG	CAT	TAT	870	
Ile	Arg	Pro	Asn	Thr	Asp	Val	Ala	Leu	Met	Leu	Gly	Met	Met	His	Tyr		
				265					270					275			
CTT	TAT	ACG	AGC	AAT	CAA	TAT	GAT	AAA	GCG	TTT	ATC	GCT	AAA	TAC	ACT	918	
Leu	Tyr	Thr	Ser	Asn	Gln	Tyr	Asp	Lys	Ala	Phe	Ile	Ala	Lys	Tyr	Thr		
			280					285					290				
GAT	GGT	TTT	GAT	AAA	TTT	TTA	CCC	TAT	TTG	CTA	GGA	GAG	AGC	GAT	AAT	966	
Asp	Gly	Phe	Asp	Lys	Phe	Leu	Pro	Tyr	Leu	Leu	Gly	Glu	Ser	Asp	Asn		
		295					300					305					
GCG	CCT	AAG	ACT	TTA	GAA	TGG	GCG	TCT	CAA	ATC	ACT	GGA	GTG	AGC	GCA	1014	
Ala	Pro	Lys	Thr	Leu	Glu	Trp	Ala	Ser	Gln	Ile	Thr	Gly	Val	Ser	Ala		
		310				315					320						
GAA	AAA	ATC	AAA	GAA	TTA	GCG	GAT	TTG	TTT	GTT	TCT	AAA	CGC	ACT	TTT	1062	
Glu	Lys	Ile	Lys	Glu	Leu	Ala	Asp	Leu	Phe	Val	Ser	Lys	Arg	Thr	Phe		
325					330				335						340		
TTA	GCG	GGT	AAT	TGG	GCC	ATG	CAA	AGA	GCT	CAG	TAT	GGC	GAG	CAA	CCG	1110	
Leu	Ala	Gly	Asn	Trp	Ala	Met	Gln	Arg	Ala	Gln	Tyr	Gly	Glu	Gln	Pro		
			345					350					355				
GAT	TGG	GCG	TTA	ATT	GTT	TTA	GCT	AGC	ATG	ATT	GGT	CAA	GTG	GGC	TTA	1158	
Asp	Trp	Ala	Leu	Ile	Val	Leu	Ala	Ser	Met	Ile	Gly	Gln	Val	Gly	Leu		
			360					365					370				

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 43...1584
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

AATTTGGGGT GTTTAAACAG AATGCAAGCT TGAAGGAGAA TC ATG TCC ATT TCA	54
Met Ser Ile Ser	
1	
CGC AGA AGT ATC CTA ACA AAA ATC CCA ATC GCG CTC GCT AGC GCT AAT	102
Arg Arg Ser Ile Leu Thr Lys Ile Pro Ile Ala Leu Ala Ser Ala Asn	
5 10 15 20	
GTT TTG AAA GCT GTT GGT GTT TTT GAA AAA GTA GAA TCC ATT CCG CAT	150
Val Leu Lys Ala Val Gly Val Phe Glu Lys Val Glu Ser Ile Pro His	
25 30 35	
GCA ACG CAT TTT GGC CCC TTT ATC GCA AAG GTT CAA AAT GGA GTG ATT	198
Ala Thr His Phe Gly Pro Phe Ile Ala Lys Val Gln Asn Gly Val Ile	
40 45 50	
AAA GAT ATT GTC CCC CAA AAA AGC GAT TAT AAC CCT ACT ATG ATG TTA	246
Lys Asp Ile Val Pro Gln Lys Ser Asp Tyr Asn Pro Thr Met Met Leu	
55 60 65	
AAA GCG ATG GTT GAT AGG GTG TAT TCA GAT AGT AGG GTG AAG TAT CCT	294
Lys Ala Met Val Asp Arg Val Tyr Ser Asp Ser Arg Val Lys Tyr Pro	
70 75 80	
TGC GTG CGC AAG AGC TTC TTA GAA AAC AAA AAA AAC CAC AAA GAA TTG	342
Cys Val Arg Lys Ser Phe Leu Glu Asn Lys Lys Asn His Lys Glu Leu	
85 90 95 100	
CGC GGG AGA GAA GAG TTT GTG CGT GTG AGT TGG GAT GTG GCG TTG GAT	390
Arg Gly Arg Glu Glu Phe Val Arg Val Ser Trp Asp Val Ala Leu Asp	
105 110 115	
TTA GCG GCT AAA AAG CTT AAA GAA ATC CCT AAA GAA AAC ATT TAT AAT	438
Leu Ala Ala Lys Lys Leu Lys Glu Ile Pro Lys Glu Asn Ile Tyr Asn	
120 125 130	
GCC AGT TAT GGT GGC TGG GGG CAT GCG GGC AGC TTG CAT CGT TGC CAT	486
Ala Ser Tyr Gly Gly Trp Gly His Ala Gly Ser Leu His Arg Cys His	
135 140 145	
CAT TTA GCA TGG CGT TTT TTT AAC ACG ACT TTA GGA GGG GCT ATT GGC	534

				165				170				175				
Ser	Ile	Asn	Ile	Ser	Arg	Lys	Arg	Phe	Phe	Glu	Val	Asn	Asp	Lys	Arg	
180								185				190				
Gln	Leu	Glu	Val	Ser	Lys	Glu	Leu	Leu	Glu	Ala	Thr	Glu	Pro	Val	Leu	
195								200				205				
Gly	Val	Val	Arg	Gln	Ile	Thr	Pro	Phe	Gly	Ile	Phe	Val	Glu	Ala	Lys	
210								215				220				
Gly	Ile	Glu	Gly	Leu	Val	His	Tyr	Ser	Glu	Ile	Ser	His	Lys	Gly	Pro	
225					230				235				240			
Val	Asn	Pro	Glu	Lys	Tyr	Tyr	Lys	Glu	Gly	Asp	Glu	Val	Tyr	Val	Lys	
				245				250				255				
Ala	Ile	Ala	Tyr	Asp	Ala	Glu	Lys	Arg	Arg	Leu	Ser	Leu	Ser	Ile	Lys	
				260				265				270				
Ala	Thr	Ile	Glu	Asp	Pro	Trp	Glu	Glu	Ile	Gln	Asp	Lys	Leu	Lys	Pro	
				275				280				285				
Gly	Tyr	Ala	Ile	Lys	Val	Val	Val	Ser	Asn	Ile	Glu	His	Tyr	Gly	Val	
				290				295				300				
Phe	Val	Asp	Ile	Gly	Asn	Asp	Ile	Glu	Gly	Phe	Leu	His	Val	Ser	Glu	
305					310				315				320			
Ile	Ser	Trp	Asp	Lys	Asn	Val	Ser	His	Pro	Asn	Asn	Tyr	Leu	Ser	Val	
				325				330				335				
Gly	Gln	Glu	Ile	Asp	Val	Lys	Ile	Ile	Asp	Ile	Asp	Pro	Lys	Asn	Arg	
				340				345				350				
Arg	Leu	Arg	Val	Ser	Leu	Lys	Gln	Leu	Thr	Asn	Arg	Pro	Phe	Asp	Val	
				355				360				365				
Phe	Glu	Ser	Lys	His	Gln	Val	Gly	Asp	Val	Leu	Glu	Gly	Lys	Val	Ala	
				370				375				380				
Thr	Leu	Thr	Asp	Phe	Gly	Ala	Phe	Leu	Asn	Leu	Gly	Gly	Val	Asp	Gly	
385					390				395				400			
Leu	Leu	His	Asn	His	Asp	Ala	Phe	Trp	Asp	Lys	Asp	Lys	Lys	Cys	Lys	
				405				410				415				
Asp	His	Tyr	Lys	Ile	Gly	Asp	Val	Ile	Lys	Val	Lys	Ile	Leu	Lys	Ile	
				420				425				430				
Asn	Lys	Lys	Asp	Lys	Lys	Ile	Ser	Leu	Ser	Ala	Lys	His	Leu	Val	Thr	
				435				440				445				
Ser	Pro	Thr	Glu	Glu	Phe	Ala	Gln	Lys	His	Lys	Thr	Asp	Ser	Val	Ile	
				450				455				460				
Gln	Gly	Lys	Val	Val	Ser	Ile	Lys	Asp	Phe	Gly	Val	Phe	Ile	Asn	Ala	
465					470				475				480			
Asp	Gly	Ile	Asp	Val	Leu	Ile	Lys	Asn	Glu	Asp	Leu	Asn	Pro	Leu	Lys	
				485				490				495				
Lys	Asp	Glu	Ile	Lys	Ile	Gly	Gln	Glu	Ile	Thr	Cys	Val	Val	Val	Ala	
				500				505				510				
Ile	Glu	Lys	Ser	Asn	Asn	Lys	Val	Arg	Ala	Ser	Val	His	Arg	Leu	Glu	
				515				520				525				
Arg	Lys	Lys	Glu	Lys	Glu	Glu	Leu	Gln	Ala	Phe	Asn	Thr	Ser	Asp	Asp	
				530				535				540				
Lys	Met	Thr	Leu	Gly	Asp	Ile	Leu	Lys	Glu	Lys	Leu					
				545				550				555				

(2) INFORMATION FOR SEQ ID NO:1299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1636 base pairs

(B) TYPE: nucleic acid

```

AAA AAT GAA GAT TTG AAC CCC TTG AAA AAA GAT GAA ATT AAA ATA GGC      1542
Lys Asn Glu Asp Leu Asn Pro Leu Lys Lys Asp Glu Ile Lys Ile Gly
      490                      495                      500

CAA GAA ATC ACA TGC GTG GTG GTT GCG ATT GAA AAA TCT AAC AAC AAG      1590
Gln Glu Ile Thr Cys Val Val Val Ala Ile Glu Lys Ser Asn Asn Lys
      505                      510                      515

GTG CGT GCT TCT GTG CAT AGG TTA GAG CGC AAA AAA GAA AAA GAA GAA      1638
Val Arg Ala Ser Val His Arg Leu Glu Arg Lys Lys Glu Lys Glu Glu
      520                      525                      530                      535

TTG CAA GCT TTT AAC ACG AGC GAT GAT AAA ATG ACT TTA GGG GAT ATT      1686
Leu Gln Ala Phe Asn Thr Ser Asp Asp Lys Met Thr Leu Gly Asp Ile
      540                      545                      550

CTT AAA GAA AAA CTC TAAAGAGTGA TTTTAAAAGC ATGAGAATGG CATGAGATTT A      1742
Leu Lys Glu Lys Leu
      555

AGGGTG                                                                    1748

```

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

```

Met Ser Lys Ile Ala Asp Asp Gln Asn Phe Asn Asp Glu Glu Glu Asn
  1           5           10           15
Phe Ala Lys Leu Phe Lys Lys Glu Leu Glu Lys Glu Glu Thr Leu Glu
      20           25           30
Lys Gly Thr Ile Lys Glu Gly Leu Val Val Ser Ile Asn Glu Asn Asp
      35           40           45
Gly Tyr Ala Met Val Ser Val Gly Gly Lys Thr Glu Gly Arg Leu Ala
      50           55           60
Leu Asn Glu Ile Thr Asp Glu Lys Gly Gln Leu Leu Tyr Gln Lys Asn
      65           70           75           80
Asp Pro Ile Ile Val His Val Ser Glu Lys Gly Glu His Pro Ser Val
      85           90           95
Ser Tyr Lys Lys Ala Ile Ser Gln Gln Lys Ile Gln Ala Lys Ile Glu
      100          105          110
Glu Leu Gly Glu Asn Tyr Glu Asn Ala Ile Ile Glu Gly Lys Ile Val
      115          120          125
Gly Lys Asn Lys Gly Gly Tyr Ile Val Glu Ser Gln Gly Val Glu Tyr
      130          135          140
Phe Leu Ser Arg Ser His Ser Ser Leu Lys Asn Asp Ala Asn His Ile
      145          150          155          160
Gly Lys Arg Val Lys Ala Cys Ile Ile Arg Val Asp Lys Glu Asn His

```

AAA AGA CGC CTT TCA CTC TCC ATA AAA GCG ACT ATA GAA GAC CCA TGG	870
Lys Arg Arg Leu Ser Leu Ser Ile Lys Ala Thr Ile Glu Asp Pro Trp	
265 270 275	
GAA GAG ATT CAA GAC AAG CTA AAA CCC GGA TAC GCC ATT AAG GTA GTG	918
Glu Glu Ile Gln Asp Lys Leu Lys Pro Gly Tyr Ala Ile Lys Val Val	
280 285 290 295	
GTG AGC AAC ATT GAA CAT TAT GGG GTG TTT GTG GAT ATT GGT AAT GAT	966
Val Ser Asn Ile Glu His Tyr Gly Val Phe Val Asp Ile Gly Asn Asp	
300 305 310	
ATT GAA GGC TTT TTG CAT GTT TCT GAA ATC TCT TGG GAT AAA AAT GTC	1014
Ile Glu Gly Phe Leu His Val Ser Glu Ile Ser Trp Asp Lys Asn Val	
315 320 325	
AGC CAC CCT AAC AAT TAC TTG AGC GTG GGG CAA GAG ATT GAT GTG AAA	1062
Ser His Pro Asn Asn Tyr Leu Ser Val Gly Gln Glu Ile Asp Val Lys	
330 335 340	
ATC ATT GAC ATT GAT CCA AAA AAT CGC CGC TTA AGG GTT TCT TTA AAG	1110
Ile Ile Asp Ile Asp Pro Lys Asn Arg Arg Leu Arg Val Ser Leu Lys	
345 350 355	
CAA CTC ACT AAC AGG CCT TTT GAT GTT TTT GAA TCT AAA CAC CAA GTG	1158
Gln Leu Thr Asn Arg Pro Phe Asp Val Phe Glu Ser Lys His Gln Val	
360 365 370 375	
GGG GAT GTT TTA GAA GGC AAA GTG GCG ACT TTA ACG GAT TTT GGG GCG	1206
Gly Asp Val Leu Glu Gly Lys Val Ala Thr Leu Thr Asp Phe Gly Ala	
380 385 390	
TTT TTA AAT CTG GGT GGG GTG GAT GGT TTG CTC CAC AAT CAC GAC GCT	1254
Phe Leu Asn Leu Gly Gly Val Asp Gly Leu Leu His Asn His Asp Ala	
395 400 405	
TTT TGG GAT AAA GAT AAA AAA TGC AAA GAC CAC TAT AAA ATT GGC GAT	1302
Phe Trp Asp Lys Asp Lys Lys Cys Lys Asp His Tyr Lys Ile Gly Asp	
410 415 420	
GTG ATC AAA GTG AAA ATC CTT AAA ATC AAC AAA AAA GAT AAA AAG ATT	1350
Val Ile Lys Val Lys Ile Leu Lys Ile Asn Lys Lys Asp Lys Lys Ile	
425 430 435	
TCT TTG AGC GCG AAG CAC TTG GTG ACT TCC CCT ACA GAA GAA TTC GCT	1398
Ser Leu Ser Ala Lys His Leu Val Thr Ser Pro Thr Glu Glu Phe Ala	
440 445 450 455	
CAA AAG CAT AAA ACA GAC AGC GTG ATT CAA GGC AAA GTG GTG AGT ATT	1446
Gln Lys His Lys Thr Asp Ser Val Ile Gln Gly Lys Val Val Ser Ile	
460 465 470	
AAG GAT TTT GGC GTT TTC ATT AAT GCT GAT GGC ATT GAT GTG CTG ATC	1494
Lys Asp Phe Gly Val Phe Ile Asn Ala Asp Gly Ile Asp Val Leu Ile	
475 480 485	

CTA GTC GTT TCC ATC AAT GAG AAT GAT GGT TAT GCC ATG GTG AGC GTG	198
Leu Val Val Ser Ile Asn Glu Asn Asp Gly Tyr Ala Met Val Ser Val	
40 45 50 55	
GGC GGT AAG ACA GAA GGC CGT TTG GCT TTG AAT GAG ATC ACC GAT GAA	246
Gly Gly Lys Thr Glu Gly Arg Leu Ala Leu Asn Glu Ile Thr Asp Glu	
60 65 70	
AAG GGG CAG TTG CTG TAT CAA AAA AAT GAC CCC ATT ATC GTG CAT GTG	294
Lys Gly Gln Leu Leu Tyr Gln Lys Asn Asp Pro Ile Ile Val His Val	
75 80 85	
TCC GAA AAA GGT GAA CAC CCT AGC GTT TCC TAC AAA AAG GCC ATT TCC	342
Ser Glu Lys Gly Glu His Pro Ser Val Ser Tyr Lys Lys Ala Ile Ser	
90 95 100	
CAA CAA AAG ATT CAA GCT AAA ATT GAA GAA TTA GGC GAA AAC TAT GAA	390
Gln Gln Lys Ile Gln Ala Lys Ile Glu Glu Leu Gly Glu Asn Tyr Glu	
105 110 115	
AAC GCC ATT ATT GAA GGC AAG ATT GTA GGC AAG AAT AAA GGG GGT TAT	438
Asn Ala Ile Ile Glu Gly Lys Ile Val Gly Lys Asn Lys Gly Gly Tyr	
120 125 130 135	
ATC GTG GAG TCT CAA GGC GTG GAG TAT TTC CTC TCC CGC TCG CAC TCT	486
Ile Val Glu Ser Gln Gly Val Glu Tyr Phe Leu Ser Arg Ser His Ser	
140 145 150	
TCT TTA AAG AAT GAC GCA AAC CAT ATC GGC AAA CGC GTT AAA GCG TGC	534
Ser Leu Lys Asn Asp Ala Asn His Ile Gly Lys Arg Val Lys Ala Cys	
155 160 165	
ATC ATT CGT GTG GAT AAG GAA AAC CAT TCT ATC AAT ATT TCT CGC AAA	582
Ile Ile Arg Val Asp Lys Glu Asn His Ser Ile Asn Ile Ser Arg Lys	
170 175 180	
CGA TTC TTT GAA GTC AAT GAC AAA CGA CAA CTT GAG GTT TCT AAG GAA	630
Arg Phe Phe Glu Val Asn Asp Lys Arg Gln Leu Glu Val Ser Lys Glu	
185 190 195	
TTG TTA GAA GCC ACA GAG CCG GTG TTA GGG GTT GTG CGC CAG ATC ACC	678
Leu Leu Glu Ala Thr Glu Pro Val Leu Gly Val Val Arg Gln Ile Thr	
200 205 210 215	
CCT TTT GGC ATT TTT GTA GAA GCT AAG GGG ATT GAG GGC TTG GTC CAT	726
Pro Phe Gly Ile Phe Val Glu Ala Lys Gly Ile Glu Gly Leu Val His	
220 225 230	
TAT TCT GAA ATC AGC CAT AAG GGA CCA GTC AAT CCT GAA AAA TAC TAC	774
Tyr Ser Glu Ile Ser His Lys Gly Pro Val Asn Pro Glu Lys Tyr Tyr	
235 240 245	
AAA GAG GGC GAT GAA GTC TAT GTC AAA GCC ATC GCT TAT GAT GCA GAA	822
Lys Glu Gly Asp Glu Val Tyr Val Lys Ala Ile Ala Tyr Asp Ala Glu	
250 255 260	

```

Phe Ser Ser Gln Ile His Lys Gly Val Cys Gln Lys Ile Glu Leu Ser
      340      345      350
Leu Cys Gly Glu Ile Asn Gln Phe Lys Asp Ala Leu Val Ala Phe Met
      355      360      365
Leu Val Gly Val Leu Lys Pro Val Val Gly Asp Lys Ile Asn Tyr Ile
      370      375      380
Asn Ala Pro Phe Val Ala Lys Glu Arg Gly Ile Glu Ile Lys Val Ser
385      390      395      400
Leu Lys Glu Ser Ala Ser Pro Tyr Lys Asn Met Leu Ser Leu Thr Leu
      405      410      415
Asn Ala Ala Asn Gly Thr Ile Ser Val Ser Gly Thr Val Phe Glu Glu
      420      425      430
Asp Ile Leu Lys Leu Thr Glu Ile Asp Gly Phe His Ile Asp Ile Glu
      435      440      445
Pro Lys Gly Lys Met Leu Leu Phe Arg Asn Thr Asp Ile Pro Gly Val
      450      455      460
Ile Gly Ser Val Gly Asn Ala Phe Ala Arg His Gly Ile Asn Ile Ala
465      470      475      480
Asp Phe Arg Leu Gly Arg Asn Thr Gln Lys Glu Ala Leu Ala Leu Ile
      485      490      495
Ile Val Asp Glu Glu Val Ser Leu Glu Val Leu Glu Glu Leu Lys Asn
      500      505      510
Ile Pro Ala Cys Leu Ser Val His Tyr Val Val Ile
      515      520

```

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1701
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

```

GGATTTTATA TTTATTTTAT AGTAAGGCAG TCA ATG AGC AAG ATA GCA GAT GAT      54
                               Met Ser Lys Ile Ala Asp Asp
                               1           5

CAG AAC TTT AAT GAC GAG GAG GAA AAC TTC GCA AAA CTC TTT AAA AAA      102
Gln Asn Phe Asn Asp Glu Glu Glu Asn Phe Ala Lys Leu Phe Lys Lys
      10           15           20

GAA TTA GAA AAA GAA GAA ACC CTA GAA AAA GGC ACT ATC AAA GAA GGG      150
Glu Leu Glu Lys Glu Glu Thr Leu Glu Lys Gly Thr Ile Lys Glu Gly
      25           30           35

```

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

```

Met Tyr Gln Val Ala Ile Cys Asp Pro Ile His Ala Lys Gly Ile Gln
 1           5           10           15
Ile Leu Glu Ala Gln Lys Asp Ile Val Leu His Asp Tyr Ser Lys Cys
          20           25           30
Pro Lys Lys Glu Leu Leu Glu Lys Leu Thr Pro Met Asp Ala Leu Ile
          35           40           45
Thr Arg Ser Met Thr Pro Ile Thr Ser Asp Phe Leu Lys Pro Leu Thr
          50           55           60
His Leu Lys Ser Ile Val Arg Ala Gly Val Gly Val Asp Asn Ile Asp
65           70           75           80
Leu Glu Ser Cys Ser Gln Lys Gly Ile Val Val Met Asn Ile Pro Thr
          85           90           95
Ala Asn Thr Ile Ala Ala Val Glu Leu Thr Met Ala His Leu Ile Asn
          100          105          110
Ala Val Arg Ser Phe Pro Cys Ala Asn Asp Gln Ile Lys His Gln Arg
          115          120          125
Leu Trp Lys Arg Glu Asp Trp Tyr Gly Thr Glu Leu Lys Asn Lys Lys
          130          135          140
Leu Gly Ile Ile Gly Phe Gly Asn Ile Gly Ser Arg Val Gly Ile Arg
145          150          155          160
Ala Lys Ala Phe Glu Met Glu Val Leu Ala Tyr Asp Pro Tyr Ile Pro
          165          170          175
Ser Ser Lys Ala Thr Asp Leu Gly Val Ile Tyr Thr Lys Asn Phe Glu
          180          185          190
Asp Ile Leu Gln Cys Asp Met Ile Thr Ile His Thr Pro Lys Asn Lys
          195          200          205
Glu Thr Ile Asn Met Ile Gly Ala Lys Glu Ile Glu Arg Met Lys Lys
          210          215          220
Gly Val Ile Leu Leu Asn Cys Ala Arg Gly Gly Leu Tyr Asn Glu Asp
225          230          235          240
Ala Leu Tyr Glu Ala Leu Glu Thr Lys Lys Val Arg Trp Leu Gly Ile
          245          250          255
Asp Val Phe Ser Lys Glu Pro Gly Ile His Asn Lys Leu Leu Asp Leu
          260          265          270
Pro Asn Val Tyr Ala Thr Pro His Ile Gly Ala Asn Thr Leu Glu Ser
          275          280          285
Gln Glu Glu Ile Ser Lys Gln Ala Ala Gln Gly Val Met Glu Ser Leu
          290          295          300
Arg Gly Ser Ser His Pro His Ala Leu Asn Leu Pro Met Gln Ala Phe
305          310          315          320
Asp Ala Ser Ala Lys Ala Tyr Leu Asn Leu Ala Gln Lys Leu Gly Tyr
          325          330          335

```

TTA CCC ATG CAA GCT TTT GAC GCG AGC GCA AAA GCC TAC TTG AAT TTA	1011
Leu Pro Met Gln Ala Phe Asp Ala Ser Ala Lys Ala Tyr Leu Asn Leu	
315 320 325 330	
GCG CAA AAA TTG GGT TAT TTT TCC AGT CAA ATC CAT AAG GGC GTG TGC	1059
Ala Gln Lys Leu Gly Tyr Phe Ser Ser Gln Ile His Lys Gly Val Cys	
335 340 345	
CAA AAA ATT GAG CTC AGT CTT TGT GGG GAG ATC AAC CAA TTT AAA GAC	1107
Gln Lys Ile Glu Leu Ser Leu Cys Gly Glu Ile Asn Gln Phe Lys Asp	
350 355 360	
GCT CTT GTA GCC TTT ATG TTA GTG GGG GTG TTA AAA CCT GTT GTA GGG	1155
Ala Leu Val Ala Phe Met Leu Val Gly Val Leu Lys Pro Val Val Gly	
365 370 375	
GAT AAA ATC AAT TAC ATT AAC GCC CCC TTT GTG GCC AAA GAA AGA GGT	1203
Asp Lys Ile Asn Tyr Ile Asn Ala Pro Phe Val Ala Lys Glu Arg Gly	
380 385 390	
ATT GAG ATT AAG GTT AGC CTT AAA GAA AGC GCT TCG CCC TAT AAG AAC	1251
Ile Glu Ile Lys Val Ser Leu Lys Glu Ser Ala Ser Pro Tyr Lys Asn	
395 400 405 410	
ATG CTC TCT TTA ACC CTC AAT GCG GCT AAT GGC ACA ATC AGC GTG AGC	1299
Met Leu Ser Leu Thr Leu Asn Ala Ala Asn Gly Thr Ile Ser Val Ser	
415 420 425	
GGC ACG GTG TTT GAA GAA GAT ATT TTA AAA CTC ACT GAG ATT GAT GGG	1347
Gly Thr Val Phe Glu Glu Asp Ile Leu Lys Leu Thr Glu Ile Asp Gly	
430 435 440	
TTT CAT ATT GAT ATA GAG CCA AAG GGT AAA ATG CTT TTA TTC AGG AAT	1395
Phe His Ile Asp Ile Glu Pro Lys Gly Lys Met Leu Leu Phe Arg Asn	
445 450 455	
ACG GAT ATT CCA GGC GTT ATT GGG AGT GTG GGG AAT GCG TTC GCT AGG	1443
Thr Asp Ile Pro Gly Val Ile Gly Ser Val Gly Asn Ala Phe Ala Arg	
460 465 470	
CAT GGC ATT AAC ATC GCT GAT TTT CGT TTG GGG CGT AAC ACG CAA AAA	1491
His Gly Ile Asn Ile Ala Asp Phe Arg Leu Gly Arg Asn Thr Gln Lys	
475 480 485 490	
GAA GCC CTA GCA CTC ATT ATT GTA GAT GAA GAA GTT TCT TTG GAA GTT	1539
Glu Ala Leu Ala Leu Ile Ile Val Asp Glu Glu Val Ser Leu Glu Val	
495 500 505	
TTA GAA GAG CTT AAA AAC ATT CCT GCG TGC TTA AGC GTT CAT TAT GTG	1587
Leu Glu Glu Leu Lys Asn Ile Pro Ala Cys Leu Ser Val His Tyr Val	
510 515 520	
GTT ATT TAAGGTAGTT GGATGCGAGA TTTTAAATAA CTTTAAATAA	1633
Val Ile	

GTG	ATG	AAT	ATC	CCT	ACC	GCT	AAC	ACG	ATT	GCC	GCT	GTG	GAA	TTG	ACC	339
Val	Met	Asn	Ile	Pro	Thr	Ala	Asn	Thr	Ile	Ala	Ala	Val	Glu	Leu	Thr	
				95					100					105		
ATG	GCG	CAT	TTG	ATC	AAT	GCA	GTG	CGT	TCG	TTC	CCT	TGT	GCA	AAC	GAT	387
Met	Ala	His	Leu	Ile	Asn	Ala	Val	Arg	Ser	Phe	Pro	Cys	Ala	Asn	Asp	
			110					115					120			
CAA	ATC	AAA	CAC	CAA	AGG	TTA	TGG	AAA	AGA	GAA	GAT	TGG	TAT	GGC	ACG	435
Gln	Ile	Lys	His	Gln	Arg	Leu	Trp	Lys	Arg	Glu	Asp	Trp	Tyr	Gly	Thr	
		125					130					135				
GAA	TTG	AAA	AAT	AAA	AAG	CTG	GGC	ATC	ATT	GGT	TTT	GGG	AAT	ATT	GGC	483
Glu	Leu	Lys	Asn	Lys	Lys	Leu	Gly	Ile	Ile	Gly	Phe	Gly	Asn	Ile	Gly	
	140					145				150						
TCT	AGG	GTG	GGC	ATT	AGA	GCA	AAA	GCC	TTT	GAA	ATG	GAA	GTT	CTA	GCC	531
Ser	Arg	Val	Gly	Ile	Arg	Ala	Lys	Ala	Phe	Glu	Met	Glu	Val	Leu	Ala	
155					160					165					170	
TAT	GAT	CCT	TAT	ATC	CCT	TCT	TCA	AAA	GCC	ACT	GAT	TTA	GGA	GTC	ATT	579
Tyr	Asp	Pro	Tyr	Ile	Pro	Ser	Ser	Lys	Ala	Thr	Asp	Leu	Gly	Val	Ile	
				175				180						185		
TAC	ACG	AAA	AAT	TTT	GAA	GAC	ATT	TTG	CAA	TGC	GAT	ATG	ATC	ACT	ATC	627
Tyr	Thr	Lys	Asn	Phe	Glu	Asp	Ile	Leu	Gln	Cys	Asp	Met	Ile	Thr	Ile	
			190					195					200			
CAC	ACC	CCT	AAA	AAT	AAA	GAA	ACG	ATT	AAC	ATG	ATA	GGT	GCT	AAA	GAG	675
His	Thr	Pro	Lys	Asn	Lys	Glu	Thr	Ile	Asn	Met	Ile	Gly	Ala	Lys	Glu	
		205					210					215				
ATT	GAG	CGC	ATG	AAA	AAA	GGG	GTT	ATT	TTG	CTC	AAT	TGC	GCT	AGG	GGT	723
Ile	Glu	Arg	Met	Lys	Lys	Gly	Val	Ile	Leu	Leu	Asn	Cys	Ala	Arg	Gly	
	220					225					230					
GGG	CTT	TAT	AAT	GAA	GAC	GCT	CTT	TAT	GAG	GCT	TTA	GAA	ACC	AAA	AAA	771
Gly	Leu	Tyr	Asn	Glu	Asp	Ala	Leu	Tyr	Glu	Ala	Leu	Glu	Thr	Lys	Lys	
235					240				245					250		
GTG	CGT	TGG	CTT	GGC	ATT	GAT	GTC	TTT	TCT	AAA	GAG	CCT	GGC	ATT	CAC	819
Val	Arg	Trp	Leu	Gly	Ile	Asp	Val	Phe	Ser	Lys	Glu	Pro	Gly	Ile	His	
				255				260						265		
AAC	AAG	CTT	TTA	GAC	TTG	CCC	AAT	GTT	TAT	GCG	ACC	CCC	CAT	ATT	GGC	867
Asn	Lys	Leu	Leu	Asp	Leu	Pro	Asn	Val	Tyr	Ala	Thr	Pro	His	Ile	Gly	
		270					275						280			
GCA	AAC	ACT	TTA	GAA	TCC	CAA	GAA	GAA	ATT	TCC	AAA	CAA	GCC	GCT	CAA	915
Ala	Asn	Thr	Leu	Glu	Ser	Gln	Glu	Glu	Ile	Ser	Lys	Gln	Ala	Ala	Gln	
		285					290					295				
GGG	GTT	ATG	GAA	TCT	TTA	AGG	GGT	TCA	AGC	CAC	CCG	CAT	GCT	TTG	AAT	963
Gly	Val	Met	Glu	Ser	Leu	Arg	Gly	Ser	Ser	His	Pro	His	Ala	Leu	Asn	
	300					305					310					

130		135		140
Ile Tyr Ser Gln Ile	Ser Glu Thr Cys Lys	His Leu Lys Leu Lys Gly		
145		150		155
Leu Met Cys Ile Gly	Ala His Thr Asp Asp	Glu Lys Glu Ile Glu Lys		160
	165		170	
Ser Phe Ile Thr Thr	Lys Lys Leu Phe	Asp Gln Ile Lys Asn Ala Ser		175
	180		185	
Val Leu Ser Met Gly	Met Ser Asp Phe	Glu Leu Ala Ile Ala Cys		190
	195		200	
Gly Ala Asn Leu Leu	Arg Ile Gly Ser	Phe Leu Phe Lys Glu		205
210		215		220

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1593
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

TTTTAAATTC AAAGGATAAA A ATG TAT CAA GTA GCC ATT TGC GAC CCC ATC	51
Met Tyr Gln Val Ala Ile Cys Asp Pro Ile	
1 5 10	
CAT GCT AAA GGC ATT CAA ATT TTA GAA GCT CAA AAA GAC ATT GTC TTG	99
His Ala Lys Gly Ile Gln Ile Leu Glu Ala Gln Lys Asp Ile Val Leu	
15 20 25	
CAT GAT TAT TCC AAA TGC CCT AAA AAG GAG CTT TTA GAA AAA CTC ACT	147
His Asp Tyr Ser Lys Cys Pro Lys Lys Glu Leu Leu Glu Lys Leu Thr	
30 35 40	
CCC ATG GAT GCG CTC ATC ACT CGC AGC ATG ACC CCT ATC ACA AGC GAT	195
Pro Met Asp Ala Leu Ile Thr Arg Ser Met Thr Pro Ile Thr Ser Asp	
45 50 55	
TTT TTA AAG CCC TTA ACC CAC TTA AAA TCC ATC GTG AGA GCG GGC GTG	243
Phe Leu Lys Pro Leu Thr His Leu Lys Ser Ile Val Arg Ala Gly Val	
60 65 70	
GGA GTG GAT AAT ATT GAT TTA GAA AGC TGC TCT CAA AAA GGG ATT GTA	291
Gly Val Asp Asn Ile Asp Leu Glu Ser Cys Ser Gln Lys Gly Ile Val	
75 80 85 90	

GGG GTG GTG CCT GAA GAA GCG CTA GAA ATT TAT TCT CAA ATC AGT GAA 484
 Gly Val Val Pro Glu Glu Ala Leu Glu Ile Tyr Ser Gln Ile Ser Glu
 140 145 150

ACT TGC AAG CAC CTC AAG CTT AAG GGG CTT ATG TGT ATA GGG GCA CAC 532
 Thr Cys Lys His Leu Lys Leu Lys Gly Leu Met Cys Ile Gly Ala His
 155 160 165

ACA GAT GAT GAA AAG GAA ATT GAA AAA TCC TTT ATC ACC ACC AAA AAG 580
 Thr Asp Asp Glu Lys Glu Ile Glu Lys Ser Phe Ile Thr Thr Lys Lys
 170 175 180

CTT TTT GAC CAA ATA AAG AAT GCG AGC GTT CTT TCA ATG GGC ATG AGT 628
 Leu Phe Asp Gln Ile Lys Asn Ala Ser Val Leu Ser Met Gly Met Ser
 185 190 195

GAT GAT TTT GAA TTA GCG ATT GCT TGC GGG GCG AAT CTT TTA AGG ATT 676
 Asp Asp Phe Glu Leu Ala Ile Ala Cys Gly Ala Asn Leu Leu Arg Ile
 200 205 210 215

GGC TCT TTT TTG TTC AAA GAG TAAGATGCTA GAACTTATG CACTTAAAAA TGGG 731
 Gly Ser Phe Leu Phe Lys Glu
 220

GCTGTTTTTA TCTCTGATGC GC 753

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

Met Leu Asp Tyr Arg Gln Lys Ile Asp Ala Leu Ile Thr Lys Ile Glu
 1 5 10 15
 Lys Ala Arg Thr Ala Tyr Ser Arg His His Ile Val Lys Ile Val Ala
 20 25 30
 Val Ser Lys Asn Ala Ser Pro Glu Ala Ile Gln His Tyr Tyr Asn Cys
 35 40 45
 Ser Gln Arg Ala Phe Gly Glu Asn Lys Val Gln Asp Leu Lys Thr Lys
 50 55 60
 Met His Ser Leu Glu His Leu Pro Leu Glu Trp His Met Ile Gly Ser
 65 70 75 80
 Leu Gln Glu Asn Lys Ile Asn Ala Leu Leu Ser Leu Lys Pro Ala Leu
 85 90 95
 Leu His Ser Leu Asp Ser Leu Lys Leu Ala Leu Lys Ile Glu Lys Arg
 100 105 110
 Cys Glu Ile Leu Gly Val Asn Leu Asn Ala Leu Leu Gln Val Asn Ser
 115 120 125
 Ala Tyr Glu Glu Ser Lys Ser Gly Val Val Pro Glu Glu Ala Leu Glu

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 32...697
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

GATCTATAAA GAATAGCCAT AAAGAAGAAT T ATG TTA GAT TAT CGC CAA AAA	52
Met Leu Asp Tyr Arg Gln Lys	
1 5	
ATT GAT GCT CTC ATC ACC AAA ATA GAA AAG GCT CGC ACC GCC TAT TCA	100
Ile Asp Ala Leu Ile Thr Lys Ile Glu Lys Ala Arg Thr Ala Tyr Ser	
10 15 20	
AGG CAC CAC ATT GTC AAA ATC GTG GCT GTT TCA AAA AAC GCT TCC CCA	148
Arg His His Ile Val Lys Ile Val Ala Val Ser Lys Asn Ala Ser Pro	
25 30 35	
GAA GCT ATC CAA CAT TAT TAT AAC TGC TCT CAA AGG GCT TTT GGA GAA	196
Glu Ala Ile Gln His Tyr Tyr Asn Cys Ser Gln Arg Ala Phe Gly Glu	
40 45 50 55	
AAT AAA GTT CAA GAT TTA AAA ACT AAA ATG CAT TCT TTA GAG CAT TTG	244
Asn Lys Val Gln Asp Leu Lys Thr Lys Met His Ser Leu Glu His Leu	
60 65 70	
CCC CTT GAA TGG CAC ATG ATA GGC TCT TTA CAA GAA AAT AAA ATC AAT	292
Pro Leu Glu Trp His Met Ile Gly Ser Leu Gln Glu Asn Lys Ile Asn	
75 80 85	
GCG CTT TTG AGT TTA AAG CCC GCT CTT TTG CAT TCT TTA GAC TCT TTA	340
Ala Leu Leu Ser Leu Lys Pro Ala Leu Leu His Ser Leu Asp Ser Leu	
90 95 100	
AAA CTC GCT TTG AAA ATA GAA AAG CGT TGC GAA ATA TTG GGC GTC AAT	388
Lys Leu Ala Leu Lys Ile Glu Lys Arg Cys Glu Ile Leu Gly Val Asn	
105 110 115	
TTA AAC GCT CTT TTA CAG GTT AAT AGC GCG TAT GAG GAA AGT AAA AGC	436
Leu Asn Ala Leu Leu Gln Val Asn Ser Ala Tyr Glu Glu Ser Lys Ser	
120 125 130 135	

TTATAAAATT GTAAATACT CTTATCTCAA ACGCTAAAAA GGGGTTTTAA ATGGATG

1026

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

```

Met Ala Glu Lys Thr Ala Asn Asp Leu Lys Leu Ser Glu Ile Glu Leu
 1           5           10           15
Val Asp Phe Arg Ile Tyr Gly Met Gln Glu Gly Val Pro Tyr Glu Gly
          20           25           30
Ile Tyr Gly Ile Asn Val Ala Lys Val Gln Glu Ile Ile Pro Met Pro
          35           40           45
Thr Leu Phe Glu Tyr Pro Thr Asn Leu Asp Tyr Ile Ile Gly Val Phe
          50           55           60
Asp Leu Arg Ser Ile Ile Ile Pro Leu Ile Asp Leu Ala Lys Trp Ile
65           70           75           80
Gly Ile Ile Pro Asp Lys Ser Lys Glu Asn Glu Lys Ile Val Ile Ile
          85           90           95
Thr Glu Phe Asn Asn Val Lys Met Gly Phe Leu Val His Ser Ala Arg
          100          105          110
Arg Ile Arg Arg Ile Ser Trp Lys Asp Val Glu Pro Ala Ser Phe Ser
          115          120          125
Ala Ser Asn Ser Ile Asn Lys Glu Asn Ile Thr Gly Thr Thr Arg Ile
          130          135          140
Glu Asn Asp Lys Thr Leu Leu Ile Leu Asp Leu Glu Ser Ile Leu Asp
145          150          155          160
Asp Leu Lys Leu Asn Glu Asp Ala Lys Asn Ala Lys Asp Thr His Lys
          165          170          175
Glu Arg Phe Glu Gly Glu Val Leu Phe Leu Asp Asp Ser Lys Thr Ala
          180          185          190
Arg Lys Thr Leu Lys Asn His Leu Ser Lys Leu Gly Phe Ser Ile Thr
          195          200          205
Glu Ala Val Asp Gly Glu Asp Gly Leu Asn Lys Leu Glu Met Leu Phe
          210          215          220
Lys Lys Tyr Gly Asp Asp Leu Arg Lys His Leu Lys Phe Ile Ile Ser
225          230          235          240
Asp Val Glu Met Pro Lys Met Asp Gly Tyr His Phe Leu Phe Lys Leu
          245          250          255
Gln Lys Asp Pro Arg Phe Ala Tyr Ile Pro Val Ile Phe Asn Ser Ser
          260          265          270
Ile Cys Asp Asn Tyr Ser Ala Glu Arg Ala Lys Glu Met Gly Ala Val
          275          280          285
Ala Tyr Leu Val Lys Phe Asp Ala Glu Lys Phe Thr Glu Glu Ile Ser
          290          295          300
Lys Ile Leu Asp Lys Asn Ala
305          310

```

AAC GAA AAA ATC GTC ATT ATC ACT GAA TTT AAC AAC GTT AAA ATG GGT	342
Asn Glu Lys Ile Val Ile Ile Thr Glu Phe Asn Asn Val Lys Met Gly	
90 95 100 105	
TTT TTA GTC CAT TCG GCT AGG CGT ATC AGG CGC ATT AGC TGG AAA GAT	390
Phe Leu Val His Ser Ala Arg Arg Ile Arg Arg Ile Ser Trp Lys Asp	
110 115 120	
GTG GAG CCT GCA TCC TTT AGC GCC TCT AAT AGC ATC AAT AAA GAA AAT	438
Val Glu Pro Ala Ser Phe Ser Ala Ser Asn Ser Ile Asn Lys Glu Asn	
125 130 135	
ATT ACC GGC ACG ACA CGC ATT GAA AAC GAC AAA ACC CTG CTC ATT TTG	486
Ile Thr Gly Thr Thr Arg Ile Glu Asn Asp Lys Thr Leu Leu Ile Leu	
140 145 150	
GAT TTA GAA AGC ATT TTA GAC GAT TTA AAG CTT AAT GAA GAC GCT AAA	534
Asp Leu Glu Ser Ile Leu Asp Asp Leu Lys Leu Asn Glu Asp Ala Lys	
155 160 165	
AAC GCT AAA GAT ACC CAT AAA GAG CGT TTT GAA GGC GAA GTG TTG TTT	582
Asn Ala Lys Asp Thr His Lys Glu Arg Phe Glu Gly Glu Val Leu Phe	
170 175 180 185	
TTA GAC GAT AGC AAG ACC GCA AGA AAA ACC TTA AAA AAC CAT TTG AGC	630
Leu Asp Asp Ser Lys Thr Ala Arg Lys Thr Leu Lys Asn His Leu Ser	
190 195 200	
AAA TTA GGT TTT AGC ATC ACT GAA GCT GTG GAT GGG GAA GAC GGG TTG	678
Lys Leu Gly Phe Ser Ile Thr Glu Ala Val Asp Gly Glu Asp Gly Leu	
205 210 215	
AAC AAA TTA GAA ATG TTA TTC AAA AAA TAC GGG GAC GAT TTG AGA AAG	726
Asn Lys Leu Glu Met Leu Phe Lys Lys Tyr Gly Asp Asp Leu Arg Lys	
220 225 230	
CAT TTG AAA TTC ATT ATT TCA GAT GTT GAA ATG CCT AAA ATG GAT GGC	774
His Leu Lys Phe Ile Ile Ser Asp Val Glu Met Pro Lys Met Asp Gly	
235 240 245	
TAT CAT TTC TTA TTC AAG CTC CAA AAA GAC CCT AGG TTT GCT TAT ATT	822
Tyr His Phe Leu Phe Lys Leu Gln Lys Asp Pro Arg Phe Ala Tyr Ile	
250 255 260 265	
CCT GTG ATT TTT AAT TCT TCT ATT TGC GAT AAT TAC AGC GCT GAA AGG	870
Pro Val Ile Phe Asn Ser Ser Ile Cys Asp Asn Tyr Ser Ala Glu Arg	
270 275 280	
GCT AAA GAA ATG GGG GCT GTA GCG TAT TTA GTC AAG TTT GAC GCA GAA	918
Ala Lys Glu Met Gly Ala Val Ala Tyr Leu Val Lys Phe Asp Ala Glu	
285 290 295	
AAA TTC ACC GAA GAA ATT TCT AAG ATT TTA GAC AAG AAT GCG TAATTCTTT	969
Lys Phe Thr Glu Glu Ile Ser Lys Ile Leu Asp Lys Asn Ala	
300 305 310	

[illegible]

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 28...960
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

CCATCTCAAA	ATAAGGACGC	CTAAATC	ATG	GCA	GAA	AAA	ACA	GCT	AAC	GAT	TTA					54
			Met	Ala	Glu	Lys	Thr	Ala	Asn	Asp	Leu					
			1				5									
AAA	CTA	AGT	GAG	ATA	GAA	CTC	GTG	GAT	TTT	CGT	ATT	TAT	GGC	ATG	CAA	102
Lys	Leu	Ser	Glu	Ile	Glu	Leu	Val	Asp	Phe	Arg	Ile	Tyr	Gly	Met	Gln	
10					15					20					25	
GAG	GGC	GTC	CCT	TAT	GAG	GGG	ATT	TAT	GGT	ATC	AAT	GTG	GCT	AAA	GTC	150
Glu	Gly	Val	Pro	Tyr	Glu	Gly	Ile	Tyr	Gly	Ile	Asn	Val	Ala	Lys	Val	
				30					35					40		
CAA	GAA	ATC	ATC	CCC	ATG	CCC	ACC	CTT	TTT	GAA	TAC	CCC	ACG	AAT	TTG	198
Gln	Glu	Ile	Ile	Pro	Met	Pro	Thr	Leu	Phe	Glu	Tyr	Pro	Thr	Asn	Leu	
			45					50					55			
GAT	TAC	ATT	ATC	GGC	GTG	TTT	GAT	TTG	CGC	TCC	ATA	ATC	ATT	CCG	CTT	246
Asp	Tyr	Ile	Ile	Gly	Val	Phe	Asp	Leu	Arg	Ser	Ile	Ile	Ile	Pro	Leu	
		60					65					70				
ATA	GAC	TTG	GCT	AAA	TGG	ATA	GGG	ATT	ATC	CCA	GAT	AAA	AGC	AAG	GAA	294
Ile	Asp	Leu	Ala	Lys	Trp	Ile	Gly	Ile	Ile	Pro	Asp	Lys	Ser	Lys	Glu	
	75					80					85					

```

TTA GCC GCT AAA TTA AAA ATC CCT TTT TTG GTT TGT GAA ATG GGG TAT      723
Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr
                225                      230                      235

GAC CAG TTG AAA AGC TTG AAA GAA TGC TTG GAA TTT TGC GGT TAT GAT      771
Asp Gln Leu Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp
                240                      245                      250

GCA GAG TTT TAC AAG GAT TTG AGC GGC TTT GAT AGA GGG TTT GTG GGC      819
Ala Glu Phe Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly
                255                      260                      265

GTT TTA AAA AGT TTT TTA AGA TAAATTAAAA CTTAATTACC CTTTGTAGTGT TACA      874
Val Leu Lys Ser Phe Leu Arg
                270                      275

ATAAAAACAC TTAA                                                    888

```

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

```

Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Gly Leu Ser Gln
 1          5          10          15
Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu Gly Phe Val
          20          25          30
Leu Gln Lys Glu Arg Val Phe Leu His Thr His Ala Tyr Leu Glu Leu
          35          40          45
Asn His Glu Glu Glu Val Arg Phe Phe Glu Leu Val Glu Lys Arg Leu
          50          55          60
Asn Asn Cys Pro Ile Glu Tyr Leu Leu Glu Ser Cys Asp Phe Tyr Gly
          65          70          75          80
Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg Pro Glu Thr
          85          90          95
Glu Ile Leu Val Gln Lys Ala Leu Asp Ile Ile Ser Gln Tyr His Leu
          100          105          110
Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val Ser Val Ser
          115          120          125
Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser Asp Ile Ser
          130          135          140
Pro Asn Ala Leu Glu Val Ala Ser Lys Asn Ile Glu His Phe Cys Leu
          145          150          155          160
Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp His Met Pro
          165          170          175
Met Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala Arg Asn Tyr
          180          185          190
Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala Leu Phe Gly

```

Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Gly																	
1					5					10							
TTA	TCG	CAA	AAA	GGT	TTT	AGG	GGG	GGC	TTA	GAA	TCT	GAA	ATT	TTA	TTA		99
Leu	Ser	Gln	Lys	Gly	Phe	Arg	Gly	Gly	Leu	Glu	Ser	Glu	Ile	Leu	Leu		
15					20					25							
GGC	TTT	GTC	TTG	CAA	AAA	GAA	AGG	GTT	TTT	TTG	CAC	ACG	CAT	GCC	TAT		147
Gly	Phe	Val	Leu	Gln	Lys	Glu	Arg	Val	Phe	Leu	His	Thr	His	Ala	Tyr		
30					35					40							45
TTA	GAG	TTA	AAC	CAC	GAA	GAA	GAG	GTG	CGT	TTT	TTT	GAA	TTG	GTA	GAA		195
Leu	Glu	Leu	Asn	His	Glu	Glu	Glu	Val	Arg	Phe	Phe	Glu	Leu	Val	Glu		
50					55					60							
AAG	CGC	TTG	AAT	AAC	TGC	CCC	ATA	GAG	TAT	TTA	TTA	GAA	AGC	TGT	GAT		243
Lys	Arg	Leu	Asn	Asn	Cys	Pro	Ile	Glu	Tyr	Leu	Leu	Glu	Ser	Cys	Asp		
65					70					75							
TTT	TAT	GGG	CGC	TCT	TTT	TTT	GTG	AAT	GAG	CAT	GTT	TTA	ATC	CCA	CGA		291
Phe	Tyr	Gly	Arg	Ser	Phe	Phe	Val	Asn	Glu	His	Val	Leu	Ile	Pro	Arg		
80					85					90							
CCT	GAA	ACC	GAG	ATT	TTG	GTC	CAA	AAA	GCC	CTT	GAT	ATT	ATT	TCT	CAA		339
Pro	Glu	Thr	Glu	Ile	Leu	Val	Gln	Lys	Ala	Leu	Asp	Ile	Ile	Ser	Gln		
95					100					105							
TAC	CAT	TTA	AAA	GAG	ATA	GGC	GAA	ATC	GGC	ATA	GGG	AGC	GGA	TGC	GTG		387
Tyr	His	Leu	Lys	Glu	Ile	Gly	Glu	Ile	Gly	Ile	Gly	Ser	Gly	Cys	Val		
110					115					120							125
TCT	GTG	AGT	TTG	GCT	TTA	GAA	AAC	CCT	AAT	CTC	TCT	ATT	TAT	GCG	AGC		435
Ser	Val	Ser	Leu	Ala	Leu	Glu	Asn	Pro	Asn	Leu	Ser	Ile	Tyr	Ala	Ser		
130					135					140							
GAT	ATT	TCA	CCA	AAC	GCT	TTA	GAA	GTG	GCG	TCC	AAA	AAT	ATT	GAG	CAC		483
Asp	Ile	Ser	Pro	Asn	Ala	Leu	Glu	Val	Ala	Ser	Lys	Asn	Ile	Glu	His		
145					150					155							
TTT	TGT	CTA	AAA	GAG	CGT	GTT	TTT	TTA	AAA	CAA	ACA	CGC	CTT	TGG	GAT		531
Phe	Cys	Leu	Lys	Glu	Arg	Val	Phe	Leu	Lys	Gln	Thr	Arg	Leu	Trp	Asp		
160					165					170							
CAT	ATG	CCC	ATG	ATA	GAA	ATG	CTT	GTC	TCT	AAC	CCG	CCC	TAT	ATC	GCT		579
His	Met	Pro	Met	Ile	Glu	Met	Leu	Val	Ser	Asn	Pro	Pro	Tyr	Ile	Ala		
175					180					185							
AGA	AAT	TAT	CCT	TTG	GAA	AAA	TCC	GTC	CTC	AAA	GAA	CCG	CAT	GAA	GCC		627
Arg	Asn	Tyr	Pro	Leu	Glu	Lys	Ser	Val	Leu	Lys	Glu	Pro	His	Glu	Ala		
190					195					200							205
CTT	TTT	GGG	GGG	GTT	AAA	GGC	GAT	GAG	ATC	TTA	AAA	GAA	ATC	GTT	TTT		675
Leu	Phe	Gly	Gly	Val	Lys	Gly	Asp	Glu	Ile	Leu	Lys	Glu	Ile	Val	Phe		
210					215					220							

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

```

Met Arg Phe Val Tyr His Pro Leu Ala Lys Glu Pro Val Leu Lys Ile
 1           5           10           15
Glu Gly Glu Ser Tyr Thr His Leu Tyr Arg Ser Arg Arg Val Lys Ser
          20           25           30
Ala Ser Arg Leu Asp Leu Arg Asn Leu Lys Asp Gly Phe Leu Tyr Thr
          35           40           45
Tyr Glu His Ala Glu Ile Thr Lys Lys His Ala Leu Leu Lys Leu Val
          50           55           60
Gly Ala Arg Leu Leu Glu Val Met Ala Ser Lys Lys Thr His Leu Ile
65           70           75           80
Leu Ser Val Ile Glu Ile Lys Asn Ile Glu Lys Ile Leu Pro Phe Leu
          85           90           95
Asn Gln Leu Gly Val Ser Lys Leu Ser Leu Phe Tyr Ala Asp Phe Ser
          100          105          110
Gln Arg Asn Glu Lys Ile Asp Ile Ala Lys Leu Glu Arg Phe Gln Lys
          115          120          125
Ile Leu Ile His Ser Cys Glu Gln Cys Gly Arg Ser Ala Leu Met Glu
          130          135          140
Leu Glu Val Phe Ser Asn Thr Lys Glu Ala Leu Lys Ala Tyr Pro Lys
145          150          155          160
Ala Ser Val Leu Asp Phe Lys Gly Glu Thr Leu Xaa Ala Ser Ala Asp
          165          170          175
Phe Glu Lys Gly Val Ile Ile Gly Pro Glu Gly Gly Phe Ser Glu Pro
          180          185          190
Glu Arg Gly Tyr Phe Lys Glu Arg Glu Ile Tyr Arg Ile Pro Leu Asp
          195          200          205
Met Val Leu Lys Ser Glu Ser Ala Cys Val Phe Val Ala Ser Ile Ala
210          215          220
Gln Val
225

```

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...840
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

TTATGAAATT GA ATG ACC CTT TCG CAA GCC CTA AAC AAA GCC AAA AAA GGA 51

Phe	Leu	Tyr	Thr	Tyr	Glu	His	Ala	Glu	Ile	Thr	Lys	Lys	His	Ala	Leu		
45					50					55					60		
TTA	AAG	CTA	GTG	GGC	GCG	CGA	TTA	TTA	GAG	GTT	ATG	GCC	AGT	AAA	AAA		242
Leu	Lys	Leu	Val	Gly	Ala	Arg	Leu	Leu	Glu	Val	Met	Ala	Ser	Lys	Lys		
				65					70					75			
ACG	CAT	TTG	ATT	TTA	AGC	GTG	ATT	GAA	ATC	AAA	AAC	ATT	GAA	AAA	ATC		290
Thr	His	Leu	Ile	Leu	Ser	Val	Ile	Glu	Ile	Lys	Asn	Ile	Glu	Lys	Ile		
			80					85					90				
CTA	CCC	TTT	TTA	AAT	CAG	TTA	GGC	GTG	AGC	AAG	TTG	AGT	TTA	TTC	TAT		338
Leu	Pro	Phe	Leu	Asn	Gln	Leu	Gly	Val	Ser	Lys	Leu	Ser	Leu	Phe	Tyr		
		95					100					105					
GCG	GAT	TTT	AGC	CAA	CGC	AAT	GAA	AAA	ATA	GAC	ATC	GCT	AAA	TTA	GAG		386
Ala	Asp	Phe	Ser	Gln	Arg	Asn	Glu	Lys	Ile	Asp	Ile	Ala	Lys	Leu	Glu		
	110					115					120						
CGC	TTT	CAA	AAG	ATT	TTG	ATC	CAT	TCT	TGC	GAG	CAG	TGT	GGT	AGG	AGT		434
Arg	Phe	Gln	Lys	Ile	Leu	Ile	His	Ser	Cys	Glu	Gln	Cys	Gly	Arg	Ser		
	125				130					135					140		
GCT	TTA	ATG	GAA	TTG	GAA	GTG	TTT	TCA	AAC	ACT	AAA	GAG	GCG	CTA	AAA		482
Ala	Leu	Met	Glu	Leu	Glu	Val	Phe	Ser	Asn	Thr	Lys	Glu	Ala	Leu	Lys		
				145					150					155			
GCC	TAT	CCT	AAG	GCG	AGC	GTT	TTG	GAT	TTT	AAG	GGC	GAA	ACC	TTA	NCC		530
Ala	Tyr	Pro	Lys	Ala	Ser	Val	Leu	Asp	Phe	Lys	Gly	Glu	Thr	Leu	Xaa		
			160					165					170				
GCA	AGC	GCG	GAT	TTT	GAA	AAG	GGC	GTT	ATC	ATA	GGG	CCT	GAG	GGG	GGC		578
Ala	Ser	Ala	Asp	Phe	Glu	Lys	Gly	Val	Ile	Ile	Gly	Pro	Glu	Gly	Gly		
		175					180					185					
TTT	AGC	GAA	CCA	GAA	AGA	GGG	TAT	TTT	AAA	GAG	CGT	GAA	ATT	TAT	CGC		626
Phe	Ser	Glu	Pro	Glu	Arg	Gly	Tyr	Phe	Lys	Glu	Arg	Glu	Ile	Tyr	Arg		
	190					195					200						
ATC	CCG	TTA	GAT	ATG	GTG	CTA	AAG	TCT	GAG	AGT	GCA	TGC	GTG	TTT	GTA		674
Ile	Pro	Leu	Asp	Met	Val	Leu	Lys	Ser	Glu	Ser	Ala	Cys	Val	Phe	Val		
	205				210				215					220			
GCG	AGT	ATC	GCA	CAA	GTT	TAGGGGGTTA	TTGGGGGATTT	TAAATCCTAA	AAAATC								728
Ala	Ser	Ile	Ala	Gln	Val												
				225													

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```

Glu Lys Met Lys Leu Phe Arg Ser His Gly Met Leu Lys Lys Asp Phe
      115                      120                      125
Phe Glu Gly Glu Val Lys Ser Ile Gly His Asn Phe Arg Leu Asn Glu
      130                      135                      140
Ile Gln Ser Ala Leu Gly Leu Ser Gln Leu Lys Lys Ala Pro Phe Leu
      145                      150                      155                      160
Met Gln Lys Arg Glu Ala Ala Leu Thr Tyr Asp Arg Ile Phe Lys
      165                      170                      175
Asp Asn Pro Tyr Phe Thr Pro Leu His Pro Leu Leu Lys Asp Lys Ser
      180                      185                      190
Ser Asn His Leu Tyr Pro Ile Leu Met His Gln Lys Phe Phe Thr Cys
      195                      200                      205
Lys Lys Leu Ile Leu Glu Ser Leu His Lys Arg Gly Ile Leu Ala Gln
      210                      215                      220
Val His Tyr Lys Pro Ile Tyr Gln Tyr Gln Leu Tyr Gln Gln Leu Phe
      225                      230                      235                      240
Asn Thr Ala Pro Leu Lys Ser Ala Glu Asp Phe Tyr His Ala Glu Ile
      245                      250                      255
Ser Leu Pro Cys His Ala Asn Leu Asn Leu Glu Ser Val Gln Asn Ile
      260                      265                      270
Ala His Ser Val Leu Lys Thr Phe Glu Ser Phe Lys Ile Glu
      275                      280                      285

```

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 15...692
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

```

TAATGGGCCT TTGA ATG CGT TTT GTC TAT CAC CCT TTA GCC AAA GAG CCT      50
      Met Arg Phe Val Tyr His Pro Leu Ala Lys Glu Pro
      1                      5                      10

GTT TTA AAA ATA GAA GGC GAG AGT TAT ACG CAT TTA TAC CGA TCA AGG      98
Val Leu Lys Ile Glu Gly Glu Ser Tyr Thr His Leu Tyr Arg Ser Arg
      15                      20                      25

CGT GTC AAA AGT GCG AGT CGT TTG GAT TTG AGA AAT TTA AAA GAC GGC      146
Arg Val Lys Ser Ala Ser Arg Leu Asp Leu Arg Asn Leu Lys Asp Gly
      30                      35                      40

TTT TTA...TAC ACC TAT GAG CAT GCA GAA ATC ACT AAA AAA CAC GCC CTT      194

```



```

Pro Tyr Phe Thr Pro Leu His Pro Leu Leu Lys Asp Lys Ser Ser Asn
 180                               185                               190

CAC CTT TAT CCT ATT TTA ATG CAC CAA AAA TTT TTT ACA TGC AAA AAA      680
His Leu Tyr Pro Ile Leu Met His Gln Lys Phe Phe Thr Cys Lys Lys
195                               200                               205                               210

CTC ATT TTA GAA AGT TTG CAC AAG CGT GGC ATT TTA GCC CAA GTG CAT      728
Leu Ile Leu Glu Ser Leu His Lys Arg Gly Ile Leu Ala Gln Val His
                               215                               220                               225

TAC AAG CCC ATT TAT CAA TAC CAA TTG TAC CAA CAG CTC TTC AAT ACA      776
Tyr Lys Pro Ile Tyr Gln Tyr Gln Leu Tyr Gln Gln Leu Phe Asn Thr
                               230                               235                               240

GCC CCA TTA AAA AGC GCA GAG GAT TTC TAT CAC GCT GAA ATT TCC TTG      824
Ala Pro Leu Lys Ser Ala Glu Asp Phe Tyr His Ala Glu Ile Ser Leu
                               245                               250                               255

CCT TGT CAT GCG AAT TTA AAT TTA GAG AGC GTT CAA AAC ATC GCT CAT      872
Pro Cys His Ala Asn Leu Asn Leu Glu Ser Val Gln Asn Ile Ala His
                               260                               265                               270

AGC GTT TTA AAA ACT TTT GAG AGT TTT AAA ATA GAA TGAGTTTCAT TTAGGG      924
Ser Val Leu Lys Thr Phe Glu Ser Phe Lys Ile Glu
275                               280                               285

CTTCAAATCT TAATCATTA GAATGGTGCG GAAGAAA      961

```

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

```

Met Leu Leu Glu Ser Gly Tyr Thr Pro Val Phe Ala Gly Ile Lys Asn
 1                               5                               10                               15
Asp Gly Asn Ile Asp Glu Leu Ala Leu Glu Lys Leu Ile Asn Glu Arg
                               20                               25                               30
Thr Lys Ala Ile Val Ser Val Asp Tyr Ala Gly Lys Ser Val Glu Val
                               35                               40                               45
Glu Ser Val Gln Lys Leu Cys Lys Lys His Ser Leu Ser Phe Leu Ser
                               50                               55                               60
Asp Ser Ser His Ala Leu Gly Ser Glu Tyr Gln Asn Lys Lys Val Gly
65                               70                               75                               80
Gly Phe Ala Leu Ala Ser Val Phe Ser Phe His Ala Ile Lys Pro Ile
                               85                               90                               95
Thr Thr Ala Glu Gly Gly Ala Val Val Thr Asn Asp Ser Glu Leu His
                               100                               105                               110

```

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

ATCGTAATGA AATAATCACC ACCCCTATAA GCTTTGTAGC GACGGCTAAC	ATG CTT	56
	Met Leu	
	1	
TTA GAA AGC GGT TAT ACA CCC GTA TTT GCT GGA ATT AAA AAC GAT GGC		104
Leu Glu Ser Gly Tyr Thr Pro Val Phe Ala Gly Ile Lys Asn Asp Gly		
5 10 15		
AAT ATA GAT GAA TTA GCC CTA GAA AAG CTC ATT AAC GAA AGA ACC AAA		152
Asn Ile Asp Glu Leu Ala Leu Glu Lys Leu Ile Asn Glu Arg Thr Lys		
20 25 30		
GCC ATA GTG AGC GTG GAT TAT GCC GGT AAA AGC GTG GAA GTA GAA AGC		200
Ala Ile Val Ser Val Asp Tyr Ala Gly Lys Ser Val Glu Val Glu Ser		
35 40 45 50		
GTT CAA AAG CTT TGC AAA AAG CAT TCT TTG AGC TTT CTT TCT GAC AGC		248
Val Gln Lys Leu Cys Lys Lys His Ser Leu Ser Phe Leu Ser Asp Ser		
55 60 65		
TCG CAT GCT CTA GGA AGC GAG TAT CAA AAC AAA AAA GTA GGA GGC TTT		296
Ser His Ala Leu Gly Ser Glu Tyr Gln Asn Lys Lys Val Gly Gly Phe		
70 75 80		
GCG TTA GCG AGC GTG TTT AGT TTC CAT GCC ATT AAG CCC ATC ACT ACG		344
Ala Leu Ala Ser Val Phe Ser Phe His Ala Ile Lys Pro Ile Thr Thr		
85 90 95		
GCT GAA GGG GGA GCG GTC GTT ACT AAC GAT AGC GAA TTG CAT GAA AAA		392
Ala Glu Gly Gly Ala Val Val Thr Asn Asp Ser Glu Leu His Glu Lys		
100 105 110		
ATG AAA TTG TTT CGC TCT CAT GGC ATG CTC AAA AAA GAT TTT TTT GAA		440
Met Lys Leu Phe Arg Ser His Gly Met Leu Lys Lys Asp Phe Phe Glu		
115 120 125 130		
GGC GAA GTC AAA AGC ATA GGG CAT AAC TTC CGC TTG AAT GAA ATC CAA		488
Gly Glu Val Lys Ser Ile Gly His Asn Phe Arg Leu Asn Glu Ile Gln		
135 140 145		
AGC GCT TTG GGT TTG AGC CAG CTT AAA AAA GCC CCC TTT TTA ATG CAA		536
Ser Ala Leu Gly Leu Ser Gln Leu Lys Lys Ala Pro Phe Leu Met Gln		
150 155 160		
AAA AGA GAA GAA GCC GCT CTA ACC TAT GAC AGG ATT TTT AAA GAT AAC		584
Lys Arg Glu Glu Ala Ala Leu Thr Tyr Asp Arg Ile Phe Lys Asp Asn		
165 170 175		
CCT TAT TTC ACC CCT TTA CAC CCC TTG TTA AAA GAT AAA AGC TCT AAC		632

```

      195              200              205
Arg Phe Leu Val Ser Lys Ala Leu Tyr Phe Leu Gln Lys Glu Ser Leu
  210              215              220
Gly Ala Met Gly Phe Leu Arg Gln Arg Glu Val Phe Arg Lys Arg Ser
  225              230              235              240
Leu Lys Ala Ser Asp Ile Ser Phe Asn Ile Ala Pro Leu Ile Asn Ser
      245              250              255
Ala Gly Arg Met Gln Asp Ala Lys Met Ala Leu Asp Phe Leu Ser Ala
      260              265              270
Asn Asn Ser Gln Asp Gly Tyr Ser Leu Tyr Glu Arg Leu Lys Ala Cys
      275              280              285
Asn Leu Lys Arg Lys Met Ile Gln Gln Gln Val Phe Glu Glu Ala Phe
      290              295              300
Lys His Ala Met Val Gly Glu Lys Ile Ile Val Ala Phe Lys Asp Asn
  305              310              315              320
Trp His Glu Gly Val Leu Gly Ile Val Ala Ser Lys Leu Val Glu Ala
      325              330              335
Thr Gln Lys Pro Ser Leu Val Phe Thr Phe Lys Glu Gly Val Tyr Lys
      340              345              350
Gly Ser Ala Arg Ser Ser Ser Asn Ile Asp Leu Ile Asp Ala Leu Asn
      355              360              365
Gly Val Ser Ser Leu Leu Leu Gly Tyr Gly Gly His Arg Gln Ala Cys
      370              375              380
Gly Leu Ser Val Glu Lys Asn Asn Ile Ile Ser Leu Phe Glu Thr Leu
  385              390              395              400
Glu Asn Phe Asp Phe Lys Val Leu Pro Phe Cys Lys Thr Glu Pro Pro
      405              410              415
Leu Thr Leu Lys Leu Lys Asp Ile Asp Arg Glu Leu Leu Glu Ile Ile
      420              425              430
Glu Met Gly Glu Pro Tyr Gly Gln Glu Asn Pro Glu Pro Leu Phe Gln
      435              440              445
Ala Lys Asn Leu Glu Val Ile Glu Glu Lys Ile Ile Lys Glu Ser His
      450              455              460
Gln Val Leu Arg Phe Lys Asp Lys Glu Cys Val Lys Glu Ala Ile Tyr
  465              470              475              480
Phe Ser Ala Glu Arg Phe Leu Lys Ala Gly Glu Lys Val Ser Val Leu
      485              490              495
Phe Ser Val Glu Leu Asp Glu Cys Ser Asn Glu Pro Lys Met Phe Val
      500              505              510
Lys Ser Leu Leu
      515

```

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...908

```

ATC ATT AAA GAA AGC CAC CAG GTT TTG CGT TTT AAG GAT AAA GAA TGC      1442
Ile Ile Lys Glu Ser His Gln Val Leu Arg Phe Lys Asp Lys Glu Cys
    460                      465                      470

GTC AAA GAG GCT ATT TAT TTT AGC GCT GAG CGG TTT TTG AAA GCG GGC      1490
Val Lys Glu Ala Ile Tyr Phe Ser Ala Glu Arg Phe Leu Lys Ala Gly
    475                      480                      485                      490

GAA AAG GTG AGC GTG CTT TTT AGC GTG GAA TTA GAT GAG TGT TCT AAT      1538
Glu Lys Val Ser Val Leu Phe Ser Val Glu Leu Asp Glu Cys Ser Asn
                      495                      500                      505

GAG CCT AAA ATG TTT GTT AAA AGT TTG TTG TAGTGCCTTT TGTTGAAGAA GAA      1591
Glu Pro Lys Met Phe Val Lys Ser Leu Leu
                      510                      515

TTTGAAATTT TAAACCCAC CAAAGCCTTG TTTTTT                                1627

```

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

```

Met Lys Gln Lys Leu Lys Ala Gln Ile Lys Glu Arg Met Ala Ser Ile
  1           5           10           15
Ala Tyr Asn Glu Lys Gly Phe Pro Ser Pro Phe Leu Phe Lys Asp Leu
          20           25           30
Lys Lys Ala Ala Leu Lys Ile Ile Glu Ala Met Arg Thr Asn Thr Glu
          35           40           45
Ile Leu Val Val Gly Asp Tyr Asp Ala Asp Gly Val Ile Ser Ser Ala
          50           55           60
Ile Met Ala Lys Phe Phe Glu Ser Leu Asn Tyr Lys His Val Arg Ile
          65           70           75           80
Ala Ile Pro Asn Arg Phe Met Asp Gly Tyr Gly Ile Ser Lys Lys Phe
          85           90           95
Leu Glu Lys His His Ala Pro Leu Ile Ile Thr Val Asp Asn Gly Ile
          100          105          110
Asn Ala Phe Glu Ala Ala Arg Phe Cys Lys Glu Lys Asn Tyr Thr Leu
          115          120          125
Ile Ile Thr Asp His His Cys Leu His His Asp Glu Val Pro Asp Ala
          130          135          140
Tyr Ala Val Ile Asn Pro Lys Gln Pro Asp Cys Asp Phe Ile Gln Lys
          145          150          155          160
Glu Val Cys Gly Ala Leu Val Ala Phe Tyr Leu Cys Tyr Gly Ile His
          165          170          175
Gln Leu Leu Gly Lys Glu Lys Ser His Ser Ser Glu Leu Leu Cys Leu
          180          185          190
Ala Gly Val Ala Thr Ile Ala Asp Met Met Pro Leu Thr Phe Phe Asn

```

GTT TTT AGA AAA CGC TCT TTA AAA GCG AGT GAT ATT TCT TTT AAT ATC	770
Val Phe Arg Lys Arg Ser Leu Lys Ala Ser Asp Ile Ser Phe Asn Ile	
235 240 245 250	
GCC CCC TTA ATC AAC TCC GCA GGG CGC ATG CAA GAT GCG AAA ATG GCT	818
Ala Pro Leu Ile Asn Ser Ala Gly Arg Met Gln Asp Ala Lys Met Ala	
255 260 265	
TTA GAT TTT TTA AGC GCG AAT AAT TCT CAA GAT GGC TAT TCT TTG TAT	866
Leu Asp Phe Leu Ser Ala Asn Asn Ser Gln Asp Gly Tyr Ser Leu Tyr	
270 275 280	
GAA CGC TTG AAA GCA TGC AAT TTG AAG CGT AAA ATG ATC CAA CAG CAG	914
Glu Arg Leu Lys Ala Cys Asn Leu Lys Arg Lys Met Ile Gln Gln Gln	
285 290 295	
GTT TTT GAA GAA GCT TTT AAG CAT GCG ATG GTT GGA GAA AAA ATT ATC	962
Val Phe Glu Glu Ala Phe Lys His Ala Met Val Gly Glu Lys Ile Ile	
300 305 310	
GTC GCT TTT AAG GAC AAT TGG CAT GAG GGA GTG CTG GGG ATT GTG GCT	1010
Val Ala Phe Lys Asp Asn Trp His Glu Gly Val Leu Gly Ile Val Ala	
315 320 325 330	
TCA AAA TTA GTG GAA GCC ACT CAA AAG CCA AGC CTG GTT TTT ACC TTT	1058
Ser Lys Leu Val Glu Ala Thr Gln Lys Pro Ser Leu Val Phe Thr Phe	
335 340 345	
AAA GAA GGG GTG TAT AAA GGG AGC GCT CGT AGC TCT TCA AAC ATT GAC	1106
Lys Glu Gly Val Tyr Lys Gly Ser Ala Arg Ser Ser Ser Asn Ile Asp	
350 355 360	
TTG ATT GAC GCT TTG AAT GGG GTT TCT TCT TTA TTG CTC GGC TAT GGA	1154
Leu Ile Asp Ala Leu Asn Gly Val Ser Ser Leu Leu Leu Gly Tyr Gly	
365 370 375	
GGG CAT AGG CAA GCT TGC GGG TTG AGC GTT GAA AAA AAC AAT ATC ATC	1202
Gly His Arg Gln Ala Cys Gly Leu Ser Val Glu Lys Asn Asn Ile Ile	
380 385 390	
TCG CTC TTT GAA ACT TTA GAA AAT TTT GAT TTT AAA GTT TTA CCT TTT	1250
Ser Leu Phe Glu Thr Leu Glu Asn Phe Asp Phe Lys Val Leu Pro Phe	
395 400 405 410	
TGT AAA ACA GAG CCC CCT TTA ACG CTC AAA TTA AAA GAC ATT GAC AGA	1298
Cys Lys Thr Glu Pro Leu Thr Leu Lys Leu Lys Asp Ile Asp Arg	
415 420 425	
GAG CTT TTA GAG ATT ATA GAA ATG GGC GAA CCT TAT GGG CAA GAA AAC	1346
Glu Leu Leu Glu Ile Ile Glu Met Gly Glu Pro Tyr Gly Gln Glu Asn	
430 435 440	
CCT GAA CCC CTA TTC CAA GCA AAA AAT TTA GAA GTC ATA GAA GAA AAA	1394
Pro Glu Pro Leu Phe Gln Ala Lys Asn Leu Glu Val Ile Glu Glu Lys	
445 450 455	

GAG CGC ATG GCT TCT ATC GCT TAT AAT GAA AAA GGG TTT CCT AGC CCC	98
Glu Arg Met Ala Ser Ile Ala Tyr Asn Glu Lys Gly Phe Pro Ser Pro	
15 20 25	
TTT TTA TTT AAA GAC TTG AAA AAA GCC GCG CTC AAA ATC ATA GAA GCC	146
Phe Leu Phe Lys Asp Leu Lys Lys Ala Ala Leu Lys Ile Ile Glu Ala	
30 35 40	
ATG CGC ACA AAC ACA GAA ATT TTA GTG GTG GGC GAT TAT GAC GCT GAC	194
Met Arg Thr Asn Thr Glu Ile Leu Val Val Gly Asp Tyr Asp Ala Asp	
45 50 55	
GGC GTG ATT AGC TCT GCT ATC ATG GCA AAA TTT TTT GAA AGC CTG AAC	242
Gly Val Ile Ser Ser Ala Ile Met Ala Lys Phe Phe Glu Ser Leu Asn	
60 65 70	
TAT AAG CAT GTC CGC ATT GCA ATC CCT AAT CGC TTC ATG GAT GGC TAT	290
Tyr Lys His Val Arg Ile Ala Ile Pro Asn Arg Phe Met Asp Gly Tyr	
75 80 85 90	
GGG ATT TCT AAA AAA TTT TTA GAA AAA CAC CAC GCC CCT TTA ATC ATC	338
Gly Ile Ser Lys Lys Phe Leu Glu Lys His His Ala Pro Leu Ile Ile	
95 100 105	
ACG GTG GAT AAC GGG ATT AAC GCC TTT GAA GCC GCG CGA TTT TGT AAA	386
Thr Val Asp Asn Gly Ile Asn Ala Phe Glu Ala Ala Arg Phe Cys Lys	
110 115 120	
GAA AAA AAT TAC ACC CTT ATC ATC ACA GAT CAC CAT TGC TTA CAC CAT	434
Glu Lys Asn Tyr Thr Leu Ile Ile Thr Asp His His Cys Leu His His	
125 130 135	
GAT GAA GTC CCA GAC GCT TAT GCG GTG ATC AAC CCC AAG CAA CCG GAT	482
Asp Glu Val Pro Asp Ala Tyr Ala Val Ile Asn Pro Lys Gln Pro Asp	
140 145 150	
TGT GAT TTT ATC CAA AAG GAA GTG TGC GGG GCG TTG GTA GCG TTT TAT	530
Cys Asp Phe Ile Gln Lys Glu Val Cys Gly Ala Leu Val Ala Phe Tyr	
155 160 165 170	
TTG TGC TAT GGG ATC CAT CAG CTT TTA GGA AAA GAA AAA AGC CAT TCT	578
Leu Cys Tyr Gly Ile His Gln Leu Leu Gly Lys Glu Lys Ser His Ser	
175 180 185	
AGT GAG TTA TTA TGT TTA GCG GGC GTG GCG ACT ATT GCT GAC ATG ATG	626
Ser Glu Leu Leu Cys Leu Ala Gly Val Ala Thr Ile Ala Asp Met Met	
190 195 200	
CCT TTG ACT TTT TTT AAC CGC TTT TTA GTT TCT AAA GCC TTG TAT TTT	674
Pro Leu Thr Phe Phe Asn Arg Phe Leu Val Ser Lys Ala Leu Tyr Phe	
205 210 215	
TTG CAA AAA GAA TCC TTA GGG GCG ATG GGT TTT TTG CGC CAA AGA GAA	722
Leu Gln Lys Glu Ser Leu Gly Ala Met Gly Phe Leu Arg Gln Arg Glu	
220 225 230	

TTA AGT ATG CTG AAA AAC TTT TAC CTA CCG ATA TTA TAAAAGATAA TCTTAA 395
 Leu Ser Met Leu Lys Asn Phe Tyr Leu Pro Ile Leu
 100 105 110

TAAC 399

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

Met	Glu	Asn	Asp	Val	Lys	Glu	Asp	Leu	Glu	Gln	Ala	Arg	Pro	Lys	Leu
1				5				10						15	
Glu	Pro	Glu	Lys	Gln	Lys	Gln	Glu	Pro	Glu	Glu	Gln	Lys	Gln	Glu	Lys
			20					25						30	
Gln	Asp	Lys	Gln	Glu	Gln	Lys	Pro	Lys	Gln	Glu	Lys	Glu	Glu	Ser	Lys
		35					40					45			
Ser	Lys	Glu	Gln	Glu	Glu	Asn	Lys	Lys	Gln	Lys	Arg	Ser	Ser	Tyr	Ile
	50					55					60				
Phe	Trp	Gly	Cys	Ile	Ile	Gly	Leu	Cys	Ile	Val	Val	Ile	Ile	Ala	Lys
65				70					75					80	
Ile	Ile	Ala	Phe	Gly	Gly	Ser	Ser	Glu	Glu	Ala	Lys	Ala	Asp	Lys	Pro
			85					90						95	
Lys	Asn	Ser	Leu	Ser	Met	Leu	Lys	Asn	Phe	Tyr	Leu	Pro	Ile	Leu	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...1568
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

TCTAAATCCT	AATCTAACAA	ATG	AAA	CAA	AAG	CTT	AAA	GCT	CAA	ATC	AAA	50
		Met	Lys	Gln	Lys	Leu	Lys	Ala	Gln	Ile	Lys	
		1				5					10	

```

Lys Tyr Gly Val Ser Leu Ile Tyr Leu Ile Glu Ser Thr Ile Leu Tyr
  50              55              60
Phe Val Ser Lys Asp Leu Ser Trp Ile Val Ala Leu Thr Ile Phe Ser
  65              70              75              80
Leu Ser Leu Ile Leu Val Ala Phe Lys Ile Phe Leu Leu Lys Asp Asn
              85              90              95
Pro Asn Lys Arg Phe Lys Asn Asn Lys Arg Asp Lys Lys
      100              105

```

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...379
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

```

AGCGCTCAAA TCATTTATTG GTTATCAAAA TATTTTAGGA GTGAGT ATG GAA AAT      55
                                   Met Glu Asn
                                   1

GAT GTT AAA GAA GAT CTA GAG CAA GCA AGA CCA AAG TTA GAG CCA GAA      103
Asp Val Lys Glu Asp Leu Glu Gln Ala Arg Pro Lys Leu Glu Pro Glu
  5              10              15

AAG CAA AAG CAA GAG CCA GAG GAA CAG AAA CAA GAA AAA CAA GAC AAA      151
Lys Gln Lys Gln Glu Pro Glu Glu Gln Lys Gln Glu Lys Gln Asp Lys
  20              25              30              35

CAA GAG CAG AAG CCA AAG CAA GAA AAA GAA GAG TCA AAG AGC AAG GAA      199
Gln Glu Gln Lys Pro Lys Gln Glu Lys Glu Glu Ser Lys Ser Lys Glu
              40              45              50

CAA GAA GAA AAC AAA AAA CAA AAG AGA TCT AGC TAT ATT TTT TGG GGA      247
Gln Glu Glu Asn Lys Lys Gln Lys Arg Ser Ser Tyr Ile Phe Trp Gly
              55              60              65

TGT ATT ATT GGT TTG TGT ATA GTT GTT ATT ATT GCC AAA ATT ATT GCG      295
Cys Ile Ile Gly Leu Cys Ile Val Val Ile Ile Ala Lys Ile Ile Ala
              70              75              80

TTT GGC GGA TCT AGT GAG GAG GCA AAA GCA GAC AAA CCA AAA AAC TCT      343
Phe Gly Gly Ser Ser Glu Glu Ala Lys Ala Asp Lys Pro Lys Asn Ser
  85              90              95

```


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

```

TAAAACGCTC TTGAAAGGGT GAGCGTGGAA TTTGCTTCTA TCGTTTGGTT GCTCATAGTC      60
AATATTCTGA TTTTATTCT C ATG CTG GTG GAT AAA AAT TCG GCT GAT CAA      111
                      Met Leu Val Asp Lys Asn Ser Ala Asp Gln
                      1             5             10

AAA ATG TGG CGT ATT CCT GAA AAA GCT TTG TGG GTT TTA TCG CTC CTT      159
Lys Met Trp Arg Ile Pro Glu Lys Ala Leu Trp Val Leu Ser Leu Leu
                      15             20             25

GGC GGG TCT GTC GGG TTT TTG GTC GCT ATG GTT GTG TCC CAC CAT AAG      207
Gly Gly Ser Val Gly Phe Leu Val Ala Met Val Val Ser His His Lys
                      30             35             40

ATC TTA AAG CCT GAG TTT AAA TAC GGC GTT TCG CTC ATT TAC TTG ATA      255
Ile Leu Lys Pro Glu Phe Lys Tyr Gly Val Ser Leu Ile Tyr Leu Ile
                      45             50             55

GAG AGC ACA ATC CTT TAC TTT GTC AGC AAA GAT CTT TCT TGG ATA GTA      303
Glu Ser Thr Ile Leu Tyr Phe Val Ser Lys Asp Leu Ser Trp Ile Val
                      60             65             70

GCG CTA ACG ATA TTC TCA CTA TCT TTG ATA CTG GTA GCG TTT AAG ATC      351
Ala Leu Thr Ile Phe Ser Leu Ser Leu Ile Leu Val Ala Phe Lys Ile
                      75             80             85             90

TTC CTC CTT AAA GAC AAC CCT AAC AAA CGC TTC AAA AAC AAC AAG AGG      399
Phe Leu Leu Lys Asp Asn Pro Asn Lys Arg Phe Lys Asn Asn Lys Arg
                      95             100             105

GAT AAA AAA TAATGTCTTA TTTTTTTAAA ATCATTCTGG GCACAAGCGT GATCGTGGG      457
Asp Lys Lys

GG                                                                 459

```

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

```

Met Leu Val Asp Lys Asn Ser Ala Asp Gln Lys Met Trp Arg Ile Pro
 1             5             10             15
Glu Lys Ala Leu Trp Val Leu Ser Leu Leu Gly Gly Ser Val Gly Phe
                20             25             30
Leu Val Ala Met Val Val Ser His His Lys Ile Leu Lys Pro Glu Phe
          35             40             45

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

```

Met Lys Ser His Phe Gln Tyr Ser Thr Leu Glu Asn Ile Pro Lys Ala
 1           5           10           15
Phe Asp Ile Leu Lys Asp Pro Pro Lys Lys Leu Tyr Cys Val Gly Asp
           20           25           30
Thr Lys Leu Leu Asp Thr Pro Leu Lys Val Ala Ile Ile Gly Thr Arg
           35           40           45
Arg Pro Thr Pro Tyr Ser Lys Gln His Thr Ile Thr Leu Ala Arg Glu
           50           55           60
Leu Ala Lys Asn Gly Ala Val Ile Val Ser Gly Gly Ala Leu Gly Val
65           70           75           80
Asp Ile Ile Ala Gln Glu Asn Ala Leu Pro Lys Thr Ile Met Leu Ser
           85           90           95
Pro Cys Ser Leu Asp Phe Ile Tyr Pro Thr Asn Asn His Lys Val Ile
           100          105          110
Gln Glu Ile Ala Gln Asn Gly Leu Ile Leu Ser Glu Tyr Glu Lys Asp
           115          120          125
Phe Met Pro Ile Lys Gly Ser Phe Leu Ala Arg Asn Arg Leu Val Ile
           130          135          140
Ala Leu Ser Asp Val Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly
145          150          155          160
Ser Met Ser Ser Ala Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe
           165          170          175
Val Leu Pro Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu
           180          185          190
Glu Lys Gly Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn
           195          200          205
Thr Leu Leu Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Glu Asp
           210          215          220
Glu Phe Leu Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr
225          230          235          240
Leu Lys Phe Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile
           245          250          255
Lys Arg Ile Asn His Ile Val Val Leu Ala
           260          265

```

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 82...408
- (D) OTHER INFORMATION:

ATC TAT CCT ACG AAC AAT CAT AAA GTG ATC CAA GAA ATC GCG CAA AAC	391
Ile Tyr Pro Thr Asn Asn His Lys Val Ile Gln Glu Ile Ala Gln Asn	
105 110 115	
GGC TTG ATT TTA AGC GAA TAT GAA AAG GAT TTC ATG CCC ATT AAA GGC	439
Gly Leu Ile Leu Ser Glu Tyr Glu Lys Asp Phe Met Pro Ile Lys Gly	
120 125 130	
TCT TTT TTG GCG AGA AAC CGC CTG GTG ATC GCT TTA AGC GAT GTG GTG	487
Ser Phe Leu Ala Arg Asn Arg Leu Val Ile Ala Leu Ser Asp Val Val	
135 140 145 150	
ATT ATC CCC CAA GCG GAT TTA AAA AGC GGC TCT ATG AGC AGC GCG AGA	535
Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser Met Ser Ser Ala Arg	
155 160 165	
TTA GCC CAG AAA TAC CAA AAG CCT TTA TTT GTT TTA CCC CAA CGC CTG	583
Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val Leu Pro Gln Arg Leu	
170 175 180	
AAT GAG AGC GAT GGC ACT AAT GAG CTT TTA GAA AAA GGG CAG GCT CAA	631
Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu Lys Gly Gln Ala Gln	
185 190 195	
GGG ATA TTT AAT ATT CAA AAT TTT ATA AAC ACC CTT TTA AAA GAC TAC	679
Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr Leu Leu Lys Asp Tyr	
200 205 210	
CAT TTA AAA GAA ATG CCT GAA ATG GAA GAT GAA TTT TTA GAA TAT TGT	727
His Leu Lys Glu Met Pro Glu Met Glu Asp Glu Phe Leu Glu Tyr Cys	
215 220 225 230	
GCC AAA AAC CCG AGC TAT GAA GAA GCG TAT CTC AAA TTT GGG GAT AAG	775
Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu Lys Phe Gly Asp Lys	
235 240 245	
CTT TTA GAA TAC GAG CTG TTG GGT AAG ATC AAG CGC ATC AAT CAC ATT	823
Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys Arg Ile Asn His Ile	
250 255 260	
GTG GTG TTA GCG TGATTTTGGC ATGCGATGTG GGGTTAAAAC GCATTGGCAT CGCTG	880
Val Val Leu Ala	
265	
CGCTTTTAAA TGGCGT	896

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

```

Lys Met Cys Glu Tyr Ala Lys Thr Leu Ala Ser Glu Phe His Arg Phe
                        485                        490                        495
Tyr Asn Ala Gly Lys Ile Leu Asp Thr Pro Lys Ala Lys Glu Leu Leu
                        500                        505                        510
Lys Ile Cys Leu Ile Val Ser Leu Ser Leu Ser Asn Ala Phe Lys Leu
                        515                        520                        525
Leu Gly Ile Glu Ile Lys Thr Lys Ile Ser Ala Arg Asp
                        530                        535                        540

```

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 38...835
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

```

AAGTAGAGAT TATATTACCT AGATAGTGAA TCAACGA ATG AAA AGC CAC TTC CAA      55
                        Met Lys Ser His Phe Gln
                        1                        5

TAC AGC ACG CTA GAA AAT ATC CCT AAA GCC TTT GAC ATT CTC AAA GAC      103
Tyr Ser Thr Leu Glu Asn Ile Pro Lys Ala Phe Asp Ile Leu Lys Asp
                        10                        15                        20

CCC CCT AAA AAA CTC TAT TGT GTG GGC GAT ACC AAG CTT TTG GAC ACG      151
Pro Pro Lys Lys Leu Tyr Cys Val Gly Asp Thr Lys Leu Leu Asp Thr
                        25                        30                        35

CCT TTA AAA GTG GCG ATC ATA GGC ACA AGA AGA CCC ACC CCT TAC AGC      199
Pro Leu Lys Val Ala Ile Ile Gly Thr Arg Arg Pro Thr Pro Tyr Ser
                        40                        45                        50

AAG CAA CAC ACG ATC ACT CTA GCT AGA GAG CTT GCT AAA AAT GGC GCG      247
Lys Gln His Thr Ile Thr Leu Ala Arg Glu Leu Ala Lys Asn Gly Ala
55                        60                        65                        70

GTT ATT GTG AGT GGG GGA GCG TTA GGC GTG GAT ATT ATC GCT CAA GAA      295
Val Ile Val Ser Gly Gly Ala Leu Gly Val Asp Ile Ile Ala Gln Glu
                        75                        80                        85

AAC GCC TTG CCA AAA ACG ATC ATG CTT TCG CCT TGC AGT TTG GAT TTC      343
Asn Ala Leu Pro Lys Thr Ile Met Leu Ser Pro Cys Ser Leu Asp Phe
                        90                        95                        100

```

35	40	45
Ile Ala Glu Glu Leu Ala Leu Lys	Ile Ser Thr His Glu Lys Thr Gln	
50	55	60
Gly Leu Phe Asp Ser Val Val Ala Cys Lys Gly Tyr Ile Asn Phe Thr		
65	70	75
Leu Ser Leu Asp Phe Leu Glu Arg Phe Thr Gln Lys Ala Leu Glu Leu		80
85	90	95
Lys Glu Lys Phe Gly Ser Gln Val Lys Ser Glu Arg Ser Gln Lys Ile		
100	105	110
Phe Leu Glu Phe Val Ser Ala Asn Pro Thr Gly Pro Leu His Ile Gly		
115	120	125
His Ala Arg Gly Ala Val Phe Gly Asp Ser Leu Ala Lys Ile Ala Arg		
130	135	140
Phe Leu Gly His Glu Val Leu Cys Glu Tyr Tyr Val Asn Asp Met Gly		
145	150	155
Ser Gln Ile Arg Leu Leu Gly Leu Ser Val Trp Leu Ala Tyr Arg Glu		160
165	170	175
His Val Leu Lys Glu Ser Val Thr Tyr Pro Glu Val Phe Tyr Lys Gly		
180	185	190
Glu Tyr Ile Ile Glu Ile Ala Lys Lys Ala Asn Asn Asp Leu Glu Pro		
195	200	205
Ser Leu Leu Lys Glu Asn Glu Glu Thr Ile Ile Glu Val Leu Ser Gly		
210	215	220
Tyr Ala Arg Asp Leu Met Leu Leu Glu Ile Lys Asp Asn Leu Asp Ala		
225	230	235
Leu Gly Ile His Phe Asp Ser Tyr Ala Ser Glu Lys Glu Val Phe Lys		240
245	250	255
His Lys Asp Ala Val Phe Glu Gln Leu Glu Lys Ala Asn Ala Leu Tyr		
260	265	270
Glu Lys Asp Ser Lys Ile Trp Leu Lys Ser Ser Leu Tyr Gln Asp Glu		
275	280	285
Ser Asp Arg Val Leu Ile Lys Glu Asp Lys Ser Tyr Thr Tyr Leu Ala		
290	295	300
Gly Asp Ile Val Tyr His Asp Glu Lys Phe Lys Gln Asp Tyr Thr Lys		
305	310	315
Tyr Ile Asn Ile Trp Gly Ala Asp His His Gly Tyr Ile Ala Arg Val		320
325	330	335
Lys Ala Ser Leu Glu Phe Leu Gly Tyr Asp Ser Asn Lys Leu Glu Val		
340	345	350
Leu Leu Ala Gln Met Val Arg Leu Leu Lys Asp Asn Glu Pro Tyr Lys		
355	360	365
Met Ser Lys Arg Ala Gly Asn Phe Ile Leu Ile Lys Asp Val Val Asp		
370	375	380
Asp Val Gly Lys Asp Ala Leu Arg Phe Ile Phe Leu Ser Lys Arg Leu		
385	390	395
Asp Thr His Leu Glu Phe Asp Val Asn Thr Leu Lys Lys Gln Asp Ser		400
405	410	415
Ser Asn Pro Ile Tyr Tyr Ile His Tyr Ala Asn Ser Arg Ile His Thr		
420	425	430
Met Leu Glu Lys Ser Pro Phe Ser Lys Glu Glu Val Leu Gln Thr Pro		
435	440	445
Leu Thr Asn Leu Asn Ala Glu Glu Lys Tyr Leu Leu Phe Ser Ala Leu		
450	455	460
Ser Leu Pro Lys Ala Ile Glu Ser Ser Phe Glu Glu Tyr Gly Leu Gln		
465	470	475
		480

ACT TTA AAA AAG CAA GAC AGC TCA AAC CCC ATT TAC TAT ATC CAT TAC	1300
Thr Leu Lys Lys Gln Asp Ser Ser Asn Pro Ile Tyr Tyr Ile His Tyr	
410 415 420 425	
GCT AAT TCG CGC ATC CAC ACC ATG CTA GAA AAA TCG CCC TTT TCT AAA	1348
Ala Asn Ser Arg Ile His Thr Met Leu Glu Lys Ser Pro Phe Ser Lys	
430 435 440	
GAA GAG GTT TTG CAA ACC CCT TTA ACC AAT TTA AAC GCT GAA GAA AAA	1396
Glu Glu Val Leu Gln Thr Pro Leu Thr Asn Leu Asn Ala Glu Glu Lys	
445 450 455	
TAC TTG CTT TTT AGC GCT TTA AGC TTG CCT AAA GCA ATT GAA TCC TCT	1444
Tyr Leu Leu Phe Ser Ala Leu Ser Leu Pro Lys Ala Ile Glu Ser Ser	
460 465 470	
TTT GAA GAA TAC GGC TTG CAA AAA ATG TGC GAA TAC GCA AAA ACC CTC	1492
Phe Glu Glu Tyr Gly Leu Gln Lys Met Cys Glu Tyr Ala Lys Thr Leu	
475 480 485	
GCA TCA GAA TTC CAC CGC TTC TAT AAC GCT GGC AAA ATC TTA GAC ACC	1540
Ala Ser Glu Phe His Arg Phe Tyr Asn Ala Gly Lys Ile Leu Asp Thr	
490 495 500 505	
CCT AAA GCT AAA GAG CTT TTA AAA ATT TGT TTA ATA GTA AGC TTG AGC	1588
Pro Lys Ala Lys Glu Leu Leu Lys Ile Cys Leu Ile Val Ser Leu Ser	
510 515 520	
TTA AGC AAC GCT TTT AAA CTT TTA GGC ATA GAG ATA AAG ACC AAA ATT	1636
Leu Ser Asn Ala Phe Lys Leu Leu Gly Ile Glu Ile Lys Thr Lys Ile	
525 530 535	
TCC GCT AGA GAT TAAGCCAATA TTTAATTTTT TGTTATAACA TTCCCCTTAT TTTTT	1693
Ser Ala Arg Asp	
540	
GAAACTAAGG AGAATATTAT	1713

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

Met His Thr Leu Ile Lys Gly Ile Leu Glu Glu Ile Leu Glu Glu Glu	
1 5 10 15	
Val Ile Val Glu Tyr Pro Lys Asp Arg Glu His Gly His Tyr Ala Thr	
20 25 30	
Pro Ile Ala Phe Asn Leu Ala Lys Val Phe Lys Lys Ser Pro Leu Ala	

Pro	Glu	Val	Phe	Tyr	Lys	Gly	Glu	Tyr	Ile	Ile	Glu	Ile	Ala	Lys	Lys	
				190					195					200		
GCG	AAC	AAC	GAT	TTA	GAA	CCA	AGC	CTT	TTA	AAA	GAA	AAC	GAA	GAA	ACG	676
Ala	Asn	Asn	Asp	Leu	Glu	Pro	Ser	Leu	Leu	Lys	Glu	Asn	Glu	Glu	Thr	
			205					210					215			
ATT	ATT	GAA	GTT	TTA	AGC	GGC	TAT	GCT	AGG	GAT	CTA	ATG	CTT	TTA	GAA	724
Ile	Ile	Glu	Val	Leu	Ser	Gly	Tyr	Ala	Arg	Asp	Leu	Met	Leu	Leu	Glu	
		220					225					230				
ATT	AAA	GAT	AAT	TTA	GAC	GCT	TTA	GGC	ATT	CAT	TTT	GAT	TCC	TAT	GCG	772
Ile	Lys	Asp	Asn	Leu	Asp	Ala	Leu	Gly	Ile	His	Phe	Asp	Ser	Tyr	Ala	
	235					240					245					
AGC	GAA	AAA	GAA	GTT	TTT	AAA	CAT	AAA	GAT	GCG	GTG	TTT	GAA	CAA	TTA	820
Ser	Glu	Lys	Glu	Val	Phe	Lys	His	Lys	Asp	Ala	Val	Phe	Glu	Gln	Leu	
250					255				260						265	
GAA	AAA	GCG	AAC	GCC	CTT	TAT	GAA	AAG	GAT	TCT	AAA	ATC	TGG	CTC	AAA	868
Glu	Lys	Ala	Asn	Ala	Leu	Tyr	Glu	Lys	Asp	Ser	Lys	Ile	Trp	Leu	Lys	
				270					275					280		
TCT	TCA	CTC	TAC	CAG	GAT	GAA	AGC	GAT	CGG	GTG	CTC	ATT	AAA	GAA	GAT	916
Ser	Ser	Leu	Tyr	Gln	Asp	Glu	Ser	Asp	Arg	Val	Leu	Ile	Lys	Glu	Asp	
			285					290					295			
AAA	AGC	TAC	ACT	TAT	TTA	GCG	GGC	GAT	ATT	GTC	TAT	CAT	GAT	GAA	AAA	964
Lys	Ser	Tyr	Thr	Tyr	Leu	Ala	Gly	Asp	Ile	Val	Tyr	His	Asp	Glu	Lys	
		300					305					310				
TTC	AAG	CAA	GAT	TAT	ACC	AAA	TAC	ATC	AAC	ATT	TGG	GGG	GCA	GAC	CAC	1012
Phe	Lys	Gln	Asp	Tyr	Thr	Lys	Tyr	Ile	Asn	Ile	Trp	Gly	Ala	Asp	His	
	315					320					325					
CAC	GGC	TAT	ATC	GCT	AGA	GTG	AAA	GCC	AGC	CTT	GAG	TTT	TTG	GGC	TAT	1060
His	Gly	Tyr	Ile	Ala	Arg	Val	Lys	Ala	Ser	Leu	Glu	Phe	Leu	Gly	Tyr	
330					335					340					345	
GAT	TCC	AAC	AAG	CTT	GAA	GTC	TTG	CTC	GCT	CAA	ATG	GTG	CGC	TTG	CTC	1108
Asp	Ser	Asn	Lys	Leu	Glu	Val	Leu	Leu	Ala	Gln	Met	Val	Arg	Leu	Leu	
				350					355					360		
AAA	GAT	AAC	GAG	CCT	TAC	AAG	ATG	AGT	AAA	AGA	GCG	GGT	AAT	TTT	ATT	1156
Lys	Asp	Asn	Glu	Pro	Tyr	Lys	Met	Ser	Lys	Arg	Ala	Gly	Asn	Phe	Ile	
			365					370					375			
TTG	ATT	AAA	GAT	GTG	GTT	GAT	GAT	GTG	GGT	AAG	GAC	GCT	TTG	AGG	TTT	1204
Leu	Ile	Lys	Asp	Val	Val	Asp	Asp	Val	Gly	Lys	Asp	Ala	Leu	Arg	Phe	
		380					385					390				
ATT	TTT	TTG	AGC	AAA	CGG	CTT	GAC	ACT	CAT	TTA	GAA	TTT	GAT	GTC	AAT	1252
Ile	Phe	Leu	Ser	Lys	Arg	Leu	Asp	Thr	His	Leu	Glu	Phe	Asp	Val	Asn	
	395					400					405					

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

TTAAAAGCAA'ACAAGAAAGT TAAGC ATG CAC ACT CTC ATT AAG GGC ATT TTA	52
Met His Thr Leu Ile Lys Gly Ile Leu	
1 5	
GAA GAG ATT TTA GAA GAA GAA GTC ATT GTT GAA TAC CCT AAA GAC AGA	100
Glu Glu Ile Leu Glu Glu Glu Val Ile Val Glu Tyr Pro Lys Asp Arg	
10 15 20 25	
GAG CAT GGG CAT TAC GCT ACG CCC ATT GCT TTC AAT CTC GCC AAA GTT	148
Glu His Gly His Tyr Ala Thr Pro Ile Ala Phe Asn Leu Ala Lys Val	
30 35 40	
TTT AAA AAA TCG CCC TTA GCC ATC GCT GAA GAG TTA GCC CTT AAA ATC	196
Phe Lys Lys Ser Pro Leu Ala Ile Ala Glu Glu Leu Ala Leu Lys Ile	
45 50 55	
AGC ACG CAT GAA AAA ACT CAA GGG CTT TTT GAC AGC GTA GTG GCT TGT	244
Ser Thr His Glu Lys Thr Gln Gly Leu Phe Asp Ser Val Val Ala Cys	
60 65 70	
AAG GGC TAT ATC AAT TTC ACG CTT TCT TTA GAT TTT TTG GAG CGT TTC	292
Lys Gly Tyr Ile Asn Phe Thr Leu Ser Leu Asp Phe Leu Glu Arg Phe	
75 80 85	
ACC CAA AAA GCT TTG GAA TTG AAA GAA AAA TTT GGC TCT CAA GTT AAA	340
Thr Gln Lys Ala Leu Glu Leu Lys Glu Lys Phe Gly Ser Gln Val Lys	
90 95 100 105	
AGC GAA CGT TCT CAA AAA ATC TTT TTA GAA TTT GTG AGC GCT AAC CCC	388
Ser Glu Arg Ser Gln Lys Ile Phe Leu Glu Phe Val Ser Ala Asn Pro	
110 115 120	
ACA GGG CCT TTA CAC ATA GGG CAT GCT AGA GGG GCG GTG TTT GGC GAT	436
Thr Gly Pro Leu His Ile Gly His Ala Arg Gly Ala Val Phe Gly Asp	
125 130 135	
AGT TTG GCT AAA ATC GCT CGC TTT TTA GGG CAT GAA GTT TTA TGC GAG	484
Ser Leu Ala Lys Ile Ala Arg Phe Leu Gly His Glu Val Leu Cys Glu	
140 145 150	
TAT TAT GTC AAT GAC ATG GGA TCT CAA ATC CGC TTG TTA GGG CTT TCT	532
Tyr Tyr Val Asn Asp Met Gly Ser Gln Ile Arg Leu Leu Gly Leu Ser	
155 160 165	
GTA TGG CTC GCT TAC AGA GAA CAT GTT TTA AAA GAA AGC GTA ACT TAC	580
Val Trp Leu Ala Tyr Arg Glu His Val Leu Lys Glu Ser Val Thr Tyr	
170 175 180 185	
CCA GAA GTC TTT TAC AAA GGC GAA TAC ATC ATT GAA ATC GCT AAA AAG	628

1		5		10		15									
Lys	Thr	Ser	Phe	Leu	Ser	Glu	Tyr	Leu	Asn	Gln	Thr	Asp	His	Gln	Gly
		20						25					30		
Val	Ala	Leu	Ile	Ile	Asn	Glu	Ile	Gly	Gln	Ala	Ala	Leu	Asp	Gln	Arg
		35						40					45		
Ile	Leu	Ser	Val	Gln	Tyr	Cys	Gly	Glu	Lys	Met	Leu	Tyr	Leu	Asn	Ala
	50					55					60				
Gly	Cys	Val	Cys	Cys	Asn	Lys	Arg	Leu	Asp	Leu	Val	Glu	Ser	Leu	Lys
65					70					75					80
Ala	Thr	Leu	Asn	Asn	Tyr	Glu	Trp	His	Gly	Glu	Ile	Leu	Arg	Arg	Ile
			85						90					95	
Ile	Ile	Glu	Thr	Thr	Gly	Leu	Ala	Asn	Pro	Ala	Pro	Ile	Leu	Trp	Thr
		100						105					110		
Ile	Leu	Ser	Asp	Thr	Phe	Leu	Gly	Val	His	Phe	Glu	Ile	Gln	Ser	Val
		115					120					125			
Val	Ala	Cys	Val	Asp	Ala	Leu	Asn	Ala	Arg	Glu	His	Leu	Thr	Asn	Asn
	130					135					140				
Glu	Ala	Lys	Glu	Gln	Ile	Val	Phe	Ala	Asp	Ser	Val	Leu	Leu	Thr	Lys
145					150				155						160
Thr	Asp	Leu	Gln	Asn	Asp	Ser	Ala	Ala	Leu	Thr	Lys	Leu	Lys	Glu	Arg
				165				170						175	
Ile	Gln	Ala	Leu	Asn	Pro	Ser	Ala	Glu	Ile	Phe	Asp	Lys	Arg	Ala	Ile
		180						185					190		
Asp	Tyr	Glu	Ser	Leu	Phe	Ser	Arg	Lys	Asn	Arg	Ala	Arg	Asn	Phe	Met
	195						200					205			
Pro	Arg	Met	Pro	Lys	Asp	Ser	His	Ser	Gln	Gly	Phe	Glu	Thr	Leu	Ser
	210					215					220				
Ile	Asn	Phe	Glu	Gly	Thr	Met	Glu	Trp	Ser	Ala	Phe	Gly	Ile	Trp	Leu
225					230					235					240
Ser	Leu	Leu	Leu	His	Gln	Tyr	Gly	Thr	Gln	Ile	Leu	Arg	Ile	Lys	Gly
			245						250					255	
Ile	Ile	Asp	Ile	Gly	Ser	Gly	Phe	Leu	Val	Ser	Ile	Asn	Gly	Val	Met
		260						265					270		
His	Val	Ile	Tyr	Pro	Pro	Lys	His	Ile	Leu	Lys	Asp	Gln	Asn	Gly	Ser
		275					280					285			
Asn	Leu	Val	Phe	Ile	Met	Arg	His	Leu	Glu	Arg	Glu	Lys	Ile	Leu	Asn
	290					295					300				
Ser	Leu	Lys	Gly	Phe	Lys	Asp	Phe	Leu	Gly	Ile	Lys	Gly	Phe	Glu	Thr
305					310				315						320
Gln															

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...1648

GCT TTA ACA AAA CTA AAA GAG AGG ATA CAA GCC CTT AAC CCT AGT GCA	641
Ala Leu Thr Lys Leu Lys Glu Arg Ile Gln Ala Leu Asn Pro Ser Ala	
170 175 180	
GAA ATT TTT GAC AAG AGG GCG ATA GAC TAT GAG AGC CTC TTT TCA CGC	689
Glu Ile Phe Asp Lys Arg Ala Ile Asp Tyr Glu Ser Leu Phe Ser Arg	
185 190 195 200	
AAA AAT AGG GCG CGA AAT TTT ATG CCA AGA ATG CCA AAA GAT TCG CAC	737
Lys Asn Arg Ala Arg Asn Phe Met Pro Arg Met Pro Lys Asp Ser His	
205 210 215	
TCG CAA GGC TTT GAG ACT TTA AGC ATT AAT TTT GAA GGC ACG ATG GAG	785
Ser Gln Gly Phe Glu Thr Leu Ser Ile Asn Phe Glu Gly Thr Met Glu	
220 225 230	
TGG AGC GCG TTT GGG ATT TGG CTG AGT TTG TTA TTG CAT CAA TAC GGC	833
Trp Ser Ala Phe Gly Ile Trp Leu Ser Leu Leu Leu His Gln Tyr Gly	
235 240 245	
ACA CAG ATT TTA CGC ATC AAG GGG ATT ATT GAC ATT GGA AGC GGC TTT	881
Thr Gln Ile Leu Arg Ile Lys Gly Ile Ile Asp Ile Gly Ser Gly Phe	
250 255 260	
TTG GTG AGT ATT AAC GGC GTG ATG CAT GTC ATT TAC CCG CCT AAG CAT	929
Leu Val Ser Ile Asn Gly Val Met His Val Ile Tyr Pro Pro Lys His	
265 270 275 280	
ATT TTA AAG GAT CAA AAC GGC TCT AAC CTC GTT TTT ATC ATG CGC CAT	977
Ile Leu Lys Asp Gln Asn Gly Ser Asn Leu Val Phe Ile Met Arg His	
285 290 295	
TTA GAG CGT GAA AAA ATC TTA AAT TCC TTA AAG GGT TTT AAG GAT TTT	1025
Leu Glu Arg Glu Lys Ile Leu Asn Ser Leu Lys Gly Phe Lys Asp Phe	
300 305 310	
CTC GGC ATC AAG GGT TTT GAA ACC CAA TAATTTTCT ATTTATGGAT AGCTGTT	1079
Leu Gly Ile Lys Gly Phe Glu Thr Gln	
315 320	
TGCATTTTGA TGGGGAAAAG A	1100

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

Met Pro Lys Ile Pro Ile Thr Leu Ile Thr Gly Phe Leu Gly Ser Gly

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 90...1052
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

```

AAGGCGCAAA ACTTAGCCAA AAAAGAGATG GACGCACTAG ATTCTCATCT GTTAGCGTTT      60
TTAAATCAAA ATGCAAATGC CATTCACTG  ATG CCC AAA ATC CCT ATC ACG CTC      113
                               Met Pro Lys Ile Pro Ile Thr Leu
                               1                               5

ATC ACC GGT TTT TTA GGC AGC GGT AAA ACG AGT TTT TTG AGC GAA TAT      161
Ile Thr Gly Phe Leu Gly Ser Gly Lys Thr Ser Phe Leu Ser Glu Tyr
    10                               15                               20

TTA AAC CAA ACA GAT CAC CAA GGC GTC GCT CTT ATC ATC AAT GAA ATC      209
Leu Asn Gln Thr Asp His Gln Gly Val Ala Leu Ile Ile Asn Glu Ile
    25                               30                               35                               40

GGT CAA GCC GCT TTG GAT CAG CGC ATC TTA AGC GTT CAA TAT TGC GGT      257
Gly Gln Ala Ala Leu Asp Gln Arg Ile Leu Ser Val Gln Tyr Cys Gly
                               45                               50                               55

GAA AAA ATG CTC TAT CTT AAC GCA GGG TGC GTG TGT TGC AAC AAA CGC      305
Glu Lys Met Leu Tyr Leu Asn Ala Gly Cys Val Cys Cys Asn Lys Arg
                               60                               65                               70

TTG GAT TTA GTG GAG TCT CTA AAA GCC ACG CTC AAC AAC TAT GAA TGG      353
Leu Asp Leu Val Glu Ser Leu Lys Ala Thr Leu Asn Asn Tyr Glu Trp
    75                               80                               85

CAC GGC GAA ATT CTA AGG CGC ATC ATC ATT GAA ACT ACC GGT TTA GCC      401
His Gly Glu Ile Leu Arg Arg Ile Ile Ile Glu Thr Thr Gly Leu Ala
    90                               95                               100

AAC CCG GCA CCG ATT TTA TGG ACG ATT TTG AGC GAC ACT TTT TTA GGA      449
Asn Pro Ala Pro Ile Leu Trp Thr Ile Leu Ser Asp Thr Phe Leu Gly
    105                               110                               115                               120

GTG CAT TTT GAG ATT CAA AGC GTG GTG GCT TGC GTG GAT GCA TTG AAT      497
Val His Phe Glu Ile Gln Ser Val Val Ala Cys Val Asp Ala Leu Asn
                               125                               130                               135

GCT AGA GAG CAT TTA ACC AAC AAT GAA GCT AAA GAG CAA ATC GTT TTT      545
Ala Arg Glu His Leu Thr Asn Asn Glu Ala Lys Glu Gln Ile Val Phe
                               140                               145                               150

GCT GAT AGC GTT TTA TTG ACC AAA ACG GAT TTA CAA AAC GAT AGC GCG      593
Ala Asp Ser Val Leu Leu Thr Lys Thr Asp Leu Gln Asn Asp Ser Ala
    155                               160                               165

```

65					70					75				80
Leu	Lys	Lys	Gly	Thr	Ser	Phe	Gly	Ala	Pro	Thr	Glu	Leu	Glu	Thr
				85					90					95
Leu	Ala	Lys	Glu	Ile	Ile	Ser	Cys	Tyr	Glu	Gly	Leu	Asp	Lys	Val
			100					105					110	
Leu	Val	Ser	Ser	Gly	Thr	Glu	Ala	Thr	Met	Ser	Ala	Ile	Arg	Leu
		115						120					125	
Arg	Ala	Tyr	Ser	Gln	Lys	Asp	Asp	Leu	Ile	Lys	Phe	Glu	Gly	Cys
		130					135					140		
His	Gly	His	Ser	Asp	Ser	Leu	Leu	Val	Lys	Ala	Gly	Ser	Gly	Cys
145					150					155				160
Thr	Phe	Gly	Ser	Pro	Ser	Ser	Leu	Gly	Val	Pro	Asn	Asp	Phe	Ser
			165						170					175
His	Thr	Leu	Val	Ala	Arg	Tyr	Asn	Asp	Leu	Asn	Ser	Thr	Glu	Glu
			180					185					190	
Phe	Lys	Lys	Gly	Asn	Val	Gly	Cys	Val	Ile	Ile	Glu	Pro	Ile	Ala
		195					200					205		
Asn	Met	Gly	Leu	Val	Pro	Ala	Gln	Lys	Glu	Phe	Leu	Leu	Gly	Leu
	210					215					220			
Ala	Leu	Cys	Glu	Lys	Tyr	Gln	Ala	Val	Leu	Ile	Leu	Asp	Glu	Val
225					230					235				240
Ser	Gly	Phe	Arg	Ala	Ser	Leu	Ser	Gly	Ser	Gln	Glu	Phe	Tyr	Gly
			245					250					255	
Val	Pro	Asp	Leu	Val	Thr	Phe	Gly	Lys	Val	Ile	Gly	Ala	Gly	Leu
		260					265						270	
Leu	Ala	Cys	Phe	Gly	Gly	Arg	Ala	Glu	Ile	Met	Asp	Leu	Leu	Ser
		275					280					285		
Ile	Gly	Ser	Val	Tyr	Gln	Ala	Gly	Thr	Leu	Ser	Gly	Asn	Pro	Leu
	290					295					300			
Val	Cys	Ala	Gly	Leu	Ser	Ala	Leu	Tyr	Lys	Ile	Lys	Arg	Asp	Lys
305					310					315				320
Leu	Tyr	Thr	Arg	Leu	Asp	Ala	Leu	Ala	Ile	Arg	Leu	Thr	Gln	Gly
			325						330				335	
Gln	Lys	Ser	Ala	Gln	Asn	Tyr	Asn	Ile	Ala	Leu	Glu	Thr	Leu	Asn
			340				345						350	
Gly	Ser	Met	Phe	Gly	Phe	Phe	Phe	Asn	Glu	Asn	Ala	Val	His	Asp
		355					360					365		
Asp	Asp	Ala	Leu	Lys	Ser	Asp	Thr	Glu	Met	Phe	Ala	Lys	Phe	His
	370					375					380			
Lys	Met	Leu	Phe	Lys	Gly	Val	Tyr	Leu	Ala	Cys	Ser	Ser	Phe	Glu
385					390					395				400
Gly	Phe	Ile	Cys	Glu	Pro	Met	Thr	Glu	Glu	Met	Ile	Asp	Leu	Thr
			405						410				415	
Ala	Lys	Ala	Asp	Glu	Ser	Phe	Asp	Glu	Ile	Ile	Lys	Gly	Val	
			420					425					430	

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

```

GGG TTG AGT GCG CTT TAT AAA ATC AAA AGA GAC AAA ACC CTT TAT ACT      1017
Gly Leu Ser Ala Leu Tyr Lys Ile Lys Arg Asp Lys Thr Leu Tyr Thr
      310                      315                      320

CGC TTA GAC GCT TTA GCT ATT CGT TTG ACT CAA GGC TTA CAA AAG AGC      1065
Arg Leu Asp Ala Leu Ala Ile Arg Leu Thr Gln Gly Leu Gln Lys Ser
      325                      330                      335

GCT CAA AAC TAT AAC ATC GCT TTA GAG ACG CTT AAC ATG GGG AGC ATG      1113
Ala Gln Asn Tyr Asn Ile Ala Leu Glu Thr Leu Asn Met Gly Ser Met
      340                      345                      350                      355

TTT GGC TTT TTC TTT AAC GAA AAT GCG GTG CAC GAT TTT GAT GAC GCT      1161
Phe Gly Phe Phe Phe Asn Glu Asn Ala Val His Asp Phe Asp Asp Ala
      360                      365                      370

TTA AAA AGC GAT ACG GAG ATG TTT GCA AAA TTC CAC CAA AAA ATG CTC      1209
Leu Lys Ser Asp Thr Glu Met Phe Ala Lys Phe His Gln Lys Met Leu
      375                      380                      385

TTT AAG GGC GTG TAT TTG GCG TGC TCA AGC TTT GAA ACC GGC TTT ATT      1257
Phe Lys Gly Val Tyr Leu Ala Cys Ser Ser Phe Glu Thr Gly Phe Ile
      390                      395                      400

TGT GAG CCT ATG ACT GAA GAG ATG ATT GAT TTA ACG ATC GCA AAA GCC      1305
Cys Glu Pro Met Thr Glu Glu Met Ile Asp Leu Thr Ile Ala Lys Ala
      405                      410                      415

GAT GAA AGT TTT GAT GAA ATC ATA AAA GGT GTG TGAATTTTTT GAAAAAGCCA      1358
Asp Glu Ser Phe Asp Glu Ile Ile Lys Gly Val
      420                      425                      430

AAGTATTATA AATTCATAGA GGGGGCGAAT TATTTGAGCT TGGGGCTT      1406

```

(2) INFORMATION FOR SEQ ID NO:1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

```

Met Glu Leu Leu His Ser Ile Asn Asp Phe Asn Glu Ala Lys Gln Val
 1           5           10           15
Ile Ala Gly Gly Val Asn Ser Pro Val Arg Ala Phe Lys Ser Val Lys
      20           25           30
Gly Thr Pro Pro Phe Ile Leu Lys Gly Lys Gly Ala Tyr Leu Tyr Asp
      35           40           45
Val Asp Asn Asn His Tyr Ile Asp Phe Val Gln Ser Trp Gly Pro Leu
      50           55           60
Ile Phe Gly His Ala Asp Glu Glu Ile Glu Glu Asn Ile Ile Asn Ala

```

GGC ACT TCT TTT GGC GCT CCC ACA GAA TTA GAA ACC ACT TTA GCT AAG	345
Gly Thr Ser Phe Gly Ala Pro Thr Glu Leu Glu Thr Thr Leu Ala Lys	
85 90 95	
GAA ATC ATT TCT TGT TAT GAA GGC TTA GAT AAG GTG CGT TTA GTC AGT	393
Glu Ile Ile Ser Cys Tyr Glu Gly Leu Asp Lys Val Arg Leu Val Ser	
100 105 110 115	
AGC GGC ACA GAA GCG ACC ATG AGC GCG ATA CGA CTC GCT AGA GCT TAT	441
Ser Gly Thr Glu Ala Thr Met Ser Ala Ile Arg Leu Ala Arg Ala Tyr	
120 125 130	
AGC CAA AAA GAT GAT TTG ATC AAG TTT GAA GGG TGC TAC CAT GGG CAT	489
Ser Gln Lys Asp Asp Leu Ile Lys Phe Glu Gly Cys Tyr His Gly His	
135 140 145	
AGC GAC TCC TTA TTG GTG AAA GCG GGT AGC GGG TGT GCT ACT TTT GGA	537
Ser Asp Ser Leu Leu Val Lys Ala Gly Ser Gly Cys Ala Thr Phe Gly	
150 155 160	
TCG CCT TCT TCT TTA GGC GTG CCG AAC GAT TTT AGC AAA CAC ACT CTA	585
Ser Pro Ser Ser Leu Gly Val Pro Asn Asp Phe Ser Lys His Thr Leu	
165 170 175	
GTG GCT CGT TAT AAC GAT TTA AAC TCC ACA GAA GAA TGC TTT AAA AAA	633
Val Ala Arg Tyr Asn Asp Leu Asn Ser Thr Glu Glu Cys Phe Lys Lys	
180 185 190 195	
GGC AAT GTG GGT TGC GTC ATC ATT GAA CCC ATT GCC GGG AAT ATG GGG	681
Gly Asn Val Gly Cys Val Ile Ile Glu Pro Ile Ala Gly Asn Met Gly	
200 205 210	
TTA GTG CCG GCT CAA AAA GAG TTT TTA TTG GGC TTA AAG GCC TTG TGT	729
Leu Val Pro Ala Gln Lys Glu Phe Leu Leu Gly Leu Lys Ala Leu Cys	
215 220 225	
GAA AAA TAC CAA GCG GTG CTG ATT TTA GAT GAA GTG ATG AGC GGT TTT	777
Glu Lys Tyr Gln Ala Val Leu Ile Leu Asp Glu Val Met Ser Gly Phe	
230 235 240	
AGA GCG AGC TTG AGC GGT TCG CAA GAA TTT TAT GGC GTG GTG CCG GAT	825
Arg Ala Ser Leu Ser Gly Ser Gln Glu Phe Tyr Gly Val Val Pro Asp	
245 250 255	
TTG GTA ACC TTT GGT AAG GTG ATA GGT GCT GGG CTT CCT TTG GCG TGT	873
Leu Val Thr Phe Gly Lys Val Ile Gly Ala Gly Leu Pro Leu Ala Cys	
260 265 270 275	
TTT GGA GGG CGT GCA GAA ATT ATG GAC TTG CTT TCG CCC ATT GGA AGC	921
Phe Gly Gly Arg Ala Glu Ile Met Asp Leu Leu Ser Pro Ile Gly Ser	
280 285 290	
GTG TAT CAA GCA GGC ACT TTG AGC GGT AAC CCC CTA GCG GTG TGC GCG	969
Val Tyr Gln Ala Gly Thr Leu Ser Gly Asn Pro Leu Ala Val Cys Ala	
295 300 305	

```

          100          105          110
Ser Leu Thr Ala Tyr Val Arg Met Asn Glu Lys Leu Val Lys Val Pro
          115          120          125
Met Gln Tyr Thr Ile Ala Glu Asp Lys Ile Val Val Lys Gly Val Leu
          130          135          140
Asp Leu Leu Asn Phe Gly Leu Lys Asn Glu Leu Ala Ser Leu Ala Lys
145          150          155          160
Arg Cys Glu Ser Phe His Glu Gly Leu Thr Trp Ser Gln Val Glu Ile
          165          170          175
Gln Phe Glu Ser Met Ile Lys Gly
          180

```

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1338
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

```

CAAGTGGAAA TCCAATTGGA AAGCATGATC AAGGGATAAT GTAAAATC ATG GAG TTG      57
                                     Met Glu Leu
                                     1

TTG CAC AGC ATT AAT GAT TTC AAT GAA GCT AAG CAG GTG ATC GCT GGG      105
Leu His Ser Ile Asn Asp Phe Asn Glu Ala Lys Gln Val Ile Ala Gly
   5              10              15

GGG GTC AAT TCA CCT GTT AGG GCG TTT AAG AGC GTT AAA GGC ACT CCC      153
Gly Val Asn Ser Pro Val Arg Ala Phe Lys Ser Val Lys Gly Thr Pro
 20              25              30              35

CCC TTT ATT TTA AAA GGC AAG GGG GCG TAT CTT TAT GAT GTG GAT AAC      201
Pro Phe Ile Leu Lys Gly Lys Gly Ala Tyr Leu Tyr Asp Val Asp Asn
          40              45              50

AAC CAT TAT ATA GAT TTT GTG CAA AGC TGG GGG CCT TTG ATT TTT GGG      249
Asn His Tyr Ile Asp Phe Val Gln Ser Trp Gly Pro Leu Ile Phe Gly
          55              60              65

CAT GCT GAT GAA GAG ATT GAA GAA AAT ATT ATT AAT GCA TTA AAA AAA      297
His Ala Asp Glu Glu Ile Glu Glu Asn Ile Ile Asn Ala Leu Lys Lys
          70              75              80

```

```

GGC GAT GAA TTG AAA AAC AAA AAT GTG AAA GAA GCT TTT TTC GCT CTT      291
Gly Asp Glu Leu Lys Asn Lys Asn Val Lys Glu Ala Phe Phe Ala Leu
      80                      85                      90

TTT AAA AAC ACT AAC ATC AAA GTA ACT TTC AGG AAT GTG ATA GAA GGC      339
Phe Lys Asn Thr Asn Ile Lys Val Thr Phe Arg Asn Val Ile Glu Gly
      95                      100                      105

GAT CAT GCA GGT TCT CTT ACG GCT TAT GTG AGA ATG AAT GAA AAG CTG      387
Asp His Ala Gly Ser Leu Thr Ala Tyr Val Arg Met Asn Glu Lys Leu
      110                      115                      120

GTG AAA GTG CCT ATG CAA TAC ACG ATT GCT GAG GAT AAG ATC GTG GTT      435
Val Lys Val Pro Met Gln Tyr Thr Ile Ala Glu Asp Lys Ile Val Val
      125                      130                      135                      140

AAA GGG GTT TTG GAT TTA TTG AAT TTT GGC TTG AAA AAC GAA TTA GCG      483
Lys Gly Val Leu Asp Leu Leu Asn Phe Gly Leu Lys Asn Glu Leu Ala
      145                      150                      155

AGC TTG GCC AAA CGA TGC GAA AGC TTT CAT GAG GGC TTG ACT TGG TCG      531
Ser Leu Ala Lys Arg Cys Glu Ser Phe His Glu Gly Leu Thr Trp Ser
      160                      165                      170

CAA GTG GAA ATC CAA TTT GAA AGC ATG ATC AAG GGA TAATGTAAAA TCATGG      583
Gln Val Glu Ile Gln Phe Glu Ser Met Ile Lys Gly
      175                      180

AGTTGTTGCA CAGCATTAAT GATTTC AATG AAGCTAAG      621

```

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

```

Met Lys Lys Met Val Leu Val Ser Val Leu Leu Ala Gly Phe Leu Gln
 1           5           10           15
Ala Val Asn Leu Asp Leu Ser Ser Ala Lys Leu Thr Trp Thr Ala Phe
      20           25           30
Lys Thr Lys Ala Lys Thr Pro Val Asn Gly Ser Phe Glu Ser Ile Thr
      35           40           45
Tyr Lys Leu Gly Lys Ser Gln Asp Ser Leu Lys Thr Leu Leu Glu Gly
      50           55           60
Ala Ser Ala Ser Met Asp Ser Leu Lys Val Asn Leu Gly Asp Glu Leu
      65           70           75           80
Lys Asn Lys Asn Val Lys Glu Ala Phe Phe Ala Leu Phe Lys Asn Thr
      85           90           95
Asn Ile Lys Val Thr Phe Arg Asn Val Ile Glu Gly Asp His Ala Gly

```



```

225          230          235          240
Arg Leu Glu Leu Glu Lys Phe Ser Ser Ala Leu Ala Asn Lys Pro Phe
          245          250          255
Gly Val Leu Leu Asn Lys Cys Asp Val Val Glu Asn Ile Asp Glu Met
          260          265          270
Thr Lys Asp Phe Cys Ala Phe Leu Asn Leu Gly Ala Gln Lys Leu Asn
          275          280          285
Glu Phe Gly Leu Glu Pro Tyr Leu Gly Phe Leu His Pro His Leu Thr
          290          295          300
Asn Asp Phe Glu Asn Asn Pro Asn Glu Gln Ser Ala Leu Phe Val Leu
305          310          315          320
Pro Leu Ser Ala Val Ser Ala Leu Asn Val His Ala Leu Lys Phe Val
          325          330          335
Leu Leu Glu Ala Leu Pro
          340

```

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...567
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

```

ATTAAAGGAT AATGA ATG AAA AAA ATG GTT TTG GTA TCG GTT TTA CTA GCA      51
      Met Lys Lys Met Val Leu Val Ser Val Leu Leu Ala
          1          5          10

GGG TTT TTG CAA GCG GTG AAT TTG GAT TTA TCT TCG GCT AAG CTA ACA      99
Gly Phe Leu Gln Ala Val Asn Leu Asp Leu Ser Ser Ala Lys Leu Thr
          15          20          25

TGG ACA GCC TTT AAA ACT AAG GCT AAA ACA CCA GTA AAT GGG AGT TTT     147
Trp Thr Ala Phe Lys Thr Lys Ala Lys Thr Pro Val Asn Gly Ser Phe
          30          35          40

GAA AGC ATC ACC TAT AAA TTG GGT AAA TCT CAA GAT AGT TTA AAA ACC     195
Glu Ser Ile Thr Tyr Lys Leu Gly Lys Ser Gln Asp Ser Leu Lys Thr
          45          50          55          60

CTT TTA GAG GGA GCG AGC GCG AGC ATG GAT AGC TTG AAA GTC AAT TTA     243
Leu Leu Glu Gly Ala Ser Ala Ser Met Asp Ser Leu Lys Val Asn Leu
          65          70          75

```

```

AAT GAT TTT GAA AAT AAC CCT AAT GAG CAA TCA GCG CTC TTT GTC TTG      1021
Asn Asp Phe Glu Asn Asn Pro Asn Glu Gln Ser Ala Leu Phe Val Leu
305                      310                      315                      320

CCC CTT TCA GCG GTT AGC GCT CTT AAT GTG CAT GCA CTC AAA TTT GTG      1069
Pro Leu Ser Ala Val Ser Ala Leu Asn Val His Ala Leu Lys Phe Val
                      325                      330                      335

TTG TTG GAA GCG TTA CCC TAAACGCTA TTTTAAAAAT AATCCATTAA AATAAAGG  1125
Leu Leu Glu Ala Leu Pro
                      340

CGAGGAATGA AAAGAT                                                    1141

```

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

```

Met Val Ser Phe Arg Arg Glu Lys Phe Val Ile Lys Gly Gly Pro Asp
 1                      5                      10                      15
Gly Gly Asp Gly Gly Asp Gly Gly Asp Val Tyr Phe Glu Val Asp Asn
                      20                      25                      30
Asn Thr Asp Thr Leu Ala Ser Phe Arg Gly Thr Lys His His Lys Ala
                      35                      40                      45
Lys Asn Gly Ala Pro Gly Gly Thr Arg Asn Cys Ala Gly Lys Lys Gly
 50                      55                      60
Glu Asp Lys Ile Ile Val Val Pro Pro Gly Thr Gln Val Phe Val Gly
 65                      70                      75                      80
Asp Glu Leu Trp Leu Asp Leu Val Glu Pro Lys Glu Arg Val Leu Ala
                      85                      90                      95
Leu Lys Gly Gly Lys Gly Gly Leu Gly Asn Ala His Phe Lys Ser Ala
                      100                     105                     110
Thr Lys Gln Pro Thr Tyr Ala Gln Lys Gly Leu Glu Gly Val Glu
                      115                     120                     125
Lys Cys Val Arg Leu Glu Leu Lys Leu Ile Ala Asp Ile Gly Leu Val
                      130                     135                     140
Gly Phe Pro Asn Ala Gly Lys Ser Thr Leu Ile Ser Thr Ile Ser Asn
 145                     150                     155                     160
Ala Lys Pro Lys Ile Ala Asn Tyr Glu Phe Thr Thr Leu Val Pro Asn
                      165                     170                     175
Leu Gly Val Val Ser Val Asp Glu Lys Ser Gly Phe Leu Met Ala Asp
                      180                     185                     190
Ile Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly Leu Gly Ile
                      195                     200                     205
Ser Phe Leu Lys His Ile Glu Arg Thr Lys Val Leu Ala Phe Val Leu
                      210                     215                     220
Asp Ala Ser Arg Leu Asp Leu Gly Ile Lys Glu Gln Tyr Gln Arg Leu

```

GAT	GAG	TTG	TGG	CTT	GAT	TTA	GTG	GAA	CCT	AAA	GAA	AGG	GTG	TTA	GCC	349
Asp	Glu	Leu	Trp	Leu	Asp	Leu	Val	Glu	Pro	Lys	Glu	Arg	Val	Leu	Ala	
				85					90					95		
TTA	AAA	GGG	GGC	AAG	GGG	GGG	TTA	GGG	AAT	GCA	CAT	TTT	AAA	AGC	GCG	397
Leu	Lys	Gly	Gly	Lys	Gly	Gly	Leu	Gly	Asn	Ala	His	Phe	Lys	Ser	Ala	
			100					105					110			
ACT	AAA	CAA	CAA	CCC	ACT	TAC	GCG	CAA	AAA	GGC	TTA	GAG	GGG	GTT	GAA	445
Thr	Lys	Gln	Gln	Pro	Thr	Tyr	Ala	Gln	Lys	Gly	Leu	Glu	Gly	Val	Glu	
		115					120					125				
AAA	TGC	GTG	CGT	TTG	GAA	TTA	AAA	CTC	ATC	GCT	GAT	ATA	GGG	TTA	GTG	493
Lys	Cys	Val	Arg	Leu	Glu	Leu	Lys	Leu	Ile	Ala	Asp	Ile	Gly	Leu	Val	
	130						135				140					
GGC	TTC	CCT	AAT	GCG	GGT	AAA	TCC	ACG	CTC	ATT	TCC	ACC	ATC	TCT	AAC	541
Gly	Phe	Pro	Asn	Ala	Gly	Lys	Ser	Thr	Leu	Ile	Ser	Thr	Ile	Ser	Asn	
145					150				155					160		
GCT	AAG	CCT	AAA	ATC	GCT	AAC	TAT	GAA	TTT	ACG	ACT	CTA	GTG	CCT	AAT	589
Ala	Lys	Pro	Lys	Ile	Ala	Asn	Tyr	Glu	Phe	Thr	Thr	Leu	Val	Pro	Asn	
				165					170					175		
TTA	GGG	GTT	GTG	AGC	GTG	GAT	GAA	AAA	AGC	GGA	TTT	CTA	ATG	GCG	GAT	637
Leu	Gly	Val	Val	Ser	Val	Asp	Glu	Lys	Ser	Gly	Phe	Leu	Met	Ala	Asp	
			180					185					190			
ATT	CCT	GGC	ATT	ATT	GAA	GGG	GCT	AGC	GAG	GGA	AAG	GGC	TTA	GGG	ATT	685
Ile	Pro	Gly	Ile	Ile	Glu	Gly	Ala	Ser	Glu	Gly	Lys	Gly	Leu	Gly	Ile	
		195					200					205				
AGC	TTT	TTA	AAG	CAT	ATT	GAA	CGC	ACC	AAA	GTT	CTA	GCT	TTT	GTT	TTA	733
Ser	Phe	Leu	Lys	His	Ile	Glu	Arg	Thr	Lys	Val	Leu	Ala	Phe	Val	Leu	
	210						215				220					
GAC	GCT	TCC	AGG	CTG	GAT	TTA	GGC	ATT	AAA	GAG	CAA	TAC	CAA	CGC	TTG	781
Asp	Ala	Ser	Arg	Leu	Asp	Leu	Gly	Ile	Lys	Glu	Gln	Tyr	Gln	Arg	Leu	
225					230				235					240		
AGG	TTG	GAG	TTG	GAA	AAA	TTT	TCA	TCC	GCT	TTG	GCC	AAT	AAG	CCT	TTT	829
Arg	Leu	Glu	Leu	Glu	Lys	Phe	Ser	Ser	Ala	Leu	Ala	Asn	Lys	Pro	Phe	
				245					250					255		
GGG	GTG	TTG	CTC	AAT	AAA	TGC	GAT	GTT	GTA	GAA	AAC	ATT	GAT	GAG	ATG	877
Gly	Val	Leu	Leu	Asn	Lys	Cys	Asp	Val	Val	Glu	Asn	Ile	Asp	Glu	Met	
			260					265					270			
ACT	AAG	GAT	TTT	TGT	GCC	TTT	TTA	AAT	TTG	GGA	GCG	CAG	AAA	TTA	AAC	925
Thr	Lys	Asp	Phe	Cys	Ala	Phe	Leu	Asn	Leu	Gly	Ala	Gln	Lys	Leu	Asn	
		275					280					285				
GAG	TTT	GGT	TTA	GAG	CCG	TAT	TTA	GGG	TTT	TTG	CAC	CCC	CAT	TTA	ACC	973
Glu	Phe	Gly	Leu	Glu	Pro	Tyr	Leu	Gly	Phe	Leu	His	Pro	His	Leu	Thr	
	290					295					300					

```

145          150          155          160
Ile Gly Ile Ala Arg Ala Leu Ile Leu His Pro Ser Val Val Ile Cys
          165          170          175
Asp Glu Pro Val Ser Ala Leu Asp Val Ser Ile Gln Ala Gln Val Leu
          180          185          190
Asn Leu Leu Leu Asp Leu Gln Lys Glu Met Gly Leu Thr Tyr Ile Phe
          195          200          205
Ile Ser His Asp Leu Gly Val Val Glu His Ile Ser Asp Lys Ile Ile
          210          215          220
Val Met Asn Gln Gly Gln Ile Val Glu Thr Gly Asp Val Asp Ser Val
225          230          235          240
Ile Ser Ala Pro Lys His Pro Tyr Thr Gln Lys Leu Leu Asn Ala Val
          245          250          255
Pro His Leu Glu Lys Ser Met Gln Arg Phe Ala Lys
          260          265

```

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...1087
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

```

TTAAGCTGTG TTTGTAGATA GCGTGGAAT TATCATCGCT TCGGGTAAGG GGGGGCCTGG      60
A ATG GTG AGT TTT AGG CGA GAA AAA TTT GTC ATC AAA GGA GGC CCT GAT      109
  Met Val Ser Phe Arg Arg Glu Lys Phe Val Ile Lys Gly Gly Pro Asp
    1              5              10              15

GGG GGC GAT GGA GGC GAT GGA GGC GAT GTG TAT TTT GAA GTG GAT AAC      157
Gly Gly Asp Gly Gly Asp Gly Gly Asp Val Tyr Phe Glu Val Asp Asn
    20              25              30

AAT ACC GAC ACT CTA GCG AGT TTT AGA GGC ACC AAA CAC CAT AAG GCT      205
Asn Thr Asp Thr Leu Ala Ser Phe Arg Gly Thr Lys His His Lys Ala
    35              40              45

AAA AAT GGG GCT CCA GGA GGT ACA CGA AAT TGC GCG GGC AAA AAG GGC      253
Lys Asn Gly Ala Pro Gly Gly Thr Arg Asn Cys Ala Gly Lys Lys Gly
    50              55              60

GAA GAC AAG ATC ATT GTC GTG CCA CCA GGA ACG CAG GTT TTT GTA GGT      301
Glu Asp Lys Ile Ile Val Val Pro Pro Gly Thr Gln Val Phe Val Gly
    65              70              75              80

```

185	190	195	
CAA AAA GAA ATG GGG CTG ACT TAT ATT TTT ATC AGC CAT GAT TTA GGG			678
Gln Lys Glu Met Gly Leu Thr Tyr Ile Phe Ile Ser His Asp Leu Gly			
200	205	210	
GTG GTG GAG CAT ATA AGC GAT AAA ATC ATC GTA ATG AAT CAG GGG CAA			726
Val Val Glu His Ile Ser Asp Lys Ile Ile Val Met Asn Gln Gly Gln			
215	220	225	230
ATC GTA GAA ACG GGG GAT GTG GAT AGC GTG ATA AGC GCT CCA AAG CAC			774
Ile Val Glu Thr Gly Asp Val Asp Ser Val Ile Ser Ala Pro Lys His			
	235	240	245
CCT TAT ACG CAG AAA TTA CTC AAT GCG GTG CCG CAT TTG GAA AAA TCC			822
Pro Tyr Thr Gln Lys Leu Leu Asn Ala Val Pro His Leu Glu Lys Ser			
	250	255	260
ATG CAA AGA TTT GCC AAA TAAAAGAAAG GATTTTAAAG CTGTGTTTGT AGATAGCG			878
Met Gln Arg Phe Ala Lys			
265			
TGGAAATTAT CATCGC			894

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

Met	Lys	Leu	Leu	Glu	Ile	Lys	Glu	Leu	Lys	Lys	Ser	Tyr	Ala	Ile	Asp
1				5					10					15	
Arg	Gly	Leu	Phe	Lys	Pro	Lys	Arg	Val	Ile	His	Ala	Leu	Asn	Gly	Ile
		20						25					30		
Ser	Phe	Glu	Val	Glu	Gln	Asn	Glu	Val	Leu	Ser	Ile	Val	Gly	Glu	Ser
	35						40					45			
Gly	Cys	Gly	Lys	Ser	Thr	Thr	Ala	Lys	Ile	Leu	Ala	Gly	Ile	Glu	Arg
	50					55					60				
Gln	Asp	Ser	Gly	Ala	Ile	Tyr	Phe	Asn	Gly	Lys	Arg	His	Leu	His	Phe
65					70				75					80	
Ser	Lys	Gln	Asp	Trp	Phe	Asp	Tyr	Arg	Lys	Lys	Val	Gln	Met	Ile	Phe
			85						90					95	
Gln	Asp	Pro	Tyr	Ser	Ser	Leu	Asn	Pro	Arg	Trp	Lys	Val	Gly	Glu	Ile
		100						105					110		
Ile	Ala	Glu	Pro	Leu	Leu	Leu	Asn	Ser	His	Phe	Ser	Lys	Lys	Glu	Ile
	115					120					125				
Lys	Thr	Lys	Val	Leu	Glu	Ile	Met	Gln	Lys	Val	Gly	Leu	Lys	Leu	Glu
	130					135					140				
Trp	Ile	Asp	Arg	Tyr	Pro	His	Gln	Phe	Ser	Gly	Gly	Gln	Arg	Gln	Arg

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

AAATGTGGAT TATTTGAGTT TTCAAAAGGA GTTGCG	ATG AAG CTC TTA GAA ATT	54
	Met Lys Leu Leu Glu Ile	
	1 5	
AAA GAA TTG AAA AAA TCC TAT GCG ATA GAC AGG GGG TTA TTC AAG CCT	102	
Lys Glu Leu Lys Lys Ser Tyr Ala Ile Asp Arg Gly Leu Phe Lys Pro		
	10 15 20	
AAA AGA GTG ATC CAT GCG CTC AAT GGG ATC AGT TTT GAA GTG GAA CAA	150	
Lys Arg Val Ile His Ala Leu Asn Gly Ile Ser Phe Glu Val Glu Gln		
	25 30 35	
AAT GAA GTT TTG AGC ATT GTG GGG GAG AGC GGT TGC GGG AAA AGC ACG	198	
Asn Glu Val Leu Ser Ile Val Gly Glu Ser Gly Cys Gly Lys Ser Thr		
	40 45 50	
ACA GCC AAA ATT TTA GCC GGG ATT GAA AGG CAA GAT AGC GGG GCG ATT	246	
Thr Ala Lys Ile Leu Ala Gly Ile Glu Arg Gln Asp Ser Gly Ala Ile		
	55 60 65 70	
TAT TTC AAT GGT AAG CGC CAT TTG CAT TTT AGC AAA CAG GAT TGG TTT	294	
Tyr Phe Asn Gly Lys Arg His Leu His Phe Ser Lys Gln Asp Trp Phe		
	75 80 85	
GAT TAC CGC AAA AAG GTG CAA ATG ATT TTT CAA GAC CCT TAT TCT AGC	342	
Asp Tyr Arg Lys Lys Val Gln Met Ile Phe Gln Asp Pro Tyr Ser Ser		
	90 95 100	
CTA AAC CCT CGG TGG AAA GTG GGC GAG ATC ATC GCT GAA CCC TTG CTT	390	
Leu Asn Pro Arg Trp Lys Val Gly Glu Ile Ile Ala Glu Pro Leu Leu		
	105 110 115	
TTA AAT TCT CAT TTT TCA AAA AAA GAA ATC AAA ACA AAA GTG CTA GAG	438	
Leu Asn Ser His Phe Ser Lys Lys Glu Ile Lys Thr Lys Val Leu Glu		
	120 125 130	
ATC ATG CAA AAA GTG GGC TTG AAA TTA GAA TGG ATC GAT CGT TAC CCC	486	
Ile Met Gln Lys Val Gly Leu Lys Leu Glu Trp Ile Asp Arg Tyr Pro		
	135 140 145 150	
CAC CAA TTT TCA GGC GGT CAA AGG CAA CGA ATC GGC ATT GCT AGG GCG	534	
His Gln Phe Ser Gly Gly Gln Arg Gln Arg Ile Gly Ile Ala Arg Ala		
	155 160 165	
CTC ATT TTG CAT CCT AGC GTG GTG ATT TGC GAT GAG CCT GTG TCT GCG	582	
Leu Ile Leu His Pro Ser Val Val Ile Cys Asp Glu Pro Val Ser Ala		
	170 175 180	
CTA GAC GTG TCC ATT CAA GCG CAA GTG TTG AAT TTG CTC TTG GAT TTG	630	
Leu Asp Val Ser Ile Gln Ala Gln Val Leu Asn Leu Leu Asp Leu		

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

```

Met Ile Leu Glu Val Lys Asp Leu Lys Thr Tyr Phe Phe Thr Asp Lys
 1           5           10           15
Gly Val Asn Lys Ala Val Asp Gly Val Ser Phe Gly Leu Lys Lys Ser
          20           25           30
Gln Thr Leu Cys Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Ile Thr
      35           40           45
Ser Leu Ser Ile Leu Gly Leu Ile Glu Lys Pro Gly Gln Ile Val Gly
 50           55           60
Gly Ser Ile Gln Phe Leu Gly Gln Asp Leu Leu Gln Leu Lys Glu Lys
65           70           75           80
Gln Met Gln Lys Glu Ile Arg Gly Lys Lys Ile Gly Met Ile Phe Gln
          85           90           95
Glu Pro Met Thr Ser Leu Asn Pro Ser Tyr Thr Val Gly Phe Gln Ile
          100          105          110
Asn Glu Val Leu Lys Ile His His Pro Asn Leu Asn Lys Lys Glu Arg
      115          120          125
Leu Glu Arg Val Val Tyr Glu Leu Glu Arg Val Gly Ile Pro His Ala
      130          135          140
Gly Asp Lys Tyr His Glu Tyr Pro Phe Asn Leu Ser Gly Gly Gln Arg
145          150          155          160
Gln Arg Val Met Ile Ala Met Ala Met Val Cys Glu Pro Glu Ile Leu
          165          170          175
Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Thr Ile Gln Ala Gln
          180          185          190
Ile Leu Glu Leu Met Lys Glu Leu Gln Gln Lys Lys Gly Thr Ser Ile
      195          200          205
Leu Phe Ile Thr His Asp Leu Gly Val Val Ala Gln Ile Ala Asp Glu
      210          215          220
Val Val Val Met Tyr Lys Gly His Val Val Glu Gln Ala Ser Ala Lys
225          230          235          240
Glu Leu Phe Ala Asp Pro Arg His Pro Tyr Thr Lys Ala Leu Leu Ser
          245          250          255
Ala Ile Pro Lys Pro Gly Lys Glu Tyr Arg Lys Lys Arg Leu Glu Thr
          260          265          270
Val Asp Glu Asn Val Asp Tyr Leu Ser Phe Gln Lys Glu Leu Arg
      275          280          285

```

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...840
- (D) OTHER INFORMATION:

105	110	115	
CAC CCT AAC CTC AAT AAA AAA GAA CGC TTA GAA AGG GTG GTT TAT GAA			436
His Pro Asn Leu Asn Lys Lys Glu Arg Leu Glu Arg Val Val Tyr Glu			
120	125	130	135
TTA GAG CGT GTG GGC ATT CCC CAT GCA GGG GAT AAA TAC CAC GAA TAC			484
Leu Glu Arg Val Gly Ile Pro His Ala Gly Asp Lys Tyr His Glu Tyr			
	140	145	150
CCT TTC AAT CTC AGC GGG GGG CAG CGC CAA AGG GTG ATG ATC GCT ATG			532
Pro Phe Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Met Ile Ala Met			
	155	160	165
GCT ATG GTG TGT GAG CCT GAA ATC TTG ATC GCT GAT GAG CCT ACG ACA			580
Ala Met Val Cys Glu Pro Glu Ile Leu Ile Ala Asp Glu Pro Thr Thr			
	170	175	180
GCC TTA GAT GTA ACC ATT CAA GCG CAA ATT TTA GAA TTG ATG AAA GAA			628
Ala Leu Asp Val Thr Ile Gln Ala Gln Ile Leu Glu Leu Met Lys Glu			
	185	190	195
TTG CAA CAA AAA AAA GGC ACT TCT ATT TTG TTT ATC ACC CAT GAT TTA			676
Leu Gln Gln Lys Lys Gly Thr Ser Ile Leu Phe Ile Thr His Asp Leu			
	200	205	210
GGC GTG GTG GCG CAA ATC GCT GAT GAA GTG GTG GTG ATG TAT AAA GGG			724
Gly Val Val Ala Gln Ile Ala Asp Glu Val Val Val Met Tyr Lys Gly			
	220	225	230
CAT GTG GTG GAG CAA GCG AGT GCG AAA GAG CTT TTT GCT GAT CCA AGA			772
His Val Val Glu Gln Ala Ser Ala Lys Glu Leu Phe Ala Asp Pro Arg			
	235	240	245
CAC CCT TAT ACG AAA GCT CTT TTA AGC GCG ATC CCT AAA CCG GGC AAA			820
His Pro Tyr Thr Lys Ala Leu Leu Ser Ala Ile Pro Lys Pro Gly Lys			
	250	255	260
GAA TAC CGC AAA AAA CGC TTA GAG ACC GTG GAT GAA AAT GTG GAT TAT			868
Glu Tyr Arg Lys Lys Arg Leu Glu Thr Val Asp Glu Asn Val Asp Tyr			
	265	270	275
TTG AGT TTT CAA AAG GAG TTG CGA TGAAGCTCTT AGAAATTAAA GAATTGAAAA			922
Leu Ser Phe Gln Lys Glu Leu Arg			
	280	285	
AATCCTATGC GATAGACAGG GGGTTATTCA AGC			955

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear


```

      290              295              300
Met Ser Leu Ile Ile Ala Met Met Tyr Ile Gly Ala Asn Leu Leu Val
305              310              315              320
Asp Ile Leu Tyr Ala Phe Ile Asp Pro Arg Ile Arg Leu Ser
      325              330

```

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 32...892
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

```

ATCCTAAACG CACCTCTTAA AAGGAGCTTG C ATG ATT TTA GAA GTT AAA GAT      52
                               Met Ile Leu Glu Val Lys Asp
                               1              5

TTA AAA ACT TAT TTT TTC ACC GAT AAG GGC GTG AAT AAA GCA GTG GAT      100
Leu Lys Thr Tyr Phe Phe Thr Asp Lys Gly Val Asn Lys Ala Val Asp
      10              15              20

GGT GTG AGT TTT GGT TTG AAA AAG TCT CAA ACG CTC TGC ATT GTA GGG      148
Gly Val Ser Phe Gly Leu Lys Lys Ser Gln Thr Leu Cys Ile Val Gly
      25              30              35

GAG AGC GGG AGC GGG AAA AGC ATC ACT TCG CTC TCT ATT TTA GGG TTG      196
Glu Ser Gly Ser Gly Lys Ser Ile Thr Ser Leu Ser Ile Leu Gly Leu
      40              45              50              55

ATT GAA AAA CCG GGT CAA ATT GTG GGA GGG AGC ATT CAA TTT TTA GGG      244
Ile Glu Lys Pro Gly Gln Ile Val Gly Gly Ser Ile Gln Phe Leu Gly
              60              65              70

CAG GAT TTG TTG CAA CTC AAA GAA AAG CAG ATG CAA AAA GAA ATT AGG      292
Gln Asp Leu Leu Gln Leu Lys Glu Lys Gln Met Gln Lys Glu Ile Arg
      75              80              85

GGT AAA AAA ATT GGC ATG ATC TTT CAA GAG CCT ATG ACA AGC CTA AAC      340
Gly Lys Lys Ile Gly Met Ile Phe Gln Glu Pro Met Thr Ser Leu Asn
      90              95              100

CCT TCC TAC ACG GTG GGG TTT CAA ATC AAT GAA GTG TTG AAA ATC CAC      388
Pro Ser Tyr Thr Val Gly Phe Gln Ile Asn Glu Val Leu Lys Ile His

```

TAC GCT TTT ATT GAT CCT AGA ATA AGG TTG TCA TAATGGAGTC TTTTAGAGAG 1070
 Tyr Ala Phe Ile Asp Pro Arg Ile Arg Leu Ser
 325 330

TTTATCCAAC 1080

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

Met	Leu	Ser	Phe	Ile	Ile	Lys	Arg	Ile	Leu	Trp	Ala	Ile	Pro	Thr	Leu
1				5					10					15	
Phe	Gly	Val	Ser	Ile	Ile	Val	Phe	Met	Met	Val	His	Leu	Val	Pro	Gly
			20					25					30		
Asp	Pro	Ala	Leu	Val	Ile	Leu	Gly	Glu	Lys	Ala	Asn	Gln	Ala	Ala	Ile
		35					40					45			
Asp	Ala	Leu	Arg	Glu	Gln	Phe	Gly	Leu	Asn	Lys	Pro	Leu	Ile	Glu	Gln
		50				55					60				
Tyr	Phe	Phe	Phe	Ile	Asn	Asn	Val	Leu	His	Gly	Asn	Phe	Gly	Thr	Ser
65					70					75					80
Ile	Met	Thr	Gly	Glu	Pro	Val	Met	His	Glu	Phe	Trp	Gln	Arg	Phe	Pro
				85					90					95	
Ala	Thr	Val	Glu	Leu	Ala	Leu	Ile	Ala	Leu	Phe	Met	Ala	Leu	Val	Leu
			100					105					110		
Gly	Ile	Ser	Val	Gly	Val	Leu	Ala	Ala	Ile	Lys	Arg	Tyr	Ser	Val	Phe
		115					120					125			
Asp	Tyr	Ser	Ser	Met	Thr	Phe	Ala	Leu	Ala	Gly	Ile	Ser	Met	Pro	Val
		130				135					140				
Phe	Trp	Leu	Gly	Leu	Met	Leu	Ile	Tyr	Ile	Phe	Ser	Val	Gln	Leu	Gly
145					150					155				160	
Trp	Leu	Pro	Val	Phe	Gly	Arg	Leu	Ser	Asp	Val	Tyr	Tyr	Leu	Asp	Gly
			165					170					175		
Pro	Thr	Gly	Leu	Tyr	Leu	Ile	Asp	Ser	Leu	Ile	Ala	Arg	Asp	Tyr	Gly
			180				185						190		
Ala	Phe	Met	Asp	Thr	Ile	Lys	His	Leu	Ile	Leu	Pro	Ser	Ile	Val	Leu
		195					200					205			
Ala	Thr	Val	Ser	Thr	Ala	Val	Ile	Ala	Arg	Met	Thr	Arg	Ala	Ser	Met
		210				215					220				
Ala	Glu	Val	Ser	Lys	Glu	Asp	Tyr	Val	Arg	Thr	Ala	Lys	Ala	Lys	Gly
225					230					235				240	
Cys	Ser	Ser	Phe	Arg	Val	Ile	Phe	Val	His	Thr	Leu	Arg	Asn	Ala	Leu
			245						250				255		
Ile	Pro	Val	Thr	Thr	Ile	Ala	Gly	Leu	Met	Leu	Ala	Gly	Leu	Leu	Gly
			260				265						270		
Gly	Ser	Met	Ile	Thr	Glu	Thr	Val	Phe	Ser	Trp	Pro	Gly	Ile	Gly	Lys
		275					280					285			
Trp	Ile	Val	Asn	Ala	Leu	Asn	Gln	Arg	Asp	Phe	Pro	Ile	Ile	Gln	Ser

Glu	Leu	Ala	Leu	Ile	Ala	Leu	Phe	Met	Ala	Leu	Val	Leu	Gly	Ile	Ser	
100					105					110					115	
GTT	GGC	GTG	TTA	GCT	GCG	ATC	AAA	CGC	TAT	AGC	GTG	TTT	GAT	TAT	TCC	441
Val	Gly	Val	Leu	Ala	Ala	Ile	Lys	Arg	Tyr	Ser	Val	Phe	Asp	Tyr	Ser	
				120					125					130		
AGC	ATG	ACT	TTT	GCT	TTA	GCC	GGG	ATT	TCT	ATG	CCG	GTG	TTT	TGG	CTA	489
Ser	Met	Thr	Phe	Ala	Leu	Ala	Gly	Ile	Ser	Met	Pro	Val	Phe	Trp	Leu	
			135					140					145			
GGG	CTC	ATG	CTG	ATT	TAT	ATC	TTT	AGC	GTG	CAA	TTG	GGG	TGG	TTG	CCT	537
Gly	Leu	Met	Leu	Ile	Tyr	Ile	Phe	Ser	Val	Gln	Leu	Gly	Trp	Leu	Pro	
	150						155					160				
GTT	TTT	GGG	CGT	TTG	AGC	GAT	GTG	TAT	TAT	TTA	GAT	GGC	CCC	ACA	GGT	585
Val	Phe	Gly	Arg	Leu	Ser	Asp	Val	Tyr	Tyr	Leu	Asp	Gly	Pro	Thr	Gly	
	165					170					175					
CTT	TAT	TTG	ATA	GAC	AGC	CTG	ATC	GCA	AGG	GAT	TAT	GGG	GCG	TTT	ATG	633
Leu	Tyr	Leu	Ile	Asp	Ser	Leu	Ile	Ala	Arg	Asp	Tyr	Gly	Ala	Phe	Met	
180				185						190					195	
GAT	ACG	ATC	AAG	CAC	TTG	ATT	TTG	CCT	AGC	ATT	GTG	TTA	GCC	ACG	GTT	681
Asp	Thr	Ile	Lys	His	Leu	Ile	Leu	Pro	Ser	Ile	Val	Leu	Ala	Thr	Val	
			200						205					210		
TCT	ACC	GCT	GTT	ATT	GCC	AGA	ATG	ACT	CGC	GCG	AGC	ATG	GCA	GAA	GTG	729
Ser	Thr	Ala	Val	Ile	Ala	Arg	Met	Thr	Arg	Ala	Ser	Met	Ala	Glu	Val	
			215					220					225			
TCT	AAA	GAA	GAT	TAT	GTG	CGT	ACC	GCT	AAA	GCT	AAG	GGG	TGT	AGC	TCC	777
Ser	Lys	Glu	Asp	Tyr	Val	Arg	Thr	Ala	Lys	Ala	Lys	Gly	Cys	Ser	Ser	
	230						235					240				
TTT	AGG	GTG	ATT	TTT	GTG	CAC	ACT	TTG	CGT	AAT	GCT	TTA	ATC	CCT	GTA	825
Phe	Arg	Val	Ile	Phe	Val	His	Thr	Leu	Arg	Asn	Ala	Leu	Ile	Pro	Val	
	245					250				255						
ACG	ACT	ATC	GCA	GGC	TTG	ATG	TTG	GCC	GGG	CTT	TTA	GGG	GGG	AGC	ATG	873
Thr	Thr	Ile	Ala	Gly	Leu	Met	Leu	Ala	Gly	Leu	Leu	Gly	Gly	Ser	Met	
260				265						270					275	
ATA	ACT	GAA	ACG	GTT	TTC	TCA	TGG	CCT	GGG	ATT	GGT	AAG	TGG	ATT	GTT	921
Ile	Thr	Glu	Thr	Val	Phe	Ser	Trp	Pro	Gly	Ile	Gly	Lys	Trp	Ile	Val	
				280					285					290		
AAT	GCG	CTC	AAC	CAG	CGC	GAT	TTC	CCG	ATT	ATC	CAG	TCC	ATG	TCT	TTG	969
Asn	Ala	Leu	Asn	Gln	Arg	Asp	Phe	Pro	Ile	Ile	Gln	Ser	Met	Ser	Leu	
			295					300					305			
ATT	ATT	GCC	ATG	ATG	TAT	ATT	GGG	GCT	AAT	CTC	TTA	GTG	GAT	ATT	TTA	1017
Ile	Ile	Ala	Met	Met	Tyr	Ile	Gly	Ala	Asn	Leu	Leu	Val	Asp	Ile	Leu	
	310						315					320				

Tyr Val Pro Leu Ala Tyr Pro Tyr Ser Val Val Pro His Leu Ser Lys
 515 520 525
 Val Lys Gly Tyr Lys Thr Thr Gly Val Ser Val Asn Arg Phe Phe Lys
 530 535 540
 Val Tyr Leu Glu Lys
 545

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1050
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

GCGTGAATCG CTTCTTTAAG GTGTATTTAG AAAAATAAAA GGGGTTGC ATG CTG AGT	57
Met Leu Ser	
1	
TTT ATC ATT AAG CGT ATT TTG TGG GCG ATC CCC ACG CTG TTT GGA GTG	105
Phe Ile Ile Lys Arg Ile Leu Trp Ala Ile Pro Thr Leu Phe Gly Val	
5 10 15	
AGT ATC ATT GTG TTT ATG ATG GTG CAT TTA GTG CCA GGA GAT CCG GCA	153
Ser Ile Ile Val Phe Met Met Val His Leu Val Pro Gly Asp Pro Ala	
20 25 30 35	
TTA GTG ATT TTA GGT GAA AAG GCC AAT CAA GCC GCT ATT GAT GCT TTA	201
Leu Val Ile Leu Gly Glu Lys Ala Asn Gln Ala Ala Ile Asp Ala Leu	
40 45 50	
AGA GAG CAA TTT GGA TTG AAT AAG CCC TTG ATA GAG CAG TAT TTT TTC	249
Arg Glu Gln Phe Gly Leu Asn Lys Pro Leu Ile Glu Gln Tyr Phe Phe	
55 60 65	
TTT ATC AAT AAT GTG TTG CAT GGC AAT TTT GGC ACT TCT ATC ATG ACC	297
Phe Ile Asn Asn Val Leu His Gly Asn Phe Gly Thr Ser Ile Met Thr	
70 75 80	
GGT GAG CCT GTG ATG CAT GAG TTT TGG CAA CGC TTC CCG GCC ACG GTG	345
Gly Glu Pro Val Met His Glu Phe Trp Gln Arg Phe Pro Ala Thr Val	
85 90 95	
GAA TTA_GCT TTG ATC GCT CTG TTT ATG GCT CTT GTT TTG GGT ATT AGC	393

65					70					75				80	
Leu	Val	Gln	Phe	Arg	Tyr	Gly	Thr	Thr	Glu	Val	Glu	Pro	Ala	Leu	Ala
				85					90					95	
Thr	Ser	Trp	Asp	Ile	Ser	Pro	Asp	Gly	Leu	Val	Tyr	Thr	Phe	His	Leu
			100					105					110		
Arg	Lys	Gly	Val	Tyr	Phe	His	Gln	Thr	Lys	Tyr	Trp	Asn	Lys	Lys	Val
		115					120					125			
Glu	Phe	Ser	Ala	Lys	Asp	Val	Leu	Phe	Ser	Phe	Glu	Arg	Gln	Met	Asp
	130					135					140				
Lys	Ala	Lys	Arg	Tyr	Tyr	Ser	Pro	Gly	Ala	Lys	Ser	Tyr	Lys	Tyr	Trp
145					150					155					160
Glu	Gly	Met	Gly	Met	Ser	His	Ile	Ile	Lys	Ser	Ile	Glu	Ala	Leu	Asp
			165						170					175	
Asp	Tyr	Thr	Ile	Arg	Phe	Thr	Leu	Asn	Gly	Pro	Glu	Ala	Pro	Phe	Leu
			180					185					190		
Ala	Asn	Leu	Gly	Met	Asp	Phe	Leu	Ser	Ile	Leu	Ser	Lys	Asp	Tyr	Ala
	195						200					205			
Asp	Tyr	Leu	Ala	Gln	Asn	Asn	Lys	Lys	Asp	Glu	Leu	Ala	Lys	Lys	Pro
	210				215					220					
Ile	Gly	Thr	Gly	Pro	Phe	Lys	Phe	Phe	Leu	Trp	Asn	Lys	Asp	Glu	Lys
225				230						235					240
Ile	Ile	Leu	Leu	Lys	Asn	Gln	Asp	Tyr	Trp	Gly	Pro	Lys	Ala	Tyr	Leu
			245						250					255	
Asp	Lys	Val	Val	Val	Arg	Thr	Ile	Pro	Asn	Ser	Ser	Thr	Arg	Ala	Leu
		260						265					270		
Ala	Leu	Arg	Thr	Gly	Glu	Ile	Met	Leu	Met	Thr	Gly	Pro	Asn	Leu	Asn
	275					280						285			
Glu	Val	Glu	Gln	Leu	Glu	Lys	Val	Pro	Asn	Ile	Val	Val	Asp	Lys	Ser
	290					295					300				
Ala	Gly	Leu	Leu	Ala	Ser	Trp	Leu	Ser	Leu	Asn	Thr	Gln	Lys	Lys	Tyr
305				310						315					320
Phe	Asp	Asn	Pro	Leu	Val	Arg	Leu	Ala	Ile	Asn	His	Ala	Ile	Asn	Ala
			325						330					335	
Asp	Asp	Tyr	Ile	Lys	Val	Leu	Tyr	Glu	Gly	Phe	Ala	Gln	Lys	Met	Val
		340						345					350		
Asn	Pro	Phe	Pro	Pro	Thr	Ile	Trp	Gly	Tyr	Asn	Tyr	Asn	Ile	Lys	Pro
	355					360						365			
Tyr	Glu	Tyr	Asp	Leu	Lys	Lys	Ala	Lys	Glu	Leu	Leu	Lys	Gln	Ala	Gly
	370					375					380				
Tyr	Pro	Asn	Gly	Phe	Lys	Thr	Thr	Ile	Phe	Thr	Thr	Ala	Thr	Arg	Asn
385				390						395					400
Pro	Lys	Gly	Ala	Val	Phe	Ile	Gln	Ala	Ser	Leu	Ala	Lys	Ile	Gly	Ile
			405						410					415	
Asp	Val	Lys	Ile	Glu	Val	Tyr	Glu	Trp	Gly	Ala	Tyr	Leu	Lys	Arg	Thr
		420						425					430		
Gly	Leu	Gly	Glu	His	Glu	Met	Ala	Phe	Ser	Gly	Trp	Met	Ala	Asp	Ile
	435					440						445			
Ala	Asp	Pro	Asp	Asn	Phe	Leu	Tyr	Thr	Leu	Trp	Ser	Glu	Gln	Ala	Ala
	450					455					460				
Ser	Ala	Ile	Pro	Thr	Gln	Asn	His	Ser	Phe	Tyr	Lys	Asn	Lys	Glu	Phe
465				470						475					480
Ser	Asn	Leu	Leu	Ile	Lys	Ala	Lys	Arg	Val	Ser	Asp	Gln	Lys	Glu	Arg
			485					490					495		
Glu	Ala	Leu	Tyr	Leu	Lys	Ala	Gln	Glu	Ile	Ile	His	Lys	Asp	Ala	Pro
		500						505					510		

```

GTG TAT GAG TGG GGG GCT TAT TTG AAA AGA ACG GGT CTG GGC GAA CAT      1350
Val Tyr Glu Trp Gly Ala Tyr Leu Lys Arg Thr Gly Leu Gly Glu His
          425                      430                      435

GAA ATG GCG TTT TCA GGC TGG ATG GCA GAC ATT GCG GAT CCG GAT AAT      1398
Glu Met Ala Phe Ser Gly Trp Met Ala Asp Ile Ala Asp Pro Asp Asn
          440                      445                      450

TTC TTA TAC ACC TTA TGG AGC GAG CAA GCC GCC TCA GCT ATA CCC ACT      1446
Phe Leu Tyr Thr Leu Trp Ser Glu Gln Ala Ala Ser Ala Ile Pro Thr
          455                      460                      465

CAA AAC CAT TCC TTT TAT AAA AAT AAG GAG TTT TCC AAT CTG CTC ATA      1494
Gln Asn His Ser Phe Tyr Lys Asn Lys Glu Phe Ser Asn Leu Leu Ile
          470                      475                      480                      485

AAG GCT AAA CGC GTT TCG GAT CAA AAA GAG AGG GAA GCC CTT TAT TTA      1542
Lys Ala Lys Arg Val Ser Asp Gln Lys Glu Arg Glu Ala Leu Tyr Leu
          490                      495                      500

AAG GCA CAA GAA ATT ATC CAT AAA GAC GCG CCT TAT GTG CCT TTA GCC      1590
Lys Ala Gln Glu Ile Ile His Lys Asp Ala Pro Tyr Val Pro Leu Ala
          505                      510                      515

TAT CCT TAT TCG GTG GTG CCG CAT TTG TCT AAA GTT AAG GGT TAT AAA      1638
Tyr Pro Tyr Ser Val Val Pro His Leu Ser Lys Val Lys Gly Tyr Lys
          520                      525                      530

ACG ACC GGA GTG AGC GTG AAT CGC TTC TTT AAG GTG TAT TTA GAA AAA T      1687
Thr Thr Gly Val Ser Val Asn Arg Phe Phe Lys Val Tyr Leu Glu Lys
          535                      540                      545

AAAAGGGGTT GCATGCTGAG TTTTATCATT AAGCG                                1722

```

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

```

Met Asn Asn Val Phe Val Lys Gly Leu Phe Phe Phe Leu Leu Leu Phe
 1                      5                      10                      15
Gly Phe Phe Leu Lys Ala Ser Glu Ser Pro Asn Ala Thr Leu Asn Pro
          20                      25                      30
Ser Lys Glu Asn Val Ser Val Glu Glu Gln Lys Arg Phe Gly Gly Val
          35                      40                      45
Leu Val Phe Ala Arg Gly Ala Asp Gly Ser Ser Met Asp Pro Ala Leu
          50                      55                      60
Val Thr Asp Gly Glu Ser Tyr Val Ala Thr Gly Asn Ile Tyr Asp Thr

```

Asp	Phe	Leu	Ser	Ile	Leu	Ser	Lys	Asp	Tyr	Ala	Asp	Tyr	Leu	Ala	Gln	
		200					205					210				
AAT	AAT	AAA	AAA	GAC	GAG	TTG	GCT	AAA	AAA	CCT	ATT	GGG	ACA	GGG	CCT	726
Asn	Asn	Lys	Lys	Asp	Glu	Leu	Ala	Lys	Lys	Pro	Ile	Gly	Thr	Gly	Pro	
	215					220				225						
TTC	AAA	TTC	TTT	TTG	TGG	AAT	AAA	GAT	GAA	AAA	ATC	ATT	CTT	TTA	AAA	774
Phe	Lys	Phe	Phe	Leu	Trp	Asn	Lys	Asp	Glu	Lys	Ile	Ile	Leu	Leu	Lys	
230					235					240					245	
AAT	CAA	GAT	TAT	TGG	GGG	CCT	AAA	GCG	TAT	TTG	GAT	AAG	GTG	GTG	GTG	822
Asn	Gln	Asp	Tyr	Trp	Gly	Pro	Lys	Ala	Tyr	Leu	Asp	Lys	Val	Val	Val	
				250					255					260		
CGC	ACC	ATT	CCT	AAT	TCT	TCC	ACT	CGC	GCT	TTA	GCG	TTG	CGC	ACC	GGC	870
Arg	Thr	Ile	Pro	Asn	Ser	Ser	Thr	Arg	Ala	Leu	Ala	Leu	Arg	Thr	Gly	
			265					270					275			
GAA	ATC	ATG	CTC	ATG	ACT	GGG	CCT	AAT	CTC	AAT	GAA	GTG	GAG	CAA	TTA	918
Glu	Ile	Met	Leu	Met	Thr	Gly	Pro	Asn	Leu	Asn	Glu	Val	Glu	Gln	Leu	
		280					285				290					
GAA	AAA	GTC	CCT	AAT	ATC	GTG	GTG	GAC	AAA	AGT	GCT	GGG	TTG	TTG	GCG	966
Glu	Lys	Val	Pro	Asn	Ile	Val	Val	Asp	Lys	Ser	Ala	Gly	Leu	Leu	Ala	
	295					300				305						
AGT	TGG	CTT	TCG	TTG	AAC	ACG	CAA	AAA	AAG	TAT	TTT	GAC	AAC	CCT	TTG	1014
Ser	Trp	Leu	Ser	Leu	Asn	Thr	Gln	Lys	Lys	Tyr	Phe	Asp	Asn	Pro	Leu	
310					315					320					325	
GTG	CGT	TTG	GCT	ATC	AAT	CAT	GCG	ATC	AAT	GCA	GAT	GAT	TAC	ATC	AAA	1062
Val	Arg	Leu	Ala	Ile	Asn	His	Ala	Ile	Asn	Ala	Asp	Asp	Tyr	Ile	Lys	
				330					335					340		
GTG	CTT	TAT	GAA	GGC	TTT	GCT	CAA	AAA	ATG	GTC	AAT	CCT	TTC	CCG	CCC	1110
Val	Leu	Tyr	Glu	Gly	Phe	Ala	Gln	Lys	Met	Val	Asn	Pro	Phe	Pro	Pro	
			345					350					355			
ACC	ATA	TGG	GGT	TAT	AAC	TAC	AAT	ATC	AAA	CCC	TAT	GAA	TAC	GAT	TTG	1158
Thr	Ile	Trp	Gly	Tyr	Asn	Tyr	Asn	Ile	Lys	Pro	Tyr	Glu	Tyr	Asp	Leu	
		360					365					370				
AAA	AAG	GCT	AAG	GAG	TTG	TTG	AAA	CAA	GCG	GGC	TAT	CCT	AAC	GGC	TTT	1206
Lys	Lys	Ala	Lys	Glu	Leu	Leu	Lys	Gln	Ala	Gly	Tyr	Pro	Asn	Gly	Phe	
	375					380				385						
AAA	ACC	ACT	ATT	TTT	ACC	ACT	GCC	ACT	CGT	AAC	CCA	AAA	GGA	GCG	GTG	1254
Lys	Thr	Thr	Ile	Phe	Thr	Thr	Ala	Thr	Arg	Asn	Pro	Lys	Gly	Ala	Val	
	390				395				400						405	
TTC	ATA	CAG	GCG	AGC	CTG	GCT	AAA	ATT	GGC	ATT	GAT	GTG	AAA	ATT	GAA	1302
Phe	Ile	Gln	Ala	Ser	Leu	Ala	Lys	Ile	Gly	Ile	Asp	Val	Lys	Ile	Glu	
				410					415					420		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

ATCTCTATCC TTTATAGAAT TTGTTGTGGA GACTGGCTT ATG AAT AAT GTT TTT	54
Met Asn Asn Val Phe	
1 5	
GTT AAG GGT TTG TTT TTT TTT CTT TTA TTG TTT GGG TTT TTT TTG AAA	102
Val Lys Gly Leu Phe Phe Phe Leu Leu Leu Phe Gly Phe Phe Leu Lys	
10 15 20	
GCT TCA GAA AGC CCA AAC GCT ACT CTT AAT CCA TCT AAA GAA AAT GTT	150
Ala Ser Glu Ser Pro Asn Ala Thr Leu Asn Pro Ser Lys Glu Asn Val	
25 30 35	
TCT GTT GAA GAG CAA AAG CGT TTT GGA GGC GTT TTA GTT TTT GCA AGA	198
Ser Val Glu Glu Gln Lys Arg Phe Gly Gly Val Leu Val Phe Ala Arg	
40 45 50	
GGC GCT GAT GGC TCG AGC ATG GAT CCT GCT TTA GTG ACT GAT GGC GAA	246
Gly Ala Asp Gly Ser Ser Met Asp Pro Ala Leu Val Thr Asp Gly Glu	
55 60 65	
AGC TAT GTA GCA ACG GGC AAT ATT TAT GAC ACG CTC GTG CAA TTC AGA	294
Ser Tyr Val Ala Thr Gly Asn Ile Tyr Asp Thr Leu Val Gln Phe Arg	
70 75 80 85	
TAC GGC ACC ACA GAA GTT GAA CCC GCC TTA GCG ACA AGC TGG GAC ATA	342
Tyr Gly Thr Thr Glu Val Glu Pro Ala Leu Ala Thr Ser Trp Asp Ile	
90 95 100	
TCC CCA GAT GGT CTT GTA TAT ACC TTT CAT TTA CGC AAA GGG GTT TAT	390
Ser Pro Asp Gly Leu Val Tyr Thr Phe His Leu Arg Lys Gly Val Tyr	
105 110 115	
TTC CAC CAA ACG AAG TAT TGG AAT AAA AAA GTA GAG TTT AGC GCT AAA	438
Phe His Gln Thr Lys Tyr Trp Asn Lys Lys Val Glu Phe Ser Ala Lys	
120 125 130	
GAT GTG CTG TTT TCG TTT GAA CGC CAG ATG GAT AAA GCT AAA CGA TAT	486
Asp Val Leu Phe Ser Phe Glu Arg Gln Met Asp Lys Ala Lys Arg Tyr	
135 140 145	
TAT AGC CCG GGG GCT AAA AGC TAT AAG TAT TGG GAA GGC ATG GGC ATG	534
Tyr Ser Pro Gly Ala Lys Ser Tyr Lys Tyr Trp Glu Gly Met Gly Met	
150 155 160 165	
TCT CAT ATT ATT AAG AGC ATT GAA GCT TTA GAT GAC TAT ACC ATT AGA	582
Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr Thr Ile Arg	
170 175 180	
TTC ACA CTT AAT GGG CCA GAA GCC CCG TTT TTA GCG AAT TTG GGC ATG	630
Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn Leu Gly Met	
185 190 195	
GAC TTT TTG AGC ATT TTG AGT AAG GAT TAC GCT GAT TAC CTG GCT CAA	678


```

Leu Pro Gly Leu Asp Leu Ile Ile Phe Pro Glu Tyr Ser Thr His Gly
 50          55          60
Ile Met Tyr Asp Arg Gln Glu Met Phe Asp Thr Ala Ala Ser Val Pro
65          70          75          80
Gly Glu Glu Thr Ala Ile Phe Ala Glu Ala Cys Lys Lys Asn Lys Val
      85          90          95
Trp Gly Val Phe Ser Leu Thr Gly Glu Lys His Glu Gln Ala Lys Lys
      100          105          110
Asn Pro Tyr Asn Thr Leu Ile Leu Val Asn Asp Lys Gly Glu Ile Val
      115          120          125
Gln Lys Tyr Arg Lys Ile Leu Pro Trp Cys Pro Ile Glu Cys Trp Tyr
      130          135          140
Pro Gly Asp Lys Thr Tyr Val Val Asp Gly Pro Lys Gly Leu Lys Val
145          150          155          160
Ser Leu Ile Ile Cys Asp Asp Gly Asn Tyr Pro Glu Ile Trp Arg Asp
      165          170          175
Cys Ala Met Arg Gly Ala Glu Leu Ile Val Arg Cys Gln Gly Tyr Met
      180          185          190
Tyr Pro Ala Lys Glu Gln Gln Ile Ala Ile Val Lys Ala Met Ala Trp
      195          200          205
Ala Asn Gln Cys Tyr Val Ala Val Ala Asn Ala Thr Gly Phe Asp Gly
      210          215          220
Val Tyr Ser Tyr Phe Gly His Ser Ser Ile Ile Gly Phe Asp Gly His
225          230          235          240
Thr Leu Gly Glu Cys Gly Glu Glu Glu Asn Gly Leu Gln Tyr Ala Gln
      245          250          255
Leu Ser Val Gln Ile Arg Asp Ala Arg Lys Tyr Asp Gln Ser Gln
      260          265          270
Asn Gln Leu Phe Lys Leu Leu His Arg Gly Tyr Ser Gly Val Phe Ala
      275          280          285
Ser Gly Asp Gly Asp Lys Gly Val Ala Glu Cys Pro Phe Glu Phe Tyr
      290          295          300
Lys Thr Trp Val Asn Asp Pro Lys Lys Ala Gln Glu Asn Val Glu Lys
305          310          315          320
Ile Thr Arg Pro Ser Val Gly Val Ala Ala Cys Pro Val Gly Asp Leu
      325          330          335
Pro Thr Lys

```

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...1686
- (D) OTHER INFORMATION:

```

Ile Ala Ile Val Lys Ala Met Ala Trp Ala Asn Gln Cys Tyr Val Ala
200                               205                               210                               215

GTA GCG AAT GCG ACC GGT TTT GAT GGG GTG TAT TCC TAT TTT GGG CAT      724
Val Ala Asn Ala Thr Gly Phe Asp Gly Val Tyr Ser Tyr Phe Gly His
                               220                               225                               230

TCT AGC ATT ATT GGT TTT GAC GGG CAT ACT TTG GGC GAA TGC GGG GAA      772
Ser Ser Ile Ile Gly Phe Asp Gly His Thr Leu Gly Glu Cys Gly Glu
                               235                               240                               245

GAA GAA AAT GGT CTT CAA TAC GCT CAA CTT TCT GTG CAA CAA ATC CGT      820
Glu Glu Asn Gly Leu Gln Tyr Ala Gln Leu Ser Val Gln Gln Ile Arg
                               250                               255                               260

GAT GCG AGA AAA TAC GAC CAA AGC CAA AAC CAA CTC TTC AAA CTC TTG      868
Asp Ala Arg Lys Tyr Asp Gln Ser Gln Asn Gln Leu Phe Lys Leu Leu
                               265                               270                               275

CAC AGA GGT TAT AGT GGG GTT TTT GCT AGT GGC GAT GGG GAT AAG GGT      916
His Arg Gly Tyr Ser Gly Val Phe Ala Ser Gly Asp Gly Asp Lys Gly
280                               285                               290                               295

GTG GCG GAA TGC CCT TTT GAG TTC TAT AAA ACT TGG GTG AAT GAC CCC      964
Val Ala Glu Cys Pro Phe Glu Phe Tyr Lys Thr Trp Val Asn Asp Pro
                               300                               305                               310

AAA AAA GCT CAA GAA AAT GTA GAA AAA ATC ACC CGC CCA AGC GTG GGT      1012
Lys Lys Ala Gln Glu Asn Val Glu Lys Ile Thr Arg Pro Ser Val Gly
                               315                               320                               325

GTG GCC GCT TGT CCT GTG GGC GAT TTG CCC ACG AAA TAAAGGGCAA AAGGAG 1064
Val Ala Ala Cys Pro Val Gly Asp Leu Pro Thr Lys
                               330                               335

GAGGGGGGGGG G                                                         1075

```

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

```

Met Arg His Gly Asp Ile Ser Ser Ser Pro Asp Thr Val Gly Val Ala
 1           5           10           15
Val Val Asn Tyr Lys Met Pro Arg Leu His Thr Lys Asn Glu Val Leu
          20           25           30
Glu Asn Cys Arg Asn Ile Ala Lys Val Ile Gly Gly Val Lys Gln Gly
          35           40           45

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

GGA	ACT	TCT	CA	TCA	AAAA	AACA	AGGA	ACATAA	T	ATG	AGA	CAT	GGA	GAT	ATT	AGT	52
										Met	Arg	His	Gly	Asp	Ile	Ser	
										1						5	
AGC	AGC	CCA	GAT	ACT	GTG	GGT	GTA	GCG	GTA	GTT	AAT	TAT	AAG	ATG	CCT	100	
Ser	Ser	Pro	Asp	Thr	Val	Gly	Val	Ala	Val	Val	Asn	Tyr	Lys	Met	Pro		
		10					15					20					
AGA	CTC	CAC	ACT	AAG	AAT	GAG	GTG	TTG	GAA	AAT	TGT	CGC	AAT	ATC	GCT	148	
Arg	Leu	His	Thr	Lys	Asn	Glu	Val	Leu	Glu	Asn	Cys	Arg	Asn	Ile	Ala		
	25					30					35						
AAG	GTG	ATT	GGT	GGG	GTC	AAA	CAG	GGT	TTG	CCT	GGG	TTG	GAT	CTG	ATT	196	
Lys	Val	Ile	Gly	Gly	Val	Lys	Gln	Gly	Leu	Pro	Gly	Leu	Asp	Leu	Ile		
40					45				50					55			
ATT	TTC	CCT	GAA	TAC	AGC	ACG	CAT	GGG	ATT	ATG	TAT	GAC	AGA	CAA	GAA	244	
Ile	Phe	Pro	Glu	Tyr	Ser	Thr	His	Gly	Ile	Met	Tyr	Asp	Arg	Gln	Glu		
			60					65						70			
ATG	TTT	GAT	ACA	GCC	GCA	AGC	GTT	CCT	GGA	GAA	GAA	ACC	GCG	ATC	TTT	292	
Met	Phe	Asp	Thr	Ala	Ala	Ser	Val	Pro	Gly	Glu	Glu	Thr	Ala	Ile	Phe		
		75					80					85					
GCT	GAA	GCT	TGT	AAG	AAA	AAC	AAG	GTT	TGG	GGA	GTG	TTC	TCT	TTG	ACA	340	
Ala	Glu	Ala	Cys	Lys	Lys	Asn	Lys	Val	Trp	Gly	Val	Phe	Ser	Leu	Thr		
	90					95						100					
GGG	GAA	AAA	CAC	GAG	CAA	GCC	AAA	AAG	AAT	CCC	TAT	AAC	ACT	TTG	ATT	388	
Gly	Glu	Lys	His	Glu	Gln	Ala	Lys	Lys	Asn	Pro	Tyr	Asn	Thr	Leu	Ile		
	105					110					115						
CTT	GTC	AAT	GAT	AAG	GGT	GAG	ATC	GTG	CAA	AAA	TAC	CGC	AAA	ATC	TTG	436	
Leu	Val	Asn	Asp	Lys	Gly	Glu	Ile	Val	Gln	Lys	Tyr	Arg	Lys	Ile	Leu		
120					125				130					135			
CCT	TGG	TGC	CCT	ATT	GAA	TGT	TGG	TAT	CCT	GGG	GAT	AAA	ACT	TAT	GTG	484	
Pro	Trp	Cys	Pro	Ile	Glu	Cys	Trp	Tyr	Pro	Gly	Asp	Lys	Thr	Tyr	Val		
			140					145						150			
GTT	GAT	GGG	CCT	AAG	GGC	TTG	AAA	GTT	TCT	TTG	ATT	ATT	TGC	GAT	GAT	532	
Val	Asp	Gly	Pro	Lys	Gly	Leu	Lys	Val	Ser	Leu	Ile	Ile	Cys	Asp	Asp		
		155				160						165					
GGA	AAC	TAC	CCT	GAA	ATT	TGG	CGC	GAT	TGC	GCG	ATG	CGT	GGG	GCA	GAA	580	
Gly	Asn	Tyr	Pro	Glu	Ile	Trp	Arg	Asp	Cys	Ala	Met	Arg	Gly	Ala	Glu		
	170					175						180					
CTC	ATT	GTG	CGC	TGT	CAA	GGT	TAC	ATG	TAT	CCG	GCT	AAG	GAG	CAA	CAA	628	
Leu	Ile	Val	Arg	Cys	Gln	Gly	Tyr	Met	Tyr	Pro	Ala	Lys	Glu	Gln	Gln		
	185					190					195						
ATT	GCA	ATA	GTA	AAA	GCT	ATG	GCG	TGG	GCC	AAT	CAA	TGT	TAT	GTA	GCG	676	

Glu Ser Asp Phe Ser Leu Leu Glu Leu Lys Asn Lys Arg Phe Ser Asp
 2595 2600 2605
 Pro Asn Pro Glu Val Phe Val Lys Tyr Ser Gln Leu Ser Lys His Pro
 2610 2615 2620
 Asn Asn Leu Trp Val Gln Gly Val Gly Gly Ala Ser Phe Ile Ser Gly
 625 2630 2635 2640
 Gly Asn Gly Thr Leu Tyr Gly Leu Asn Ala Gly Tyr Asp Arg Leu Val
 2645 2650 2655
 Lys Asn Val Ile Leu Gly Gly Tyr Val Ala Tyr Gly Tyr Ser Asp Phe
 2660 2665 2670
 Asn Gly Asn Ile Met His Ser Leu Gly Asn Asn Val Asp Val Gly Met
 2675 2680 2685
 Tyr Ala Arg Ala Phe Leu Lys Arg Asn Glu Phe Thr Leu Ser Ala Asn
 2690 2695 2700
 Glu Thr Tyr Gly Gly Asn Ala Thr Ser Ile Asn Ser Ser Asn Ser Leu
 705 2710 2715 2720
 Leu Ser Val Leu Asn Gln Arg Tyr Asn Tyr Asn Thr Trp Thr Thr Ser
 2725 2730 2735
 Val Asn Gly Asn Tyr Gly Tyr Asp Phe Met Phe Lys Gln Lys Ser Val
 2740 2745 2750
 Val Leu Lys Pro Gln Val Gly Leu Ser Tyr His Phe Ile Gly Leu Ser
 2755 2760 2765
 Gly Met Lys Gly Asn Asp Ala Ala Tyr Lys Gln Phe Leu Met His Ser
 2770 2775 2780
 Asn Pro Ser Asn Glu Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser
 785 2790 2795 2800
 Arg Lys Tyr Phe Gly Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu
 2805 2810 2815
 Gly Arg Asp Leu Leu Ile Lys Ser Lys Gly Ser Asn Thr Val Arg Phe
 2820 2825 2830
 Val Gly Glu Asn Thr Leu Leu Tyr Arg Lys Gly Glu Val Phe Asn Thr
 2835 2840 2845
 Phe Ala Ser Val Ile Thr Gly Gly Glu Met His Leu Trp Arg Leu Val
 2850 2855 2860
 Tyr Val Asn Ala Gly Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp
 865 2870 2875 2880
 Ile Asn Ile Thr Gly Asn Val Gly Met Arg Val Ala Phe
 2885 2890

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 32...1048
- (D) OTHER INFORMATION:

```

145          2150          2155          2160
Thr Thr Leu Asn Ala Ser Asn Gly Leu Lys Ile Asn Ala Ala Asn Asn
          2165          2170          2175
Asn Val Ser Val Ser Gln Gly Asn Leu Phe Val Ser Ala Ser Cys Ala
          2180          2185          2190
Gln Gln Ser Asp Pro Thr Thr Ala Asn Ile Ala Asn Pro Cys Ala Leu
          2195          2200          2205
Ser Ala Gln Ser Thr Asn Gly Ala Ser Ser Asn Asn Ala Ser Asn Asn
          2210          2215          2220
Ala Pro Ile Ala Leu Ser Asn Asn Asp Glu Ser Leu Met Val Ala Ala
225          2230          2235          2240
Asn Asp Phe Asn Phe Ser Gly Asn Ile Tyr Ala Asn Gly Val Val Asp
          2245          2250          2255
Phe Ser Lys Ile Lys Gly Ser Ala Asn Ile Lys Asn Leu Tyr Leu Tyr
          2260          2265          2270
Asn Asn Ala Gln Phe Gln Ala Asn Asn Leu Thr Ile Ser Asn Gln Ala
          2275          2280          2285
Val Leu Glu Lys Asn Ala Ser Phe Val Thr Asn Asn Leu Asn Ile Gln
          2290          2295          2300
Gly Ala Phe Asn Asn Asn Ala Thr Gln Lys Ile Glu Val Leu Gln Asn
305          2310          2315          2320
Leu Val Ile Ala Ser Asn Ala Ser Leu Ser Thr Gly Ile Tyr Gly Leu
          2325          2330          2335
Glu Val Gly Gly Ala Leu Asn Asn Ser Gly Ala Ile His Phe Asn Leu
          2340          2345          2350
Glu Asn Thr Gln Thr Pro Thr Pro Leu Ile Gln Ala Glu Gly Ile Ile
          2355          2360          2365
Asn Leu Asn Thr Thr Gln Thr Pro Phe Met Asn Val Asn Asn Ser Met
          2370          2375          2380
Ala Asn Asn Thr Thr Tyr Thr Leu Leu Lys Ser Ser Arg Tyr Ile Asp
385          2390          2395          2400
Tyr Asn Ile Asn Pro Asn Ser Leu Gln Ser Tyr Leu Asn Leu Tyr Thr
          2405          2410          2415
Leu Ile Asn Ile Asn Gly Asn His Ile Glu Glu Lys Asn Gly Ala Leu
          2420          2425          2430
Thr Tyr Leu Gly Gln Arg Val Leu Leu Gln Asp Lys Gly Leu Leu Leu
          2435          2440          2445
Ser Val Ala Leu Pro Asn Ser Asn Asn Ala Ser Gln Asn Asn Ile Leu
          2450          2455          2460
Ser Leu Ser Val Leu Tyr Asn Gln Val Lys Met Ser Cys Gly Asp Lys
465          2470          2475          2480
Ala Met Asp Phe Thr Pro Pro Thr Leu Gln Asp Tyr Ile Val Gly Ile
          2485          2490          2495
Gln Gly Gln Ser Ala Leu Asn Gln Ile Glu Ala Val Gly Gly Asn Ala
          2500          2505          2510
Ile Lys Trp Leu Ser Thr Leu Met Met Glu Thr Lys Glu Asn Pro Phe
          2515          2520          2525
Phe Ala Pro Ile Tyr Leu Lys Asn His Ser Leu Asn Glu Ile Leu Gly
          2530          2535          2540
Val Thr Lys Asp Leu Gln Asn Thr Ala Ser Leu Ile Ser Asn Pro Asn
545          2550          2555          2560
Phe Arg Asp Asn Ala Thr Asn Leu Leu Glu Leu Ala Ser Tyr Thr Gln
          2565          2570          2575
Gln Thr Ser Arg Leu Thr Lys Leu Ser Asp Phe Arg Ser Arg Glu Gly
          2580          2585          2590

```

Leu Asn Gln Leu Thr Lys Leu Ile Thr Pro Asn Asp Trp Lys Asn Ile
 1715 1720 1725
 Asn Glu Leu Ile Asp Asn Ala Asn Asn Ser Val Val Gln Asn Phe Asn
 1730 1735 1740
 Asn Gly Thr Leu Ile Val Gly Ala Thr Gln Ile Gly Gln Thr Asp Thr
 745 1750 1755 1760
 Asn Ser Ala Val Val Phe Gly Gly Leu Gly Tyr Gln Thr Pro Cys Asp
 1765 1770 1775
 Tyr Thr Asp Ile Val Cys Gln Lys Phe Arg Gly Thr Tyr Leu Gly Gln
 1780 1785 1790
 Leu Leu Glu Ser Ser Ser Ala Asp Leu Gly Tyr Ile Asp Thr Thr Phe
 1795 1800 1805
 Asn Ala Lys Glu Ile Tyr Leu Thr Gly Thr Leu Gly Ser Gly Asn Ala
 1810 1815 1820
 Trp Gly Thr Gly Gly Ser Ala Ser Val Thr Phe Asn Ser Gln Thr Ser
 825 1830 1835 1840
 Leu Ile Leu Asn Gln Ala Asn Ile Val Ser Ser Gln Thr Asp Gly Ile
 1845 1850 1855
 Phe Ser Met Leu Gly Gln Glu Gly Ile Asn Lys Val Phe Asn Gln Ala
 1860 1865 1870
 Gly Leu Ala Asn Ile Leu Gly Glu Val Ala Val Gln Ser Ile Asn Lys
 1875 1880 1885
 Ala Gly Gly Leu Gly Asn Leu Ile Val Asn Thr Leu Gly Ser Asn Ser
 1890 1895 1900
 Val Ile Gly Gly Tyr Leu Thr Pro Glu Gln Lys Asn Gln Thr Leu Ser
 905 1910 1915 1920
 Gln Leu Leu Gly Gln Asn Asn Phe Asp Asn Leu Met Asn Asp Ser Gly
 1925 1930 1935
 Leu Asn Thr Ala Ile Lys Asp Leu Ile Arg Gln Lys Leu Gly Phe Trp
 1940 1945 1950
 Thr Gly Leu Val Gly Gly Leu Ala Gly Leu Gly Gly Ile Asp Leu Gln
 1955 1960 1965
 Asn Pro Glu Lys Leu Ile Gly Ser Met Ser Ile Asn Asp Leu Leu Ser
 1970 1975 1980
 Lys Lys Gly Leu Phe Asn Gln Ile Thr Gly Phe Ile Ser Ala Asn Asp
 985 1990 1995 2000
 Ile Gly Gln Val Ile Ser Val Met Leu Gln Asp Ile Val Lys Pro Ser
 2005 2010 2015
 Asn Ala Leu Lys Asn Asp Val Ala Ala Leu Gly Lys Gln Met Ile Gly
 2020 2025 2030
 Glu Phe Leu Gly Gln Asp Thr Leu Asn Ser Leu Glu Ser Leu Leu Gln
 2035 2040 2045
 Asn Gln Gln Ile Lys Ser Val Leu Asp Lys Val Leu Ala Ala Lys Gly
 2050 2055 2060
 Leu Gly Pro Ile Tyr Glu Gln Gly Leu Gly Asp Leu Ile Pro Asn Leu
 065 2070 2075 2080
 Gly Lys Lys Gly Leu Phe Ala Pro Tyr Gly Leu Ser Gln Val Trp Gln
 2085 2090 2095
 Lys Gly Asp Phe Ser Phe Asn Ala Gln Gly Asn Val Phe Val Gln Asn
 2100 2105 2110
 Ser Thr Phe Ser Asn Ala Asn Gly Gly Thr Leu Ser Phe Asn Ala Gly
 2115 2120 2125
 Asn Ser Leu Ile Phe Ala Gly Asn Asn His Ile Ala Phe Thr Asn His
 2130 2135 2140
 Ala Gly Thr Leu Gln Leu Leu Ser Asp Gln Val Ser Asn Ile Asn Ile

265 1270 1275 1280
 Asn Ala Lys Asn Ala Ile Ser Phe Thr Asn Ser Thr Asn Leu Ser Ser
 1285 1290 1295
 Gly Leu Tyr Gln Met Gln Ala Lys Ser Val Leu Phe Asp Asn Ser Asn
 1300 1305 1310
 Leu Ser Val Ser Val Gly Thr Ser Ser Ile Lys Ala Asn Ala Ile Asn
 1315 1320 1325
 Leu Ser Gln Asn Ala Ser Ile Asn Ala Ser Asn His Ser Thr Leu Glu
 1330 1335 1340
 Leu Gln Gly Asp Leu Asn Val Asn Asp Thr Ser Ser Leu Asn Leu Asn
 345 1350 1355 1360
 Gln Ser Thr Ile Asn Val Ser Asn Asn Ala Thr Ile Asn Asp Tyr Ala
 1365 1370 1375
 Ser Leu Ile Ala Ser Asn Gly Ser His Leu Asn Phe Asn Gly Ala Val
 1380 1385 1390
 Asn Phe Asn Ser Ala Asn Ile Thr Thr Ser Leu Asn Asn Ser Ser Ile
 1395 1400 1405
 Val Phe Lys Gly Ala Val Ser Leu Gly Gly Gln Phe Asn Leu Ser Asn
 1410 1415 1420
 Asn Ser Ser Leu Asp Phe Gln Gly Ser Ser Ala Ile Thr Ser Asn Thr
 425 1430 1435 1440
 Ala Phe Asn Phe Tyr Asp Asn Ala Phe Ser Gln Ser Pro Ile Thr Phe
 1445 1450 1455
 His Gln Ala Leu Asp Ile Lys Ala Pro Leu Ser Leu Gly Gly Asn Leu
 1460 1465 1470
 Leu Asn Pro Asn Asn Ser Ser Val Leu Asp Leu Lys Asn Ser Gln Leu
 1475 1480 1485
 Val Phe Gly Asp Gln Gly Ser Leu Asn Ile Ala Asn Ile Asp Leu Leu
 1490 1495 1500
 Ser Asp Leu Asn Asp Asn Lys Asn Arg Val Tyr Asn Ile Ile Gln Ala
 505 1510 1515 1520
 Asp Met Asn Ser Asn Trp Tyr Glu Arg Ile Ser Phe Phe Gly Met His
 1525 1530 1535
 Ile Asn Asp Gly Ile Tyr Asp Ala Lys Asn Gln Thr Tyr Ser Phe Thr
 1540 1545 1550
 Asn Pro Leu Asn Asn Ala Leu Lys Ile Thr Glu Ser Phe Lys Asp Asn
 1555 1560 1565
 Gln Leu Ser Val Thr Leu Ser Gln Ile Pro Gly Ile Lys Asn Thr Leu
 1570 1575 1580
 Tyr Asn Ile Gly Ser Glu Ile Phe Asn Tyr Gln Lys Val Tyr Asn Asn
 585 1590 1595 1600
 Ala Asn Gly Val Tyr Ser Tyr Ser Asp Asp Ala Gln Gly Val Phe Tyr
 1605 1610 1615
 Leu Thr Ser Asn Val Lys Gly Tyr Tyr Asn Pro Asn Gln Ser Tyr Gln
 1620 1625 1630
 Ala Ser Gly Ser Asn Asn Thr Thr Lys Asn Asn Asn Leu Thr Ser Glu
 1635 1640 1645
 Ser Ser Ile Ile Ser Gln Thr Tyr Asn Ala Gln Gly Asn Pro Ile Ser
 1650 1655 1660
 Ala Leu His Ile Tyr Asn Lys Gly Tyr Asn Phe Asn Asn Ile Lys Ala
 665 1670 1675 1680
 Leu Gly Gln Met Ala Leu Lys Leu Tyr Pro Glu Ile Lys Lys Val Leu
 1685 1690 1695
 Gly Asn Asp Phe Ser Pro Ser Ser Leu Asn Ala Leu Asn Ser Asn Ala
 1700 1705 1710

Phe Asn Ser Gly Ser Phe Glu Ile Ser Ala Lys Asn Ala Ser Phe Asn
 835 840 845
 Asn Ala Asn Phe Asn Asn Ser Ala Ser Phe Asn Phe Asn Asn Ser Asn
 850 855 860
 Ala Thr Thr Ser Phe Val Gly Asp Phe Thr Asn Ala Asn Ser Asn Leu
 865 870 875 880
 Gln Ile Ala Gly Asn Ala Val Phe Gly Asn Ser Thr Asn Gly Ser Gln
 885 890 895
 Asn Thr Ala Asn Phe Asn Asn Thr Gly Ser Val Asn Ile Ser Gly Asn
 900 905 910
 Ala Thr Phe Asp Asn Val Val Phe Asn Gly Pro Thr Asn Thr Ser Val
 915 920 925
 Lys Gly Gln Val Thr Leu Asn Asn Ile Thr Leu Lys Asn Leu Asn Ala
 930 935 940
 Pro Leu Ser Phe Gly Asp Gly Thr Ile Thr Phe Asn Ala His Ser Val
 945 950 955 960
 Ile Asn Ile Ala Glu Ser Ile Thr Asn Gly Asn Pro Ile Thr Leu Val
 965 970 975
 Ser Ser Ser Lys Glu Ile Glu Tyr Asn Asn Ala Phe Ser Lys Asn Leu
 980 985 990
 Trp Gln Leu Ile Asn Tyr Gln Gly His Gly Ala Ser Ser Glu Lys Leu
 995 1000 1005
 Val Ser Ser Ala Gly Asn Gly Val Tyr Asp Val Val Tyr Ser Phe Asn
 1010 1015 1020
 Asn Gln Thr Tyr Asn Phe Gln Glu Val Phe Ser Gln Asn Ser Ile Ser
 1025 1030 1035 1040
 Ile Arg Arg Leu Gly Val Asn Met Val Phe Asp Tyr Val Asp Met Glu
 1045 1050 1055
 Lys Ser Asp His Leu Tyr Tyr Gln Asn Ala Leu Gly Phe Met Thr Tyr
 1060 1065 1070
 Met Pro Asn Ser Tyr Asn Asn Asn Leu Gly Asn Ala Asn Asn Thr Ile
 1075 1080 1085
 Tyr Tyr Tyr Asp Lys Ser Ile Asp Phe Tyr Ala Ser Gly Lys Thr Leu
 1090 1095 1100
 Phe Thr Lys Ala Glu Phe Ser Gln Thr Phe Thr Gly Gln Asn Ser Ala
 1105 1110 1115 1120
 Ile Val Phe Gly Ala Lys Ser Ile Trp Thr Ser Leu Ser Asp Ala Pro
 1125 1130 1135
 Gln Ser Asn Thr Ile Ile Arg Phe Gly Asp Asn Lys Gly Ala Gly Ser
 1140 1145 1150
 Asn Asp Ala Ser Gly His Cys Trp Asn Leu Gln Cys Ile Gly Phe Ile
 1155 1160 1165
 Thr Gly His Tyr Glu Ala Gln Lys Ile Tyr Ile Thr Gly Ser Ile Glu
 1170 1175 1180
 Ser Gly Asn Arg Ile Ser Ser Gly Gly Gly Ala Ser Leu Asn Phe Asn
 1185 1190 1195 1200
 Gly Leu Gln Gly Ile Leu Leu Thr Asn Ala Thr Leu Tyr Asn Arg Ala
 1205 1210 1215
 Ala Gly Thr Gln Ser Ser Ser Met Asn Phe Ile Ser Asn Ser Ala Asn
 1220 1225 1230
 Ile Gln Ala Gln Asn Ser Tyr Phe Ile Asp Asp Thr Ala Gln Asn Gly
 1235 1240 1245
 Gly Asn Pro Asn Phe Ser Phe Asn Ala Leu Asn Leu Asp Phe Ser Asn
 1250 1255 1260
 Ser Ser Phe Arg Gly Tyr Val Gly Lys Thr Gln Ser Val Phe Lys Phe


```

385          390          395          400
Ala Thr Phe Asn Asn Thr Gly Lys Ile Thr Ile Glu Lys Asp Ala Ser
          405          410          415
Phe Asn Asn Thr Thr Phe Asn Thr Ser Val Asp Thr Asn Asn Met Ser
          420          425          430
Val Thr Gly Gly Val Thr Leu Ser Gly Lys Asn Asp Leu Lys Asn Gly
          435          440          445
Ser Thr Leu Asp Phe Gly Ser Lys Ile Thr Leu Ala Gln Gly Thr
          450          455          460
Thr Phe Asn Leu Thr Ser Leu Gly Ser Glu Lys Ser Val Thr Ile Leu
465          470          475          480
Asn Ser Ser Gly Gly Ile Thr Tyr Ser Asn Leu Leu Asn His Ala Ile
          485          490          495
Asn Gly Leu Thr Ser Ala Leu Lys Thr Asn Glu Ser Leu Ser Asn Pro
          500          505          510
Gln Ser Phe Ala Gln Gly Leu Trp Asp Ile Ile Thr Tyr Asn Gly Val
          515          520          525
Thr Gly Gln Leu Leu Asn Glu Asn Ala Ala Thr Ser Lys Pro Thr Asp
          530          535          540
Ser Ser Pro Ser Lys Ser Ser Thr Asn Ser Thr Gln Val Tyr Gln Val
545          550          555          560
Gly Tyr Lys Ile Gly Asp Thr Ile Tyr Lys Leu Gln Glu Thr Phe Ser
          565          570          575
His Asn Ser Ile Ile Ile Gln Ala Leu Glu Ser Gly Thr Tyr Thr Pro
          580          585          590
Pro Pro Val Ile Asn Gly Ser Lys Phe Asp Leu Ser Ala Ser Asn Tyr
          595          600          605
Ile Asn Ala Asp Met Pro Trp Tyr Asp His Lys Tyr Tyr Ile Pro Lys
          610          615          620
Ser Gln Asn Phe Thr Glu Ser Gly Thr Tyr Tyr Leu Pro Ser Val Gln
625          630          635          640
Ile Trp Gly Ser Tyr Thr Asn Ser Phe Lys Gln Thr Phe Ser Ala Asn
          645          650          655
Gly Ser Asn Leu Val Ile Gly Tyr Asn Ser Thr Trp Thr Asp His Asn
          660          665          670
Val Ser Ser Ser Gly Thr Val Ser Phe Gly Asp Thr Ser Gly Ser Ala
          675          680          685
Leu Asn Gly His Cys Gly Pro Trp Pro Tyr Tyr Gln Cys Thr Gly Thr
          690          695          700
Thr Asn Gly Thr Tyr Ser Ala Tyr His Val Tyr Ile Thr Ala Asn Leu
705          710          715          720
Arg Ser Gly Asn Arg Ile Gly Thr Gly Gly Ala Ala Asn Leu Ile Phe
          725          730          735
Asn Gly Val Asp Ser Ile Asn Ile Ala Asn Ala Thr Ile Thr Gln His
          740          745          750
Asn Ala Gly Ile Tyr Ser Ser Ser Met Thr Phe Ser Thr Gln Ser Met
          755          760          765
Asp Asn Ser Gln Asn Leu Asn Gly Leu Asn Ser Asn Gly Lys Leu Ser
          770          775          780
Val Tyr Gly Thr Thr Phe Thr Asn Glu Ala Lys Asp Gly Lys Phe Ile
785          790          795          800
Phe Asn Ala Gly Gln Ala Val Phe Glu Asn Thr Asn Phe Asn Gly Gly
          805          810          815
Ser Tyr Gln Phe Ser Gly Asp Ser Leu Asn Phe Ser Asn Asn Asn Gln
          820          825          830

```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

```

Met Lys Lys Phe Lys Lys Lys Pro Lys Ser Ile Lys Arg Ser His Gln
 1           5           10           15
Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Met Pro Leu Leu
          20           25           30
Ile Ser Gly Phe Ala Ser Gly Val Tyr Ala Asn Asn Leu Trp Asp Leu
          35           40           45
Leu Asn Pro Lys Val Gly Gly Glu Tyr Val His Trp Val Lys Gly Ser
          50           55           60
Gln Tyr Cys Ala Trp Trp Glu Phe Ala Gly Cys Leu Lys Asn Val Trp
65           70           75           80
Gly Ala Asn His Lys Gly Tyr Asp Ala Gly Asn Ala Ala Asn Tyr Leu
          85           90           95
Ser Ser Gln Asn Tyr Gln Ala Ile Ser Val Gly Ser Gly Asn Glu Thr
          100          105          110
Gly Thr Tyr Ser Leu Ser Gly Phe Thr Asn Tyr Val Gly Gly Asn Leu
          115          120          125
Thr Ile Asn Leu Gly Asn Ser Val Val Leu Asp Leu Ser Gly Ser Asn
          130          135          140
Ser Phe Thr Ser Tyr Gln Gly Tyr Asn Gln Gly Lys Asp Asp Val Thr
145          150          155          160
Phe Thr Val Gly Ala Ile Asn Leu Asn Gly Thr Leu Glu Val Gly Asn
          165          170          175
Arg Val Gly Ser Gly Ala Gly Thr His Thr Gly Thr Ala Thr Leu Asn
          180          185          190
Leu Asn Ala Asn Lys Val Asn Ile Asn Ser Asn Ile Asn Ala Tyr Lys
          195          200          205
Thr Ser Gln Val Asn Ile Gly Asn Ala Asn Ser Val Ile Thr Ile Gly
          210          215          220
Ser Val Ser Leu Ser Gly Asp Val Cys Ser Ser Leu Ala Ser Val Gly
225          230          235          240
Ile Gly Ala Asn Cys Ser Thr Ser Gly Pro Ser Tyr Ser Phe Lys Gly
          245          250          255
Thr Thr Asn Ala Thr Asn Thr Ala Phe Ser Asn Ala Ser Gly Ser Phe
          260          265          270
Thr Phe Glu Glu Asn Ala Thr Phe Ser Gly Ala Lys Trp Asn Gly Gly
          275          280          285
Thr Tyr Thr Phe Asn Lys Glu Phe Ser Ala Thr Asn Asn Thr Ala Phe
          290          295          300
Ser Ser Gly Ser Phe Asn Phe Lys Gly Val Ser Ser Phe Asn Gly Thr
305          310          315          320
Ser Phe Ser Asn Ala Ser Tyr Thr Phe Asp Asn Gln Ala Thr Phe Gln
          325          330          335
Asn Ser Ser Phe Asn Gly Gly Thr Phe Thr Phe Asn Asn Gln Thr Asn
          340          345          350
Pro Thr Asn Asn Ala Gln His Pro Gln Ile Gln Asn Ser Ser Phe Ser
          355          360          365
Gly Asn Ala Thr Thr Leu Lys Gly Phe Val Asn Phe Gln Gln Ala Phe
          370          375          380
Asn Asn Ser Asn His Gln Leu Thr Ile Gln Asn Ala Ser Phe Asn Asn

```

TCT AAT TCT TTG CTC TCT GTG TTG AAC CAA CGC TAC AAC TAC AAC ACC	8211
Ser Asn Ser Leu Leu Ser Val Leu Asn Gln Arg Tyr Asn Tyr Asn Thr	
2720 2725 2730	
TGG ACA ACG AGC GTG AAC GGG AAT TAC GGC TAT GAT TTC ATG TTC AAA	8259
Trp Thr Thr Ser Val Asn Gly Asn Tyr Gly Tyr Asp Phe Met Phe Lys	
2735 2740 2745	
CAA AAA AGC GTG GTG CTA AAA CCT CAA GTG GGT TTG AGC TAT CAT TTC	8307
Gln Lys Ser Val Val Leu Lys Pro Gln Val Gly Leu Ser Tyr His Phe	
2750 2755 2760	
ATA GGT CTA AGT GGG ATG AAA GGC AAT GAT GCC GCT TAC AAA CAA TTC	8355
Ile Gly Leu Ser Gly Met Lys Gly Asn Asp Ala Ala Tyr Lys Gln Phe	
2765 2770 2775 2780	
CTC ATG CAT TCA AAC CCC TCT AAC GAA TCG GTT TTA ACG CTC AAC ATG	8403
Leu Met His Ser Asn Pro Ser Asn Glu Ser Val Leu Thr Leu Asn Met	
2785 2790 2795	
GGG TTG GAG AGC CGT AAA TAT TTT GGT AAA AAT TCC TAT TAT TTT GTA	8451
Gly Leu Glu Ser Arg Lys Tyr Phe Gly Lys Asn Ser Tyr Tyr Phe Val	
2800 2805 2810	
ACG GCG AGA CTA GGT AGG GAT CTT TTG ATC AAA TCT AAA GGC AGC AAT	8499
Thr Ala Arg Leu Gly Arg Asp Leu Leu Ile Lys Ser Lys Gly Ser Asn	
2815 2820 2825	
ACG GTG CGT TTT GTG GGC GAA AAC ACT TTA TTG TAT CGC AAG GGG GAA	8547
Thr Val Arg Phe Val Gly Glu Asn Thr Leu Leu Tyr Arg Lys Gly Glu	
2830 2835 2840	
GTT TTT AAC ACT TTT GCG AGC GTG ATT ACA GGG GGC GAA ATG CAT TTG	8595
Val Phe Asn Thr Phe Ala Ser Val Ile Thr Gly Gly Glu Met His Leu	
2845 2850 2855 2860	
TGG CGT TTG GTG TAT GTG AAT GCG GGG GTG GGG CTT AAG ATG GGC TTG	8643
Trp Arg Leu Val Tyr Val Asn Ala Gly Val Gly Leu Lys Met Gly Leu	
2865 2870 2875	
CAA TAC CAA GAT ATT AAT ATA ACC GGG AAT GTG GGC ATG CGA GTG GCG	8691
Gln Tyr Gln Asp Ile Asn Ile Thr Gly Asn Val Gly Met Arg Val Ala	
2880 2885 2890	
TTT TAGCTTTTTT GCTATAATGC TTCGTTCAAA TTTTATGGTT AGGTTTTTCT ATGT	8748
Phe	

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

ATT GTG GGC ATT CAA GGG CAA AGC GCG CTC AAT CAA ATT GAA GCT GTT Ile Val Gly Ile Gln Gly Gln Ser Ala Leu Asn Gln Ile Glu Ala Val 2495 2500 2505	7539
GGG GGG AAC GCT ATC AAG TGG CTT TCA ACA TTG ATG ATG GAG ACT AAA Gly Gly Asn Ala Ile Lys Trp Leu Ser Thr Leu Met Met Glu Thr Lys 2510 2515 2520	7587
GAA AAC CCG TTT TTT GCG CCG ATT TAT TTA AAA AAC CAC TCT TTG AAT Glu Asn Pro Phe Phe Ala Pro Ile Tyr Leu Lys Asn His Ser Leu Asn 2525 2530 2535 2540	7635
GAA ATC TTA GGC GTA ACA AAA GAT CTT CAA AAC ACC GCA AGC TTG ATT Glu Ile Leu Gly Val Thr Lys Asp Leu Gln Asn Thr Ala Ser Leu Ile 2545 2550 2555	7683
TCT AAC CCT AAT TTT AGA GAT AAC GCT ACC AAT CTT TTA GAA TTG GCG Ser Asn Pro Asn Phe Arg Asp Asn Ala Thr Asn Leu Leu Glu Leu Ala 2560 2565 2570	7731
AGT TAC ACC CAA CAA ACC AGC CGT TTA ACA AAA CTC TCT GAT TTT AGA Ser Tyr Thr Gln Gln Thr Ser Arg Leu Thr Lys Leu Ser Asp Phe Arg 2575 2580 2585	7779
TCT AGA GAG GGA GAG TCT GAT TTT TCT TTG TTA GAG CTT AAA AAC AAG Ser Arg Glu Gly Glu Ser Asp Phe Ser Leu Leu Glu Leu Lys Asn Lys 2590 2595 2600	7827
CGT TTT AGC GAT CCT AAT CCA GAG GTT TTT GTC AAA TAC TCT CAA CTT Arg Phe Ser Asp Pro Asn Pro Glu Val Phe Val Lys Tyr Ser Gln Leu 2605 2610 2615 2620	7875
AGC AAA CAC CCA AAT AAC CTT TGG GTT CAA GGG GTG GGA GGA GCG AGC Ser Lys His Pro Asn Asn Leu Trp Val Gln Gly Val Gly Gly Ala Ser 2625 2630 2635	7923
TTT ATT TCT GGG GGC AAT GGC ACG CTT TAT GGC TTG AAT GCG GGC TAT Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly Leu Asn Ala Gly Tyr 2640 2645 2650	7971
GAC AGG TTG GTT AAA AAT GTG ATC CTT GGG GGT TAT GTG GCT TAT GGC Asp Arg Leu Val Lys Asn Val Ile Leu Gly Gly Tyr Val Ala Tyr Gly 2655 2660 2665	8019
TAT AGC GAC TTT AAT GGG AAC ATC ATG CAT TCT TTG GGT AAT AAT GTG Tyr Ser Asp Phe Asn Gly Asn Ile Met His Ser Leu Gly Asn Asn Val 2670 2675 2680	8067
GAT GTG GGG ATG TAT GCG AGG GCT TTT TTA AAA AGG AAC GAA TTC ACT Asp Val Gly Met Tyr Ala Arg Ala Phe Leu Lys Arg Asn Glu Phe Thr 2685 2690 2695 2700	8115
TTG AGC GCG AAT GAA ACT TAT GGA GGC AAT GCA ACT AGT ATC AAT TCT Leu Ser Ala Asn Glu Thr Tyr Gly Gly Asn Ala Thr Ser Ile Asn Ser 2705 2710 2715	8163

CTG TAT CTT TAC AAT AAC GCT CAA TTC CAA GCC AAC AAT CTC ACT ATT	6867
Leu Tyr Leu Tyr Asn Asn Ala Gln Phe Gln Ala Asn Asn Leu Thr Ile	
2270 2275 2280	
TCC AAT CAA GCG GTG TTA GAA AAA AAC GCC AGC TTT GTA ACG AAT AAT	6915
Ser Asn Gln Ala Val Leu Glu Lys Asn Ala Ser Phe Val Thr Asn Asn	
2285 2290 2295 2300	
TTA AAC ATT CAA GGA GCG TTT AAC AAC AAC GCC ACG CAA AAA ATA GAG	6963
Leu Asn Ile Gln Gly Ala Phe Asn Asn Asn Ala Thr Gln Lys Ile Glu	
2305 2310 2315	
GTG CTT CAA AAT TTA GTG ATC GCT TCA AAC GCT TCT TTA AGC ACC GGG	7011
Val Leu Gln Asn Leu Val Ile Ala Ser Asn Ala Ser Leu Ser Thr Gly	
2320 2325 2330	
ATT TAT GGG TTA GAA GTA GGG GGG GCT TTG AAT AAT TCT GGA GCG ATC	7059
Ile Tyr Gly Leu Glu Val Gly Gly Ala Leu Asn Asn Ser Gly Ala Ile	
2335 2340 2345	
CAT TTT AAT TTA GAA AAT ACC CAA ACG CCA ACG CCG CTC ATT CAA GCA	7107
His Phe Asn Leu Glu Asn Thr Gln Thr Pro Thr Pro Leu Ile Gln Ala	
2350 2355 2360	
GAG GGG ATC ATT AAC CTC AAC ACC ACC CAA ACG CCT TTT ATG AAT GTC	7155
Glu Gly Ile Ile Asn Leu Asn Thr Thr Gln Thr Pro Phe Met Asn Val	
2365 2370 2375 2380	
AAT AAC AGC ATG GCC AAT AAT ACG ACT TAC ACT TTA TTA AAA AGC AGC	7203
Asn Asn Ser Met Ala Asn Asn Thr Thr Tyr Thr Leu Leu Lys Ser Ser	
2385 2390 2395	
CGT TAC ATT GAT TAC AAT ATC AAC CCC AAC AGC TTG CAA TCG TAT TTG	7251
Arg Tyr Ile Asp Tyr Asn Ile Asn Pro Asn Ser Leu Gln Ser Tyr Leu	
2400 2405 2410	
AAT CTC TAC ACT TTA ATC AAT ATC AAC GGG AAC CAC ATA GAG GAA AAA	7299
Asn Leu Tyr Thr Leu Ile Asn Ile Asn Gly Asn His Ile Glu Glu Lys	
2415 2420 2425	
AAC GGC GCA TTG ACT TAT TTG GGC CAA CGG GTT TTG TTG CAA GAT AAG	7347
Asn Gly Ala Leu Thr Tyr Leu Gly Gln Arg Val Leu Leu Gln Asp Lys	
2430 2435 2440	
GGG TTA TTG TTA AGC GTA GCG CTG CCC AAC TCA AAC AAC GCT TCT CAA	7395
Gly Leu Leu Leu Ser Val Ala Leu Pro Asn Ser Asn Asn Ala Ser Gln	
2445 2450 2455 2460	
AAC AAC ATT TTA AGC CTT TCT GTC CTT TAT AAC CAA GTT AAA ATG TCT	7443
Asn Asn Ile Leu Ser Leu Ser Val Leu Tyr Asn Gln Val Lys Met Ser	
2465 2470 2475	
TGC GGC GAT AAA GCG ATG GAT TTT ACC CCC CCT ACC TTA CAA GAT TAC	7491
Cys Gly Asp Lys Ala Met Asp Phe Thr Pro Pro Thr Leu Gln Asp Tyr	
2480 2485 2490	

- 1837 -

AGC GGG AAC GCA TGG GGG ACT GGG GGG AGC GCG AGC GTA ACT TTT AAC	5523
Ser Gly Asn Ala Trp Gly Thr Gly Gly Ser Ala Ser Val Thr Phe Asn	
1825 1830 1835	
AGC CAA ACT TCG CTC ATT CTC AAT CAG GCT AAT ATC GTA AGC TCG CAA	5571
Ser Gln Thr Ser Leu Ile Leu Asn Gln Ala Asn Ile Val Ser Ser Gln	
1840 1845 1850	
ACC GAT GGG ATC TTT AGC ATG CTG GGT CAA GAG GGT ATT AAT AAG GTT	5619
Thr Asp Gly Ile Phe Ser Met Leu Gly Gln Glu Gly Ile Asn Lys Val	
1855 1860 1865	
TTC AAT CAA GCC GGG CTC GCT AAT ATT TTG GGC GAA GTG GCG GTG CAA	5667
Phe Asn Gln Ala Gly Leu Ala Asn Ile Leu Gly Glu Val Ala Val Gln	
1870 1875 1880	
TCC ATC AAC AAA GCC GGG GGA TTA GGG AAT TTG ATA GTA AAT ACG CTA	5715
Ser Ile Asn Lys Ala Gly Gly Leu Gly Asn Leu Ile Val Asn Thr Leu	
1885 1890 1895 1900	
GGG AGT AAT AGC GTG ATT GGG GGG TAT TTA ACG CCT GAA CAA AAA AAT	5763
Gly Ser Asn Ser Val Ile Gly Gly Tyr Leu Thr Pro Glu Gln Lys Asn	
1905 1910 1915	
CAA ACC CTA AGC CAG CTT TTA GGG CAG AAT AAC TTT GAT AAT CTC ATG	5811
Gln Thr Leu Ser Gln Leu Leu Gly Gln Asn Asn Phe Asp Asn Leu Met	
1920 1925 1930	
AAC GAT AGC GGT TTG AAT ACG GCG ATT AAG GAT TTG ATC AGA CAA AAA	5859
Asn Asp Ser Gly Leu Asn Thr Ala Ile Lys Asp Leu Ile Arg Gln Lys	
1935 1940 1945	
TTA GGC TTT TGG ACC GGG CTA GTG GGG GGA TTA GCC GGA CTA GGG GGC	5907
Leu Gly Phe Trp Thr Gly Leu Val Gly Gly Leu Ala Gly Leu Gly Gly	
1950 1955 1960	
ATT GAT TTG CAA AAC CCT GAA AAG CTT ATA GGC AGC ATG TCA ATC AAT	5955
Ile Asp Leu Gln Asn Pro Glu Lys Leu Ile Gly Ser Met Ser Ile Asn	
1965 1970 1975 1980	
GAT TTA TTG AGT AAA AAA GGG TTG TTC AAT CAG ATC ACC GGC TTT ATT	6003
Asp Leu Leu Ser Lys Lys Gly Leu Phe Asn Gln Ile Thr Gly Phe Ile	
1985 1990 1995	
TCC GCT AAC GAT ATA GGG CAA GTC ATA AGC GTA ATG TTG CAA GAT ATT	6051
Ser Ala Asn Asp Ile Gly Gln Val Ile Ser Val Met Leu Gln Asp Ile	
2000 2005 2010	
GTC AAA CCG AGC AAC GCT TTA AAA AAC GAT GTA GCG GCT TTA GGC AAG	6099
Val Lys Pro Ser Asn Ala Leu Lys Asn Asp Val Ala Ala Leu Gly Lys	
2015 2020 2025	
CAA ATG ATT GGC GAA TTT TTA GGC CAA GAC ACG CTC AAT TCT TTA GAA	6147
Gln Met Ile Gly Glu Phe Leu Gly Gln Asp Thr Leu Asn Ser Leu Glu	
2030 2035 2040	

GTT TAT AAC AAC GCT AAT GGC GTG TAT TCT TAT AGC GAT GAT GCA CAA	4851
Val Tyr Asn Asn Ala Asn Gly Val Tyr Ser Tyr Ser Asp Asp Ala Gln	
1600 1605 1610	
GGC GTG TTT TAT CTC ACA AGC AAC GTG AAA GGC TAT TAC AAC CCT AAC	4899
Gly Val Phe Tyr Leu Thr Ser Asn Val Lys Gly Tyr Tyr Asn Pro Asn	
1615 1620 1625	
CAA TCC TAT CAA GCC AGC GGC AGT AAC AAC ACC ACG AAA AAT AAT AAT	4947
Gln Ser Tyr Gln Ala Ser Gly Ser Asn Asn Thr Thr Lys Asn Asn Asn	
1630 1635 1640	
CTA ACC TCT GAA TCT TCT ATC ATC TCG CAA ACC TAT AAC GCG CAA GGC	4995
Leu Thr Ser Glu Ser Ser Ile Ile Ser Gln Thr Tyr Asn Ala Gln Gly	
1645 1650 1655 1660	
AAC CCT ATT AGC GCG TTG CAC ATC TAT AAC AAG GGC TAT AAT TTC AAC	5043
Asn Pro Ile Ser Ala Leu His Ile Tyr Asn Lys Gly Tyr Asn Phe Asn	
1665 1670 1675	
AAT ATC AAA GCG TTA GGG CAA ATG GCT CTC AAA CTC TAC CCT GAA ATC	5091
Asn Ile Lys Ala Leu Gly Gln Met Ala Leu Lys Leu Tyr Pro Glu Ile	
1680 1685 1690	
AAA AAG GTA TTA GGG AAT GAT TTT TCG CCC TCA AGT TTG AAC GCT TTA	5139
Lys Lys Val Leu Gly Asn Asp Phe Ser Pro Ser Ser Leu Asn Ala Leu	
1695 1700 1705	
AAC TCT AAT GCG CTA AAC CAA CTT ACC AAA CTC ATC ACG CCT AAC GAC	5187
Asn Ser Asn Ala Leu Asn Gln Leu Thr Lys Leu Ile Thr Pro Asn Asp	
1710 1715 1720	
TGG AAA AAC ATT AAC GAG TTG ATT GAT AAC GCA AAC AAT TCG GTG GTG	5235
Trp Lys Asn Ile Asn Glu Leu Ile Asp Asn Ala Asn Asn Ser Val Val	
1725 1730 1735 1740	
CAA AAT TTC AAT AAC GGC ACT TTG ATT GTG GGA GCG ACT CAA ATA GGG	5283
Gln Asn Phe Asn Asn Gly Thr Leu Ile Val Gly Ala Thr Gln Ile Gly	
1745 1750 1755	
CAA ACA GAC ACC AAT AGC GCG GTT GTT TTT GGG GGC TTG GGC TAT CAA	5331
Gln Thr Asp Thr Asn Ser Ala Val Val Phe Gly Gly Leu Gly Tyr Gln	
1760 1765 1770	
ACA CCT TGT GAT TAT ACT GAT ATT GTG TGC CAA AAA TTT AGA GGC ACT	5379
Thr Pro Cys Asp Tyr Thr Asp Ile Val Cys Gln Lys Phe Arg Gly Thr	
1775 1780 1785	
TAT TTA GGA CAG CTT TTA GAG TCC AGC TCG GCT GAT TTG GGC TAT ATT	5427
Tyr Leu Gly Gln Leu Leu Glu Ser Ser Ser Ala Asp Leu Gly Tyr Ile	
1790 1795 1800	
GAC ACG ACT TTT AAC GCT AAA GAA ATT TAT CTT ACC GGC ACT TTA GGG	5475
Asp Thr Thr Phe Asn Ala Lys Glu Ile Tyr Leu Thr Gly Thr Leu Gly	
1805 1810 1815 1820	

AAC GAT TAT GCG AGC TTG ATT GCG AGT AAT GGC TCT CAC CTT AAT TTT Asn Asp Tyr Ala Ser Leu Ile Ala Ser Asn Gly Ser His Leu Asn Phe 1375 1380 1385	4179
AAC GGG GCG GTT AAT TTC AAT TCA GCG AAT ATT ACT ACG AGT TTG AAT Asn Gly Ala Val Asn Phe Asn Ser Ala Asn Ile Thr Thr Ser Leu Asn 1390 1395 1400	4227
AAT TCC TCT ATC GTG TTT AAG GGG GCG GTC TCT TTA GGA GGG CAG TTT Asn Ser Ser Ile Val Phe Lys Gly Ala Val Ser Leu Gly Gly Gln Phe 1405 1410 1415 1420	4275
AAT TTA AGC AAT AAC TCT TCT TTA GAT TTC CAA GGC TCT AGC GCT ATC Asn Leu Ser Asn Asn Ser Ser Leu Asp Phe Gln Gly Ser Ser Ala Ile 1425 1430 1435	4323
ACC TCT AAC ACG GCG TTT AAT TTC TAT GAT AAC GCT TTT TCT CAA AGC Thr Ser Asn Thr Ala Phe Asn Phe Tyr Asp Asn Ala Phe Ser Gln Ser 1440 1445 1450	4371
CCC ATC ACT TTC CAT CAA GCC CTT GAC ATT AAA GCG CCC TTA AGT TTG Pro Ile Thr Phe His Gln Ala Leu Asp Ile Lys Ala Pro Leu Ser Leu 1455 1460 1465	4419
GGA GGC AAC CTT TTA AAC CCT AAC AAC AGC AGC GTG CTG GAT TTA AAA Gly Gly Asn Leu Leu Asn Pro Asn Asn Ser Ser Val Leu Asp Leu Lys 1470 1475 1480	4467
AAC AGC CAG CTT GTT TTT GGC GAT CAA GGG AGT TTG AAT ATC GCT AAC Asn Ser Gln Leu Val Phe Gly Asp Gln Gly Ser Leu Asn Ile Ala Asn 1485 1490 1495 1500	4515
ATT GAT TTA CTA AGC GAT CTA AAT GAT AAT AAA AAT CGT GTG TAT AAC Ile Asp Leu Leu Ser Asp Leu Asn Asp Asn Lys Asn Arg Val Tyr Asn 1505 1510 1515	4563
ATC ATT CAA GCG GAC ATG AAT AGT AAT TGG TAT GAG CGT ATC AGC TTC Ile Ile Gln Ala Asp Met Asn Ser Asn Trp Tyr Glu Arg Ile Ser Phe 1520 1525 1530	4611
TTT GGC ATG CAC ATC AAT GAC GGG ATT TAT GAT GCT AAA AAC CAA ACT Phe Gly Met His Ile Asn Asp Gly Ile Tyr Asp Ala Lys Asn Gln Thr 1535 1540 1545	4659
TAT AGT TTC ACT AAC CCC CTT AAT AAC GCC CTA AAA ATC ACC GAG AGC Tyr Ser Phe Thr Asn Pro Leu Asn Asn Ala Leu Lys Ile Thr Glu Ser 1550 1555 1560	4707
TTT AAA GAC AAC CAA CTA AGC GTT ACG CTC TCT CAA ATC CCG GGT ATT Phe Lys Asp Asn Gln Leu Ser Val Thr Leu Ser Gln Ile Pro Gly Ile 1565 1570 1575 1580	4755
AAA AAC ACG CTC TAT AAC ATT GGC TCT GAA ATT TTT AAC TAC CAA AAA Lys Asn Thr Leu Tyr Asn Ile Gly Ser Glu Ile Phe Asn Tyr Gln Lys 1585 1590 1595	4803

GGA GCA GGG AGT AAT GAT GCG AGC GGG CAT TGC TGG AAT TTG CAA TGC	3507
Gly Ala Gly Ser Asn Asp Ala Ser Gly His Cys Trp Asn Leu Gln Cys	
1150 1155 1160	
ATA GGC TTT ATT ACA GGG CAT TAT GAA GCG CAA AAG ATT TAC ATC ACC	3555
Ile Gly Phe Ile Thr Gly His Tyr Glu Ala Gln Lys Ile Tyr Ile Thr	
1165 1170 1175 1180	
GGT AGC ATT GAA AGC GGG AAT CGC ATT TCT AGC GGT GGG GGC GCG AGC	3603
Gly Ser Ile Glu Ser Gly Asn Arg Ile Ser Ser Gly Gly Gly Ala Ser	
1185 1190 1195	
CTT AAT TTT AAC GGG CTT CAA GGC ATT CTT TTA ACG AAC GCG ACT TTG	3651
Leu Asn Phe Asn Gly Leu Gln Gly Ile Leu Leu Thr Asn Ala Thr Leu	
1200 1205 1210	
TAT AAC CGC GCC GCT GGC ACG CAA AGC TCG TCT ATG AAT TTT ATC TCT	3699
Tyr Asn Arg Ala Ala Gly Thr Gln Ser Ser Ser Met Asn Phe Ile Ser	
1215 1220 1225	
AAC AGC GCG AAC ATT CAG GCT CAA AAC TCC TAT TTT ATA GAC GAT ACC	3747
Asn Ser Ala Asn Ile Gln Ala Gln Asn Ser Tyr Phe Ile Asp Asp Thr	
1230 1235 1240	
GCA CAA AAT GGC GGT AAC CCT AAT TTC AGT TTC AAC GCT TTG AAT CTG	3795
Ala Gln Asn Gly Gly Asn Pro Asn Phe Ser Phe Asn Ala Leu Asn Leu	
1245 1250 1255 1260	
GAT TTT TCT AAC AGC TCT TTT AGA GGC TAT GTG GGG AAA ACG CAA TCT	3843
Asp Phe Ser Asn Ser Ser Phe Arg Gly Tyr Val Gly Lys Thr Gln Ser	
1265 1270 1275	
GTT TTT AAA TTC AAT GCC AAG AAT GCG ATC AGT TTC ACC AAC AGC ACG	3891
Val Phe Lys Phe Asn Ala Lys Asn Ala Ile Ser Phe Thr Asn Ser Thr	
1280 1285 1290	
AAT TTA AGC TCT GGT TTG TAT CAA ATG CAA GCT AAA AGC GTG TTG TTT	3939
Asn Leu Ser Ser Gly Leu Tyr Gln Met Gln Ala Lys Ser Val Leu Phe	
1295 1300 1305	
GAC AAT TCC AAT TTA AGC GTT TCA GTG GGG ACA AGC AGT ATT AAA GCC	3987
Asp Asn Ser Asn Leu Ser Val Ser Val Gly Thr Ser Ser Ile Lys Ala	
1310 1315 1320	
AAT GCG ATC AAT CTT TCT CAA AAT GCC TCT ATT AAT GCG AGC AAC CAT	4035
Asn Ala Ile Asn Leu Ser Gln Asn Ala Ser Ile Asn Ala Ser Asn His	
1325 1330 1335 1340	
TCA ACC TTA GAA CTT CAA GGC GAT TTG AAT GTG AAC GAC ACC AGC TCG	4083
Ser Thr Leu Glu Leu Gln Gly Asp Leu Asn Val Asn Asp Thr Ser Ser	
1345 1350 1355	
CTC AAC CTC AAC CAA AGC ACG ATT AAT GTT TCC AAT AAC GCC ACG ATC	4131
Leu Asn Leu Asn Gln Ser Thr Ile Asn Val Ser Asn Asn Ala Thr Ile	
1360 1365 1370	

AAC ACG AGC GTG AAA GGG CAG GTT ACT TTA AAT AAC ATC ACT TTA AAA	2835
Asn Thr Ser Val Lys Gly Gln Val Thr Leu Asn Asn Ile Thr Leu Lys	
925 930 935 940	
AAC CTG AAC GCC CCT TTG TCT TTT GGC GAT GGG ACG ATT ACT TTT AAC	2883
Asn Leu Asn Ala Pro Leu Ser Phe Gly Asp Gly Thr Ile Thr Phe Asn	
945 950 955	
GCT CAT TCG GTG ATT AAT ATT GCT GAA TCT ATC ACT AAT GGC AAC CCT	2931
Ala His Ser Val Ile Asn Ile Ala Glu Ser Ile Thr Asn Gly Asn Pro	
960 965 970	
ATC ACT CTT GTA AGC TCT TCT AAA GAA ATT GAA TAC AAC AAC GCT TTC	2979
Ile Thr Leu Val Ser Ser Ser Lys Glu Ile Glu Tyr Asn Asn Ala Phe	
975 980 985	
AGT AAA AAT CTA TGG CAG CTC ATC AAC TAC CAA GGG CAT GGG GCA AGC	3027
Ser Lys Asn Leu Trp Gln Leu Ile Asn Tyr Gln Gly His Gly Ala Ser	
990 995 1000	
AGT GAA AAG CTC GTC TCT AGC GCG GGT AAT GGC GTT TAT GAT GTG GTG	3075
Ser Glu Lys Leu Val Ser Ser Ala Gly Asn Gly Val Tyr Asp Val Val	
1005 1010 1015 1020	
TAT TCT TTC AAT AAC CAA ACC TAC AAT TTC CAA GAG GTT TTT TCA CAA	3123
Tyr Ser Phe Asn Asn Gln Thr Tyr Asn Phe Gln Glu Val Phe Ser Gln	
1025 1030 1035	
AAC AGC ATT TCT ATC CGG CGT TTG GGC GTT AAC ATG GTG TTT GAT TAT	3171
Asn Ser Ile Ser Ile Arg Arg Leu Gly Val Asn Met Val Phe Asp Tyr	
1040 1045 1050	
GTG GAT ATG GAA AAA TCG GAT CAT TTA TAT TAT CAA AAC GCT CTC GGT	3219
Val Asp Met Glu Lys Ser Asp His Leu Tyr Tyr Gln Asn Ala Leu Gly	
1055 1060 1065	
TTT ATG ACC TAC ATG CCT AAT AGC TAT AAC AAT AAT TTA GGG AAT GCA	3267
Phe Met Thr Tyr Met Pro Asn Ser Tyr Asn Asn Asn Leu Gly Asn Ala	
1070 1075 1080	
AAC AAC ACC ATT TAC TAT TAC GAC AAG AGC ATT GAT TTT TAT GCG AGC	3315
Asn Asn Thr Ile Tyr Tyr Tyr Asp Lys Ser Ile Asp Phe Tyr Ala Ser	
1085 1090 1095 1100	
GGG AAA ACT CTA TTC ACT AAA GCG GAA TTT TCT CAA ACA TTC ACC GGG	3363
Gly Lys Thr Leu Phe Thr Lys Ala Glu Phe Ser Gln Thr Phe Thr Gly	
1105 1110 1115	
CAA AAC AGC GCG ATC GTT TTT GGG GCT AAA AGC ATA TGG ACG AGC TTA	3411
Gln Asn Ser Ala Ile Val Phe Gly Ala Lys Ser Ile Trp Thr Ser Leu	
1120 1125 1130	
AGC GAT GCA CCG CAG TCT AAC ACC ATC ATT CGC TTT GGG GAC AAT AAG	3459
Ser Asp Ala Pro Gln Ser Asn Thr Ile Ile Arg Phe Gly Asp Asn Lys	
1135 1140 1145	

TGC ACA GGC ACG ACT AAC GGC ACT TAT AGC GCC TAT CAT GTG TAT ATC Cys Thr Gly Thr Thr Asn Gly Thr Tyr Ser Ala Tyr His Val Tyr Ile 705 710 715	2163
ACA GCG AAT CTG CGT TCT GGC AAT CGT ATA GGC ACC GGT GGG GCA GCT Thr Ala Asn Leu Arg Ser Gly Asn Arg Ile Gly Thr Gly Gly Ala Ala 720 725 730	2211
AAT CTA ATC TTT AAT GGG GTA GAT AGT ATC AAT ATC GCT AAC GCT ACC Asn Leu Ile Phe Asn Gly Val Asp Ser Ile Asn Ile Ala Asn Ala Thr 735 740 745	2259
ATC ACG CAA CAT AAC GCC GGA ATC TAT TCA AGC TCT ATG ACT TTT TCC Ile Thr Gln His Asn Ala Gly Ile Tyr Ser Ser Ser Met Thr Phe Ser 750 755 760	2307
ACG CAA AGC ATG GAT AAT TCG CAG AAT TTG AAT GGT CTA AAT TCT AAC Thr Gln Ser Met Asp Asn Ser Gln Asn Leu Asn Gly Leu Asn Ser Asn 765 770 775 780	2355
GGC AAA CTT TCG GTG TAT GGC ACC ACT TTC ACT AAC GAA GCT AAA GAT Gly Lys Leu Ser Val Tyr Gly Thr Thr Phe Thr Asn Glu Ala Lys Asp 785 790 795	2403
GGG AAA TTC ATT TTC AAT GCA GGG CAA GCG GTT TTT GAA AAC ACC AAC Gly Lys Phe Ile Phe Asn Ala Gly Gln Ala Val Phe Glu Asn Thr Asn 800 805 810	2451
TTT AAT GGA GGG AGT TAC CAA TTC AGC GGC GAT AGC TTG AAT TTT TCA Phe Asn Gly Gly Ser Tyr Gln Phe Ser Gly Asp Ser Leu Asn Phe Ser 815 820 825	2499
AAC AAC AAC CAG TTC AAT AGC GGT TCG TTT GAA ATT AGC GCA AAA AAC Asn Asn Asn Gln Phe Asn Ser Gly Ser Phe Glu Ile Ser Ala Lys Asn 830 835 840	2547
GCT TCG TTC AAT AAC GCT AAC TTT AAC AAC AGC GCT TCT TTT AAT TTC Ala Ser Phe Asn Asn Ala Asn Phe Asn Asn Ser Ala Ser Phe Asn Phe 845 850 855 860	2595
AAT AAT TCT AAC GCG ACC ACT TCG TTT GTG GGG GAT TTC ACT AAC GCT Asn Asn Ser Asn Ala Thr Thr Ser Phe Val Gly Asp Phe Thr Asn Ala 865 870 875	2643
AAT TCA AAT TTG CAA ATC GCC GGG AAC GCT GTT TTT GGG AAC TCT ACT Asn Ser Asn Leu Gln Ile Ala Gly Asn Ala Val Phe Gly Asn Ser Thr 880 885 890	2691
AAT GGC TCT CAA AAT ACC GCT AAT TTT AAT AAT ACC GGC TCT GTT AAT Asn Gly Ser Gln Asn Thr Ala Asn Phe Asn Asn Thr Gly Ser Val Asn 895 900 905	2739
ATT TCA GGG AAT GCA ACC TTT GAT AAT GTG GTG TTT AAT GGC CCT ACG Ile Ser Gly Asn Ala Thr Phe Asp Asn Val Val Phe Asn Gly Pro Thr 910 915 920	2787

GTA ACG ATT TTA AAT TCT AGC GGT GGG ATC ACT TAT AGT AAC CTT TTA	1491
Val Thr Ile Leu Asn Ser Ser Gly Gly Ile Thr Tyr Ser Asn Leu Leu	
480 485 490	
AAC CAT GCA ATC AAC GGC TTG ACA AGT GCC TTA AAA ACG AAC GAA AGC	1539
Asn His Ala Ile Asn Gly Leu Thr Ser Ala Leu Lys Thr Asn Glu Ser	
495 500 505	
CTT TCA AAT CCG CAA AGT TTC GCT CAA GGT TTG TGG GAT ATA ATC ACT	1587
Leu Ser Asn Pro Gln Ser Phe Ala Gln Gly Leu Trp Asp Ile Ile Thr	
510 515 520	
TAC AAT GGG GTT ACC GGG CAG CTT TTG AAT GAA AAC GCT GCA ACA TCT	1635
Tyr Asn Gly Val Thr Gly Gln Leu Leu Asn Glu Asn Ala Ala Thr Ser	
525 530 535 540	
AAA CCC ACT GAC TCT TCG CCC TCT AAA TCC TCT ACA AAC TCT ACG CAA	1683
Lys Pro Thr Asp Ser Ser Pro Ser Lys Ser Ser Thr Asn Ser Thr Gln	
545 550 555	
GTC TAT CAA GTG GGT TAC AAA ATA GGG GAT ACT ATC TAC AAA CTG CAA	1731
Val Tyr Gln Val Gly Tyr Lys Ile Gly Asp Thr Ile Tyr Lys Leu Gln	
560 565 570	
GAA ACT TTC AGC CAC AAT TCC ATT ATT ATT CAG GCT TTA GAG AGC GGG	1779
Glu Thr Phe Ser His Asn Ser Ile Ile Ile Gln Ala Leu Glu Ser Gly	
575 580 585	
ACT TAC ACG CCA CCC CCT GTC ATT AAC GGC TCC AAA TTT GAC TTA TCC	1827
Thr Tyr Thr Pro Pro Pro Val Ile Asn Gly Ser Lys Phe Asp Leu Ser	
590 595 600	
GCT TCA AAT TAT ATC AAT GCT GAC ATG CCT TGG TAT GAC CAT AAA TAT	1875
Ala Ser Asn Tyr Ile Asn Ala Asp Met Pro Trp Tyr Asp His Lys Tyr	
605 610 615 620	
TAC ATC CCT AAA TCC CAA AAT TTT ACA GAG AGC GGG ACT TAT TAC TTG	1923
Tyr Ile Pro Lys Ser Gln Asn Phe Thr Glu Ser Gly Thr Tyr Tyr Leu	
625 630 635	
CCG AGC GTC CAA ATA TGG GGG AGC TAC ACT AAC TCG TTT AAA CAA ACT	1971
Pro Ser Val Gln Ile Trp Gly Ser Tyr Thr Asn Ser Phe Lys Gln Thr	
640 645 650	
TTT AGC GCA AAT GGT AGT AAT CTG GTG ATT GGG TAT AAC TCA ACA TGG	2019
Phe Ser Ala Asn Gly Ser Asn Leu Val Ile Gly Tyr Asn Ser Thr Trp	
655 660 665	
ACT GAT CAT AAT GTC TCT TCT AGC GGC ACG GTG TCT TTT GGG GAC ACT	2067
Thr Asp His Asn Val Ser Ser Ser Gly Thr Val Ser Phe Gly Asp Thr	
670 675 680	
TCA GGG AGC GCT CTT AAT GGG CAT TGC GGA CCT TGG CCG TAT TAC CAA	2115
Ser Gly Ser Ala Leu Asn Gly His Cys Gly Pro Trp Pro Tyr Tyr Gln	
685 690 695 700	

TCT	TTT	AAA	GGG	ACG	ACT	AAC	GCT	ACT	AAC	ACG	GCG	TTT	AGT	AAT	GCA	819
Ser	Phe	Lys	Gly	Thr	Thr	Asn	Ala	Thr	Asn	Thr	Ala	Phe	Ser	Asn	Ala	
		255					260					265				
AGC	GGC	AGT	TTC	ACT	TTT	GAA	GAG	AAC	GCC	ACT	TTT	AGC	GGG	GCG	AAA	867
Ser	Gly	Ser	Phe	Thr	Phe	Glu	Glu	Asn	Ala	Thr	Phe	Ser	Gly	Ala	Lys	
	270					275					280					
TGG	AAT	GGG	GGG	ACT	TAT	ACC	TTT	AAT	AAA	GAG	TTT	AGC	GCT	ACC	AAT	915
Trp	Asn	Gly	Gly	Thr	Tyr	Thr	Phe	Asn	Lys	Glu	Phe	Ser	Ala	Thr	Asn	
285					290					295					300	
AAC	ACC	GCC	TTT	AGT	AGC	GGT	AGT	TTT	AAT	TTT	AAA	GGT	GTA	AGC	TCT	963
Asn	Thr	Ala	Phe	Ser	Ser	Gly	Ser	Phe	Asn	Phe	Lys	Gly	Val	Ser	Ser	
				305					310					315		
TTT	AAT	GGT	ACT	TCG	TTT	AGT	AAC	GCT	TCT	TAT	ACT	TTT	GAC	AAT	CAA	1011
Phe	Asn	Gly	Thr	Ser	Phe	Ser	Asn	Ala	Ser	Tyr	Thr	Phe	Asp	Asn	Gln	
			320					325					330			
GCC	ACT	TTC	CAA	AAC	AGC	TCC	TTT	AAT	GGG	GGG	ACT	TTT	ACT	TTT	AAT	1059
Ala	Thr	Phe	Gln	Asn	Ser	Ser	Phe	Asn	Gly	Gly	Thr	Phe	Thr	Phe	Asn	
		335					340					345				
AAC	CAA	ACT	AAT	CCA	ACT	AAC	AAC	GCT	CAG	CAC	CCC	CAA	ATT	CAA	AAC	1107
Asn	Gln	Thr	Asn	Pro	Thr	Asn	Asn	Ala	Gln	His	Pro	Gln	Ile	Gln	Asn	
	350					355					360					
AGC	TCT	TTT	AGT	GGT	AAC	GCT	ACC	ACT	CTT	AAG	GGC	TTT	GTG	AAT	TTC	1155
Ser	Ser	Phe	Ser	Gly	Asn	Ala	Thr	Thr	Leu	Lys	Gly	Phe	Val	Asn	Phe	
365					370					375					380	
CAG	CAA	GCC	TTT	AAC	AAT	TCA	AAC	CAC	CAA	CTA	ACG	ATC	CAA	AAC	GCT	1203
Gln	Gln	Ala	Phe	Asn	Asn	Ser	Asn	His	Gln	Leu	Thr	Ile	Gln	Asn	Ala	
				385					390					395		
TCC	TTT	AAT	AAC	GCC	ACT	TTT	AAC	AAT	ACC	GGT	AAA	ATC	ACT	ATA	GAA	1251
Ser	Phe	Asn	Asn	Ala	Thr	Phe	Asn	Asn	Thr	Gly	Lys	Ile	Thr	Ile	Glu	
				400				405					410			
AAA	GAT	GCG	AGT	TTT	AAT	AAC	ACG	ACA	TTC	AAC	ACT	TCT	GTT	GAT	ACA	1299
Lys	Asp	Ala	Ser	Phe	Asn	Asn	Thr	Thr	Phe	Asn	Thr	Ser	Val	Asp	Thr	
		415					420					425				
AAC	AAC	ATG	AGT	GTT	ACC	GGT	GGC	GTT	ACT	TTA	AGC	GGT	AAA	AAT	GAC	1347
Asn	Asn	Met	Ser	Val	Thr	Gly	Gly	Val	Thr	Leu	Ser	Gly	Lys	Asn	Asp	
	430					435					440					
TTG	AAA	AAT	GGC	TCA	ACC	CTT	GAT	TTT	GGG	AGT	TCT	AAA	ATC	ACT	CTC	1395
Leu	Lys	Asn	Gly	Ser	Thr	Leu	Asp	Phe	Gly	Ser	Ser	Lys	Ile	Thr	Leu	
445					450					455					460	
GCT	CAA	GGG	ACG	ACT	TTC	AAC	CTC	ACA	AGT	TTA	GGC	AGT	GAG	AAG	AGC	1443
Ala	Gln	Gly	Thr	Thr	Phe	Asn	Leu	Thr	Ser	Leu	Gly	Ser	Glu	Lys	Ser	
				465					470					475		

ATG CCT TTA CTC ATC AGC GGG TTT GCT AGT GGG GTG TAT GCG AAT AAT	147
Met Pro Leu Leu Ile Ser Gly Phe Ala Ser Gly Val Tyr Ala Asn Asn	
30 35 40	
CTG TGG GAT TTG TTA AAC CCA AAA GTG GGG GGT GAG TAT GTG CAT TGG	195
Leu Trp Asp Leu Leu Asn Pro Lys Val Gly Gly Glu Tyr Val His Trp	
45 50 55 60	
GTT AAG GGC AGT CAG TAT TGT GCA TGG TGG GAA TTT GCT GGG TGT TTA	243
Val Lys Gly Ser Gln Tyr Cys Ala Trp Trp Glu Phe Ala Gly Cys Leu	
65 70 75	
AAG AAT GTA TGG GGG GCA AAT CAT AAA GGC TAT GAT GCT GGA AAC GCC	291
Lys Asn Val Trp Gly Ala Asn His Lys Gly Tyr Asp Ala Gly Asn Ala	
80 85 90	
GCT AAC TAT TTG TCT TCT CAA AAC TAT CAA GCT ATT TCG GTG GGT AGT	339
Ala Asn Tyr Leu Ser Ser Gln Asn Tyr Gln Ala Ile Ser Val Gly Ser	
95 100 105	
GGG AAT GAA ACG GGG ACT TAT AGT TTA AGC GGT TTT ACC AAT TAT GTT	387
Gly Asn Glu Thr Gly Thr Tyr Ser Leu Ser Gly Phe Thr Asn Tyr Val	
110 115 120	
GGG GGC AAT CTC ACG ATC AAT CTA GGC AAT AGC GTT GTT TTA GAT TTA	435
Gly Gly Asn Leu Thr Ile Asn Leu Gly Asn Ser Val Val Leu Asp Leu	
125 130 135 140	
AGC GGT TCT AAT AGT TTC ACT TCG TAT CAA GGT TAT AAT CAA GGC AAA	483
Ser Gly Ser Asn Ser Phe Thr Ser Tyr Gln Gly Tyr Asn Gln Gly Lys	
145 150 155	
GAT GAT GTA ACA TTT ACG GTT GGC GCA ATC AAT TTA AAC GGC ACT TTA	531
Asp Asp Val Thr Phe Thr Val Gly Ala Ile Asn Leu Asn Gly Thr Leu	
160 165 170	
GAA GTG GGT AAT CGT GTG GGA TCG GGA GCT GGC ACG CAC ACC GGC ACA	579
Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly Thr His Thr Gly Thr	
175 180 185	
GCC ACT TTA AAC TTG AAC GCT AAT AAG GTC AAT ATC AAT TCC AAT ATC	627
Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Asn Ile Asn Ser Asn Ile	
190 195 200	
AAC GCG TAT AAA ACT TCG CAA GTG AAT ATA GGC AAC GCT AAC AGC GTT	675
Asn Ala Tyr Lys Thr Ser Gln Val Asn Ile Gly Asn Ala Asn Ser Val	
205 210 215 220	
ATT ACC ATT GGT TCG GTT TCT TTG AGT GGG GAT GTT TGC AGT TCT TTA	723
Ile Thr Ile Gly Ser Val Ser Leu Ser Gly Asp Val Cys Ser Ser Leu	
225 230 235	
GCT AGC GTT GGG ATA GGG GCT AAT TGC TCC ACT TCT GGG CCT AGC TAT	771
Ala Ser Val Gly Ile Gly Ala Asn Cys Ser Thr Ser Gly Pro Ser Tyr	
240 245 250	

130	135	140															
Leu	Asn	Lys	Glu	Gly	Gln	Ala	Ile	Thr	Leu	Cys	Met	His	Phe	Gly	Tyr		
145					150					155					160		
Trp	Glu	Ala	Val	Gly	Thr	Thr	Leu	Ala	Gln	Tyr	Tyr	Glu	Asn	Tyr	Gly		
				165					170						175		
Arg	Gly	Cys	Leu	Gly	Arg	Leu	Thr	Lys	Phe	Ala	Pro	Ile	Asn	His	Met		
			180					185					190				
Ile	Met	Ser	Arg	Arg	Glu	Ala	Phe	Gly	Val	Arg	Phe	Val	Asn	Lys	Ile		
		195					200				205						
Gly	Ala	Met	Lys	Glu	Leu	Ile	Lys	Met	Tyr	Asn	Gln	Gly	Asn	Gly	Leu		
	210					215					220						
Val	Gly	Ile	Leu	Val	Asp	Gln	Asn	Val	Val	Pro	Lys	Asp	Gly	Val	Val		
225					230					235					240		
Val	Lys	Phe	Phe	Asp	Arg	Asp	Ala	Thr	His	Thr	Thr	Ile	Ala	Ser	Ile		
			245					250						255			
Leu	Ser	Arg	Arg	Tyr	Asn	Ile	Asp	Ile	Gln	Pro	Val	Phe	Ile	Asp	Phe		
			260				265					270					
Asn	Asp	Asp	Tyr	Ser	His	Tyr	Thr	Ala	Thr	Tyr	Tyr	Pro	Ser	Ile	Arg		
	275					280					285						
Ser	Gln	Ile	Thr	Asp	Asn	Ala	Gln	Asn	Asp	Ile	Leu	Glu	Cys	Thr	Gln		
	290				295					300							
Ala	Gln	Ala	Ser	Leu	Cys	Glu	Glu	Val	Ile	Arg	Asn	His	Pro	Glu	Ser		
305				310					315						320		
Tyr	Phe	Trp	Phe	His	Arg	Arg	Phe	Lys	Ser	Thr	His	Pro	Glu	Ile	Tyr		
			325					330						335			
Gln	Arg																

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...8694
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

AGAGGGTAGC	ATTTA	ATG	AAA	AAG	TTT	AAA	AAG	AAA	CCA	AAA	AGT	ATC	AAA	51		
	Met	Lys	Lys	Phe	Lys	Lys	Lys	Pro	Lys	Ser	Ile	Lys				
	1				5						10					
CGA	TCG	CAT	CAA	AAT	CAA	AAA	ACA	ATC	TTA	AAG	CGT	CCT	TTA	TGG	CTT	99
Arg	Ser	His	Gln	Asn	Gln	Lys	Thr	Ile	Leu	Lys	Arg	Pro	Leu	Trp	Leu	
	15					20					25					


```

TTG TCG CGC CGT TAT AAT ATA GAT ATT CAG CCG GTA TTC ATT GAT TTT      875
Leu Ser Arg Arg Tyr Asn Ile Asp Ile Gln Pro Val Phe Ile Asp Phe
                260                      265                      270

AAT GAC GAT TAT TCG CAT TAT ACA GCG ACC TAT TAT CCG AGT ATC CGC      923
Asn Asp Asp Tyr Ser His Tyr Thr Ala Thr Tyr Tyr Pro Ser Ile Arg
                275                      280                      285

TCT CAA ATC ACC GAT AAC GCG CAA AAC GAT ATT TTA GAA TGC ACG CAA      971
Ser Gln Ile Thr Asp Asn Ala Gln Asn Asp Ile Leu Glu Cys Thr Gln
                290                      295                      300

GCC CAA GCG AGT TTG TGC GAA GAG GTG ATT AGA AAC CAC CCG GAA AGT      1019
Ala Gln Ala Ser Leu Cys Glu Glu Val Ile Arg Asn His Pro Glu Ser
305                      310                      315                      320

TAT TTT TGG TTC CAT AGG CGT TTT AAA AGC ACC CAC CCT GAG ATT TAT      1067
Tyr Phe Trp Phe His Arg Arg Phe Lys Ser Thr His Pro Glu Ile Tyr
                325                      330                      335

CAA AGA TAGGGTTTTG TTTTAATCAA AAATTAAAAA CTAAAGCCTT ATTTTAAAGA AAA  1126
Gln Arg

CTTT                                                                    1130

```

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

```

Met Arg Phe Lys His Leu Lys Gly Lys Arg Met Thr Tyr Lys Glu Arg
 1          5          10          15
Leu Ile His Glu Lys Ile Leu Lys Gln Asp Asp Lys Gly Phe Lys Thr
          20          25          30
Glu Leu Arg Ile Leu Ser Ile Phe Ile Val Glu Ser Leu Val Asn Ile
          35          40          45
Leu Gly Phe Ile Leu Ala Lys Met Pro His Ser Trp Phe Leu Arg Cys
          50          55          60
Ile Lys Ala Val Ala Trp Leu Met Lys Thr Phe Asp Lys Cys Arg Tyr
          65          70          75          80
Phe Asp Ala Lys Ala Asn Leu Asp Phe Val Phe Gly Asp Ser Lys Ser
          85          90          95
Glu Glu Glu Lys Lys Arg Ile Ile Lys Lys Gly Tyr Glu Asn Phe Ala
          100          105          110
Phe Ile Ile Leu Glu Thr Ile Arg Val Ile Phe Ile Pro Lys Asp Glu
          115          120          125
Tyr Asp Ala Arg Phe Thr Leu Ile Asn Glu Glu Asn Val Trp Lys Ser

```

GAA CTG CGC ATT TTG AGT ATT TTT ATC GTG GAA TCT TTA GTG AAT ATT Glu Leu Arg Ile Leu Ser Ile Phe Ile Val Glu Ser Leu Val Asn Ile 35 40 45	203
TTG GGG TTT ATT TTA GCT AAA ATG CCC CAT TCG TGG TTT TTA AGG TGC Leu Gly Phe Ile Leu Ala Lys Met Pro His Ser Trp Phe Leu Arg Cys 50 55 60	251
ATT AAA GCG GTG GCG TGG CTC ATG AAA ACT TTT GAT AAG TGC CGT TAT Ile Lys Ala Val Ala Trp Leu Met Lys Thr Phe Asp Lys Cys Arg Tyr 65 70 75 80	299
TTT GAC GCT AAG GCC AAT TTG GAT TTT GTG TTT GGG GAT TCT AAA AGC Phe Asp Ala Lys Ala Asn Leu Asp Phe Val Phe Gly Asp Ser Lys Ser 85 90 95	347
GAA GAA GAG AAA AAA AGG ATC ATT AAA AAG GGT TAT GAA AAT TTT GCT Glu Glu Glu Lys Lys Arg Ile Ile Lys Lys Gly Tyr Glu Asn Phe Ala 100 105 110	395
TTC ATT ATT TTA GAA ACT ATT AGA GTG ATC TTT ATC CCT AAA GAT GAA Phe Ile Ile Leu Glu Thr Ile Arg Val Ile Phe Ile Pro Lys Asp Glu 115 120 125	443
TAC GAC GCT CGT TTC ACG CTC ATC AAT GAA GAA AAT GTG TGG AAA TCT Tyr Asp Ala Arg Phe Thr Leu Ile Asn Glu Glu Asn Val Trp Lys Ser 130 135 140	491
TTA AAC AAG GAA GGC CAA GCG ATC ACT TTA TGC ATG CAT TTT GGC TAT Leu Asn Lys Glu Gly Gln Ala Ile Thr Leu Cys Met His Phe Gly Tyr 145 150 155 160	539
TGG GAA GCG GTA GGC ACG ACT TTA GCG CAA TAT TAT GAA AAT TAT GGT Trp Glu Ala Val Gly Thr Thr Leu Ala Gln Tyr Tyr Glu Asn Tyr Gly 165 170 175	587
AGG GGG TGT TTG GGG CGT TTG ACT AAA TTT GCC CCT ATC AAT CAC ATG Arg Gly Cys Leu Gly Arg Leu Thr Lys Phe Ala Pro Ile Asn His Met 180 185 190	635
ATT ATG AGT AGG CGA GAG GCG TTT GGG GTG CGT TTT GTC AAT AAA ATA Ile Met Ser Arg Arg Glu Ala Phe Gly Val Arg Phe Val Asn Lys Ile 195 200 205	683
GGG GCG ATG AAA GAA CTC ATT AAA ATG TAT AAT CAA GGC AAT GGT CTG Gly Ala Met Lys Glu Leu Ile Lys Met Tyr Asn Gln Gly Asn Gly Leu 210 215 220	731
GTG GGG ATT TTA GTG GAT CAA AAT GTC GTG CCT AAA GAT GGG GTG GTG Val Gly Ile Leu Val Asp Gln Asn Val Val Pro Lys Asp Gly Val Val 225 230 235 240	779
GTG AAA TTC TTT GAT AGA GAC GCT ACG CAC ACC ACG ATC GCT TCT ATT Val Lys Phe Phe Asp Arg Asp Ala Thr His Thr Thr Ile Ala Ser Ile 245 250 255	827

```

Pro Asn Ile Asn Pro Ser Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro
305          310          315          320
His Glu Lys His Ser Gln Lys Val Lys Lys Glu Cys Val Lys Leu Phe
          325          330          335
Glu Ala Leu Ser Pro Leu His Lys Ile Asp Glu Lys Tyr Leu Phe His
          340          345          350
Leu Lys Ile Ala Gly Glu Leu Ala Ser Met Gly Lys Ile Leu Ser Val
          355          360          365
Tyr Leu Ala His Lys His Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser
          370          375          380
Tyr Gly Phe Ser His Gln Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln
385          390          395          400
Phe Ser His Lys Lys Ile Pro Lys Asp Asn Ala Ile Ala His Met Ser
          405          410          415
Ala Met Met Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe Ile Leu
          420          425          430
Ser Leu Ala Glu Asn Leu Cys Leu Thr Asp Ser His His Leu Lys Tyr
          435          440          445
Thr Leu Glu Lys Asn Lys Leu Val Ile His Ser Asn Asp Thr Leu Tyr
          450          455          460
Leu Ala Lys Glu Met Leu Pro Lys Leu Val Lys Pro Ile Pro Leu Thr
465          470          475          480
Ile Glu Phe Ala

```

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...1073
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

```

GCCAACTACC ATAAAAAGGA TTTTCTATC CAAAATATAG AGCCTAAAAA AATTAAAGA      59

ATG CGT TTT AAA CAT CTT AAA GGA AAA AGA ATG ACT TAC AAA GAA CGA      107
Met Arg Phe Lys His Leu Lys Gly Lys Arg Met Thr Tyr Lys Glu Arg
  1          5          10          15

CTC ATA CAC GAA AAA ATA TTG AAA CAA GAC GAC AAG GGT TTT AAA ACA      155
Leu Ile His Glu Lys Ile Leu Lys Gln Asp Asp Lys Gly Phe Lys Thr
          20          25          30

```

GCT TGAAAATAGC GATTGTCAGG CTTTCAGCG
Ala

1530

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

```

Met Ala Lys Ile Thr Thr Val Ile Asp Ile Gly Ser Asn Ser Val Arg
 1           5           10           15
Leu Ala Val Phe Lys Lys Thr Ser Gln Phe Gly Phe Tyr Leu Leu Phe
          20           25           30
Glu Thr Lys Ser Lys Val Arg Ile Ser Glu Gly Cys Tyr Ala Phe Asn
      35           40           45
Gly Ile Leu Gln Glu Ile Pro Met Gln Arg Ala Val Lys Ala Leu Ser
      50           55           60
Glu Phe Lys Glu Ile Ala Leu Lys Tyr Lys Ser Lys Lys Ile Leu Cys
65           70           75           80
Val Ala Thr Ser Ala Val Arg Asp Ala Pro Asn Arg Leu Glu Phe Val
          85           90           95
Ala Arg Val Lys Lys Ala Cys Gly Leu Gln Ile Lys Ile Ile Asp Gly
          100          105          110
Gln Lys Glu Ala Leu Tyr Gly Gly Ile Ala Cys Ala Asn Leu Leu His
          115          120          125
Lys Asn Ser Gly Ile Thr Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys
          130          135          140
Ala Leu Ile Glu Lys Gly Lys Ile Lys Asp Leu Ile Ser Leu Asp Val
145          150          155          160
Gly Thr Ile Arg Ile Lys Glu Met Phe Leu Asp Lys Asp Leu Glu Val
          165          170          175
Lys Leu Ala Lys Ala Phe Ile Gln Lys Glu Val Ser Lys Leu Pro Phe
          180          185          190
Lys His Lys Asn Ala Phe Gly Val Gly Gly Thr Ile Arg Ala Leu Ser
          195          200          205
Lys Val Leu Met Lys Arg Phe Cys Tyr Pro Ile Asp Ser Leu His Gly
          210          215          220
Tyr Glu Ile Asp Ala His Lys Asn Leu Ala Phe Ile Glu Lys Ile Val
225          230          235          240
Met Leu Lys Glu Asp Gln Leu Arg Leu Leu Gly Val Asn Glu Glu Arg
          245          250          255
Leu Asp Ser Ile Arg Ser Gly Ala Leu Ile Leu Ser Val Val Leu Glu
          260          265          270
His Leu Lys Thr Ser Leu Met Ile Thr Ser Gly Val Gly Val Arg Glu
          275          280          285
Gly Val Phe Leu Ser Asp Leu Leu Arg His His Tyr His Lys Phe Pro
290          295          300

```

ATC AGG AGC GGG GCG TTG ATT TTA TCA GTC GTT TTG GAG CAT TTA AAA	874
Ile Arg Ser Gly Ala Leu Ile Leu Ser Val Val Leu Glu His Leu Lys	
260 265 270 275	
ACT TCT TTA ATG ATC ACT AGT GGG GTG GGG GTG AGA GAA GGC GTG TTT	922
Thr Ser Leu Met Ile Thr Ser Gly Val Gly Val Arg Glu Gly Val Phe	
280 285 290	
TTG AGC GAT TTA TTG CGC CAT CAT TAC CAT AAA TTC CCC CCC AAT ATC	970
Leu Ser Asp Leu Leu Arg His His Tyr His Lys Phe Pro Pro Asn Ile	
295 300 305	
AAC CCC TCT CTC ATC TCT TTA AAA GAT CGC TTT TTG CCC CAT GAA AAG	1018
Asn Pro Ser Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro His Glu Lys	
310 315 320	
CAC AGC CAA AAG GTC AAA AAA GAA TGC GTG AAA TTG TTT GAA GCC TTA	1066
His Ser Gln Lys Val Lys Lys Glu Cys Val Lys Leu Phe Glu Ala Leu	
325 330 335	
TCG CCT TTG CAT AAA ATA GAT GAA AAA TAC CTT TTC CAT TTA AAG ATT	1114
Ser Pro Leu His Lys Ile Asp Glu Lys Tyr Leu Phe His Leu Lys Ile	
340 345 350 355	
GCG GGG GAA TTA GCG AGC ATG GGT AAG ATT TTA AGC GTC TAT TTA GCC	1162
Ala Gly Glu Leu Ala Ser Met Gly Lys Ile Leu Ser Val Tyr Leu Ala	
360 365 370	
CAC AAG CAC AGC GCG TAT TTT ATT TTA AAC GCT TTG AGT TAT GGC TTT	1210
His Lys His Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser Tyr Gly Phe	
375 380 385	
AGC CAC CAG GAT AGA GCG ATC ATT TGC TTA TTA GCC CAA TTC AGC CAT	1258
Ser His Gln Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln Phe Ser His	
390 395 400	
AAA AAA ATC CCT AAA GAC AAC GCT ATC GCC CAC ATG AGC GCG ATG ATG	1306
Lys Lys Ile Pro Lys Asp Asn Ala Ile Ala His Met Ser Ala Met Met	
405 410 415	
CCA AGC CTT TTA ACC TTA CAA TGG CTG AGT TTT ATC CTT TCT TTA GCC	1354
Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe Ile Leu Ser Leu Ala	
420 425 430 435	
GAA AAT TTG TGC CTA ACA GAC AGC CAT CAT TTA AAA TAC ACG CTA GAA	1402
Glu Asn Leu Cys Leu Thr Asp Ser His His Leu Lys Tyr Thr Leu Glu	
440 445 450	
AAA AAC AAG CTT GTG ATC CAT TCT AAT GAC ACG CTT TAC TTG GCT AAA	1450
Lys Asn Lys Leu Val Ile His Ser Asn Asp Thr Leu Tyr Leu Ala Lys	
455 460 465	
GAA ATG CTC CCC AAA CTC GTT AAG CCC ATT CCT TTG ACG ATA GAG TTT	1498
Glu Met Leu Pro Lys Leu Val Lys Pro Ile Pro Leu Thr Ile Glu Phe	
470 475 480	

TCT AAG GTT AGG ATT TCA GAG GGC TGT TAT GCG TTT AAT GGA ATC TTG	202
Ser Lys Val Arg Ile Ser Glu Gly Cys Tyr Ala Phe Asn Gly Ile Leu	
40 45 50	
CAA GAA ATC CCC ATG CAA CGA GCC GTT AAA GCC TTG AGC GAA TTT AAA	250
Gln Glu Ile Pro Met Gln Arg Ala Val Lys Ala Leu Ser Glu Phe Lys	
55 60 65	
GAA ATC GCT CTC AAA TAC AAA AGC AAA AAA ATC CTG TGC GTG GCG ACC	298
Glu Ile Ala Leu Lys Tyr Lys Ser Lys Lys Ile Leu Cys Val Ala Thr	
70 75 80	
TCA GCG GTG CGC GAT GCC CCT AAT CGG CTG GAG TTT GTA GCG AGG GTG	346
Ser Ala Val Arg Asp Ala Pro Asn Arg Leu Glu Phe Val Ala Arg Val	
85 90 95	
AAA AAG GCT TGC GGT TTG CAA ATC AAA ATC ATT GAT GGG CAA AAA GAA	394
Lys Lys Ala Cys Gly Leu Gln Ile Lys Ile Ile Asp Gly Gln Lys Glu	
100 105 110 115	
GCG CTC TAT GGC GGG ATT GCG TGC GCG AAT TTG TTG CAT AAA AAT TCA	442
Ala Leu Tyr Gly Gly Ile Ala Cys Ala Asn Leu Leu His Lys Asn Ser	
120 125 130	
GGG ATC ACG ATA GAT ATT GGA GGG GGT AGC ACC GAG TGC GCG TTG ATT	490
Gly Ile Thr Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys Ala Leu Ile	
135 140 145	
GAA AAA GGC AAG ATT AAG GAC TTA ATC TCG CTT GAT GTT GGG ACG ATT	538
Glu Lys Gly Lys Ile Lys Asp Leu Ile Ser Leu Asp Val Gly Thr Ile	
150 155 160	
CGC ATT AAA GAA ATG TTT TTA GAC AAA GAC TTA GAG GTC AAA TTG GCT	586
Arg Ile Lys Glu Met Phe Leu Asp Lys Asp Leu Glu Val Lys Leu Ala	
165 170 175	
AAA GCC TTT ATC CAA AAA GAA GTC TCT AAA CTG CCC TTT AAA CAC AAA	634
Lys Ala Phe Ile Gln Lys Glu Val Ser Lys Leu Pro Phe Lys His Lys	
180 185 190 195	
AAC GCC TTT GGG GTG GGG GGG ACG ATC AGA GCG TTG AGT AAG GTA TTG	682
Asn Ala Phe Gly Val Gly Gly Thr Ile Arg Ala Leu Ser Lys Val Leu	
200 205 210	
ATG AAA CGC TTT TGT TAC CCT ATT GAT TCT TTG CAT GGC TAT GAA ATA	730
Met Lys Arg Phe Cys Tyr Pro Ile Asp Ser Leu His Gly Tyr Glu Ile	
215 220 225	
GAT GCA CAT AAA AAT TTA GCG TTC ATT GAA AAA ATC GTC ATG CTC AAA	778
Asp Ala His Lys Asn Leu Ala Phe Ile Glu Lys Ile Val Met Leu Lys	
230 235 240	
GAA GAT CAA TTA CGG CTT TTA GGG GTG AAT GAA GAG CGT TTG GAT AGC	826
Glu Asp Gln Leu Arg Leu Leu Gly Val Asn Glu Glu Arg Leu Asp Ser	
245 250 255	

```

Pro Lys Val Cys Lys Ser Ile His Met Pro Leu Gln Ser Gly Ser Ser
                245                250                255
Ala Val Leu Lys Met Met Arg Arg Gly Tyr Ser Lys Glu Trp Phe Leu
                260                265                270
Asn Arg Val Glu Arg Leu Lys Ala Leu Val Pro Glu Val Gly Ile Ser
                275                280                285
Thr Asp Ile Ile Val Gly Phe Pro Asn Glu Ser Asp Lys Asp Phe Glu
                290                295                300
Asp Thr Met Glu Val Leu Glu Lys Val Arg Phe Asp Thr Leu Tyr Ser
305                310                315                320
Phe Ile Tyr Ser Pro Arg Pro Phe Thr Glu Ala Gly Ala Trp Lys Glu
                325                330                335
Arg Val Pro Leu Glu Val Ser Ser Ser Arg Leu Glu Arg Leu Gln Asn
                340                345                350
Arg His Lys Glu Ile Leu Glu Glu Lys Ala Lys Leu Glu Val Gly Lys
                355                360                365
Thr His Val Val Leu Val Glu Asn Arg Arg Glu Met Asp Asn Gln Ile
                370                375                380
Val Gly Phe Glu Gly Arg Ser Asp Thr Gly Lys Phe Ile Glu Val Thr
385                390                395                400
Cys Lys Glu Lys Arg Asn Pro Gly Glu Leu Val Lys Val Glu Ile Ile
                405                410                415
Ser His Ser Lys Gly Arg Leu Met Ala Ala Thr Lys Gly Asn
                420                425                430

```

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...1501
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

```

ATTGAAATAC AAATACGAAA GCTTAAAAGA GCAAGATTAA AGGCTAGCA ATG GCT AAA      58
                                     Met Ala Lys
                                     1

ATC ACA ACC GTG ATT GAT ATA GGC TCT AAT TCA GTG CGT TTG GCT GTC      106
Ile Thr Thr Val Ile Asp Ile Gly Ser Asn Ser Val Arg Leu Ala Val
    5                10                15

TTT AAA AAG ACG AGC CAG TTT GGG TTT TAC TTG CTT TTT GAG ACT AAG      154
Phe Lys Lys Thr Ser Gln Phe Gly Phe Tyr Leu Leu Phe Glu Thr Lys
20                25                30                35

```

```

ACG GGG AAA TTC ATT GAA GTA ACT TGT AAG GAA AAA AGA AAC CCG GGC      1254
Thr Gly Lys Phe Ile Glu Val Thr Cys Lys Glu Lys Arg Asn Pro Gly
      395              400              405

GAG CTT GTA AAA GTG GAG ATT ATT TCT CAT TCC AAA GGG CGC TTG ATG      1302
Glu Leu Val Lys Val Glu Ile Ile Ser His Ser Lys Gly Arg Leu Met
      410              415              420

GCG GCC ACT AAA GGC AAC TAATAAAAAAT AACCAATGAA AAAGCGGGTT TAAAGG      1356
Ala Ala Thr Lys Gly Asn
425              430

```

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

```

Met Gly Cys Ala Met Asn Ser Arg Asp Ser Glu His Leu Leu Ser Glu
 1              5              10              15
Leu Ser Lys Leu Asp Tyr Lys Glu Thr Asn Asp Pro Lys Thr Ala Asp
      20              25              30
Leu Ile Leu Ile Asn Thr Cys Ser Val Arg Glu Lys Pro Glu Arg Lys
      35              40              45
Leu Phe Ser Glu Ile Gly Gln Phe Ala Lys Ile Lys Lys Pro Asn Ala
      50              55              60
Lys Ile Gly Val Cys Gly Cys Thr Ala Ser His Met Gly Ala Asp Ile
65              70              75              80
Leu Lys Lys Ala Pro Ser Val Ser Phe Val Leu Gly Ala Arg Asn Val
      85              90              95
Ser Lys Ile Ser Gln Val Ile His Lys Glu Lys Ala Val Glu Val Ala
      100              105              110
Ile Asp Tyr Asp Glu Ser Ala Tyr Ala Phe Glu Phe Phe Glu Lys Lys
      115              120              125
Ala Gln Ile Arg Ser Leu Leu Asn Ile Ser Ile Gly Cys Asp Lys Lys
      130              135              140
Cys Ala Tyr Cys Ile Val Pro His Thr Arg Gly Lys Glu Ile Ser Ile
145              150              155              160
Pro Met Asp Leu Ile Leu Lys Glu Ala Glu Lys Leu Ala Asn Asn Gly
      165              170              175
Thr Lys Glu Leu Met Leu Leu Gly Gln Asn Val Asn Asn Tyr Gly Ala
      180              185              190
Arg Phe Ser Ser Glu His Ala Lys Val Asp Phe Ser Asp Leu Leu Asp
      195              200              205
Lys Leu Ser Glu Ile Gln Gly Ile Glu Arg Ile Arg Phe Thr Ser Pro
      210              215              220
His Pro Leu His Met Asn Asp Gly Phe Leu Glu Arg Phe Ala Lys Asn
225              230              235              240

```


GCT	GAG	AAA	TTA	GCG	AAT	AAC	GGC	ACC	AAA	GAG	CTT	ATG	CTT	TTA	GGG	582
Ala	Glu	Lys	Leu	Ala	Asn	Asn	Gly	Thr	Lys	Glu	Leu	Met	Leu	Leu	Gly	
170						175					180					
CAG	AAT	GTG	AAT	AAT	TAC	GGC	GCG	CGT	TTC	AGC	AGC	GAG	CAT	GCG	AAA	630
Gln	Asn	Val	Asn	Asn	Tyr	Gly	Ala	Arg	Phe	Ser	Ser	Glu	His	Ala	Lys	
185					190					195					200	
GTG	GAT	TTT	AGC	GAT	TTG	TTG	GAT	AAA	TTG	AGC	GAA	ATC	CAG	GGG	ATT	678
Val	Asp	Phe	Ser	Asp	Leu	Leu	Asp	Lys	Leu	Ser	Glu	Ile	Gln	Gly	Ile	
				205					210					215		
GAA	AGG	ATA	CGA	TTC	ACT	TCG	CCT	CAC	CCC	TTG	CAC	ATG	AAT	GAT	GGA	726
Glu	Arg	Ile	Arg	Phe	Thr	Ser	Pro	His	Pro	Leu	His	Met	Asn	Asp	Gly	
			220					225						230		
TTT	TTA	GAG	CGT	TTT	GCC	AAA	AAC	CCT	AAA	GTG	TGC	AAG	AGT	ATC	CAC	774
Phe	Leu	Glu	Arg	Phe	Ala	Lys	Asn	Pro	Lys	Val	Cys	Lys	Ser	Ile	His	
		235					240					245				
ATG	CCT	TTA	CAG	AGC	GGA	TCT	AGC	GCG	GTG	TTA	AAG	ATG	ATG	CGA	AGG	822
Met	Pro	Leu	Gln	Ser	Gly	Ser	Ser	Ala	Val	Leu	Lys	Met	Met	Arg	Arg	
	250					255					260					
GGT	TAT	AGT	AAG	GAG	TGG	TTT	TTA	AAT	AGG	GTG	GAG	AGG	TTA	AAA	GCT	870
Gly	Tyr	Ser	Lys	Glu	Trp	Phe	Leu	Asn	Arg	Val	Glu	Arg	Leu	Lys	Ala	
265					270					275					280	
TTA	GTG	CCT	GAA	GTG	GGC	ATT	AGC	ACG	GAT	ATT	ATC	GTA	GGC	TTC	CCT	918
Leu	Val	Pro	Glu	Val	Gly	Ile	Ser	Thr	Asp	Ile	Ile	Val	Gly	Phe	Pro	
				285					290					295		
AAT	GAG	AGC	GAT	AAG	GAT	TTT	GAA	GAC	ACA	ATG	GAG	GTG	CTA	GAA	AAA	966
Asn	Glu	Ser	Asp	Lys	Asp	Phe	Glu	Asp	Thr	Met	Glu	Val	Leu	Glu	Lys	
			300					305					310			
GTG	CGC	TTT	GAC	ACG	CTC	TAT	AGT	TTC	ATT	TAT	TCC	CCA	CGC	CCT	TTC	1014
Val	Arg	Phe	Asp	Thr	Leu	Tyr	Ser	Phe	Ile	Tyr	Ser	Pro	Arg	Pro	Phe	
		315					320					325				
ACT	GAA	GCG	GGA	GCT	TGG	AAG	GAA	AGA	GTG	CCG	TTA	GAA	GTT	TCA	TCT	1062
Thr	Glu	Ala	Gly	Ala	Trp	Lys	Glu	Arg	Val	Pro	Leu	Glu	Val	Ser	Ser	
	330					335					340					
TCA	AGG	TTG	GAG	AGG	TTG	CAA	AAC	AGG	CAC	AAA	GAA	ATT	TTA	GAA	GAA	1110
Ser	Arg	Leu	Glu	Arg	Leu	Gln	Asn	Arg	His	Lys	Glu	Ile	Leu	Glu	Glu	
345					350					355					360	
AAA	GCC	AAG	CTA	GAA	GTG	GGC	AAA	ACG	CAT	GTG	GTG	TTG	GTG	GAA	AAC	1158
Lys	Ala	Lys	Leu	Glu	Val	Gly	Lys	Thr	His	Val	Val	Leu	Val	Glu	Asn	
			365					370						375		
AGG	CGT	GAA	ATG	GAT	AAT	CAA	ATC	GTG	GGT	TTT	GAA	GGG	CGT	AGC	GAT	1206
Arg	Arg	Glu	Met	Asp	Asn	Gln	Ile	Val	Gly	Phe	Glu	Gly	Arg	Ser	Asp	
		380						385					390			

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 31...1320

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

AGGCTTGATAT	TGAAAGTTTA	TATTGAAACC	ATG GGT TGT GCC ATG AAT TCT AGG	54
			Met Gly Cys Ala Met Asn Ser Arg	
			1 5	
GAT AGT GAG CAT TTA TTG AGC GAG CTG TCC AAA CTA GAC TAT AAA GAG	102			
Asp Ser Glu His Leu Leu Ser Glu Leu Ser Lys Leu Asp Tyr Lys Glu				
10 15 20				
ACC AAT GAC CCT AAA ACA GCG GAT TTG ATT TTA ATC AAC ACT TGC AGC	150			
Thr Asn Asp Pro Lys Thr Ala Asp Leu Ile Leu Ile Asn Thr Cys Ser				
25 30 35 40				
GTG CGC GAA AAG CCT GAA CGA AAA TTG TTT TCA GAA ATC GGT CAA TTC	198			
Val Arg Glu Lys Pro Glu Arg Lys Leu Phe Ser Glu Ile Gly Gln Phe				
45 50 55				
GCT AAA ATC AAA AAA CCC AAC GCC AAA ATC GGG GTT TGC GGG TGC ACT	246			
Ala Lys Ile Lys Lys Pro Asn Ala Lys Ile Gly Val Cys Gly Cys Thr				
60 65 70				
GCA AGC CAC ATG GGA GCG GAT ATT TTG AAA AAA GCC CCA AGC GTG AGC	294			
Ala Ser His Met Gly Ala Asp Ile Leu Lys Lys Ala Pro Ser Val Ser				
75 80 85				
TTT GTG TTA GGG GCT AGG AAT GTG TCT AAA ATC TCT CAA GTG ATC CAT	342			
Phe Val Leu Gly Ala Arg Asn Val Ser Lys Ile Ser Gln Val Ile His				
90 95 100				
AAA GAA AAA GCG GTT GAA GTG GCG ATT GAT TAT GAT GAA AGC GCG TAT	390			
Lys Glu Lys Ala Val Glu Val Ala Ile Asp Tyr Asp Glu Ser Ala Tyr				
105 110 115 120				
GCG TTT GAA TTT TTT GAA AAA AAG GCT CAA ATC CGA TCG TTG CTA AAT	438			
Ala Phe Glu Phe Phe Glu Lys Lys Ala Gln Ile Arg Ser Leu Leu Asn				
125 130 135				
ATC TCT ATA GGG TGC GAT AAG AAA TGC GCT TAT TGC ATC GTC CCG CAC	486			
Ile Ser Ile Gly Cys Asp Lys Lys Cys Ala Tyr Cys Ile Val Pro His				
140 145 150				
ACT AGG GGG AAA GAA ATT TCT ATC CCT ATG GAT TTG ATT TTA AAA GAA	534			
Thr Arg Gly Lys Glu Ile Ser Ile Pro Met Asp Leu Ile Leu Lys Glu				
155 160 165				

Ala Gln Phe Phe Glu Asn Ser Val Leu Leu Pro Ala Phe Ile Asn Ala
 50 55 60
 His Thr His Phe Glu Phe Ser Asn Asn Lys Ala Ser Phe Asp Tyr Gly
 65 70 75 80
 Ser Phe Ser Gly Trp Leu Gly Ser Val Leu Asn Asn Gly Gly Ala Ile
 85 90 95
 Leu Glu Asn Cys Gln Gly Ala Ile Gln Asn Ala Ile Ser Thr Gln Leu
 100 105 110
 Lys Ser Gly Val Gly Ser Val Gly Ala Ile Ser Asn His Leu Ile Glu
 115 120 125
 Val Asn Leu Leu Lys Glu Ser Pro Leu Asn Ala Val Val Phe Leu Glu
 130 135 140
 Phe Leu Gly Ser Ser Tyr Ser Leu Glu Lys Leu Lys Ala Phe Glu Ala
 145 150 155 160
 Lys Phe Lys Glu Leu Lys Asp Leu Glu Asp Lys Lys Leu Lys Ala Ala
 165 170 175
 Leu Ala Val His Ala Pro Tyr Ser Val Gln Lys Asp Met Ala Leu Ser
 180 185 190
 Val Ile Gln Leu Ala Lys Asp Ser Gln Ser Leu Leu Ser Thr His Phe
 195 200 205
 Leu Glu Ser Leu Glu Glu Leu Glu Trp Val Glu Asn Ser Lys Gly Trp
 210 215 220
 Phe Glu Asn Phe Tyr Gln His Phe Leu Lys Glu Ser His Phe Lys Ser
 225 230 235 240
 Leu Tyr Lys Gly Ala Asn Asp Tyr Ile Asp Met Phe Lys Asp Thr His
 245 250 255
 Thr Leu Phe Val His Asn Gln Phe Ala Ser Leu Glu Ala Leu Lys Arg
 260 265 270
 Ile Lys Ser Gln Val Lys Asn Ala Phe Leu Ile Thr Cys Pro Phe Ser
 275 280 285
 Asn Arg Leu Leu Ser Gly Gln Ala Leu Asp Leu Glu Arg Thr Lys Glu
 290 295 300
 Ala Gly Leu Ser Val Ser Val Ala Thr Asp Gly Leu Ser Ser Asn Ile
 305 310 315 320
 Ser Leu Ser Leu Leu Asp Glu Leu Arg Ala Phe Leu Leu Thr His Asn
 325 330 335
 Met Pro Leu Leu Glu Leu Ala Lys Ile Ala Leu Leu Gly Ala Thr Arg
 340 345 350
 His Gly Ala Lys Ala Leu Ala Leu Asn Asn Gly Glu Ile Glu Ala Asn
 355 360 365
 Lys Arg Ala Asp Leu Ser Val Phe Gly Phe Asn Glu Lys Phe Thr Lys
 370 375 380
 Glu Gln Ala Ile Leu Gln Phe Leu Leu His Ala Lys Glu Val Glu Cys
 385 390 395 400
 Leu Phe Leu Gly Gly Lys Arg Val Ile
 405

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Gln Val Lys Asn Ala Phe Leu Ile Thr Cys Pro Phe Ser Asn Arg Leu	
280 285 290	
TTG AGC GGG CAA GCG TTG GAT TTA GAA AGA ACT AAA GAA GCC GGT TTG	967
Leu Ser Gly Gln Ala Leu Asp Leu Glu Arg Thr Lys Glu Ala Gly Leu	
295 300 305	
AGC GTG AGC GTG GCC ACT GAT GGC TTG AGT TCT AAC ATT TCG CTG AGC	1015
Ser Val Ser Val Ala Thr Asp Gly Leu Ser Ser Asn Ile Ser Leu Ser	
310 315 320	
CTT TTA GAC GAA TTA AGA GCG TTT TTG CTC ACC CAT AAC ATG CCG TTA	1063
Leu Leu Asp Glu Leu Arg Ala Phe Leu Leu Thr His Asn Met Pro Leu	
325 330 335	
TTA GAA TTA GCT AAA ATA GCC CTT TTA GGG GCG ACT AGG CAT GGG GCT	1111
Leu Glu Leu Ala Lys Ile Ala Leu Leu Gly Ala Thr Arg His Gly Ala	
340 345 350 355	
AAA GCT TTA GCT TTG AAT AAT GGC GAG ATA GAA GCC AAC AAA AGG GCG	1159
Lys Ala Leu Ala Leu Asn Asn Gly Glu Ile Glu Ala Asn Lys Arg Ala	
360 365 370	
GAT TTG AGC GTG TTT GGT TTT AAT GAA AAA TTC ACT AAA GAG CAA GCG	1207
Asp Leu Ser Val Phe Gly Phe Asn Glu Lys Phe Thr Lys Glu Gln Ala	
375 380 385	
ATT TTG CAA TTT TTA TTG CAT GCT AAA GAA GTG GAG TGC TTG TTT TTA	1255
Ile Leu Gln Phe Leu Leu His Ala Lys Glu Val Glu Cys Leu Phe Leu	
390 395 400	
GGG GGG AAA AGG GTG ATC TAATTTGTTT TAAAGACAGA ATGCGTTAAA ATGAGAAA	1311
Gly Gly Lys Arg Val Ile	
405	
TCTAAATCAA TTAAGGAAAG AGTCAATGAA ACTAGTTTT	1350

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

Met Gln Glu Ile Ile Gly Ala Ser Leu Val Phe Leu Cys Asn Glu Lys	
1 5 10 15	
Cys Glu Val Leu Glu Asp Tyr Gly Val Val Phe Asp Glu Lys Ile Val	
20 25 30	
Glu Ile Gly Asp Tyr Gln Ser Leu Thr Leu Lys Tyr Pro His Leu Lys	
35 40 45	

55					60					65						
TTT	GAA	TTT	TCC	AAC	AAC	AAG	GCG	AGT	TTT	GAT	TAC	GGG	AGT	TTT	TCT	295
Phe	Glu	Phe	Ser	Asn	Asn	Lys	Ala	Ser	Phe	Asp	Tyr	Gly	Ser	Phe	Ser	
		70					75					80				
GGC	TGG	TTA	GGG	AGC	GTG	TTA	AAC	AAT	GGG	GGG	GCG	ATT	TTA	GAA	AAT	343
Gly	Trp	Leu	Gly	Ser	Val	Leu	Asn	Asn	Gly	Gly	Ala	Ile	Leu	Glu	Asn	
	85					90					95					
TGC	CAA	GGG	GCT	ATT	CAA	AAC	GCT	ATC	AGC	ACG	CAA	TTA	AAA	AGC	GGG	391
Cys	Gln	Gly	Ala	Ile	Gln	Asn	Ala	Ile	Ser	Thr	Gln	Leu	Lys	Ser	Gly	
100					105					110					115	
GTG	GGG	AGC	GTG	GGA	GCG	ATT	TCT	AAC	CAC	CTG	ATA	GAA	GTT	AAT	TTG	439
Val	Gly	Ser	Val	Gly	Ala	Ile	Ser	Asn	His	Leu	Ile	Glu	Val	Asn	Leu	
				120					125					130		
TTA	AAA	GAA	AGC	CCT	TTG	AAT	GCT	GTC	GTG	TTT	TTA	GAG	TTT	TTA	GGG	487
Leu	Lys	Glu	Ser	Pro	Leu	Asn	Ala	Val	Val	Phe	Leu	Glu	Phe	Leu	Gly	
			135					140					145			
AGC	AGT	TAT	TCT	TTA	GAA	AAA	TTA	AAA	GCG	TTT	GAG	GCC	AAA	TTT	AAG	535
Ser	Ser	Tyr	Ser	Leu	Glu	Lys	Leu	Lys	Ala	Phe	Glu	Ala	Lys	Phe	Lys	
		150					155					160				
GAA	TTA	AAA	GAT	TTA	GAA	GAT	AAA	AAA	CTT	AAA	GCG	GCT	CTC	GCT	GTG	583
Glu	Leu	Lys	Asp	Leu	Glu	Asp	Lys	Lys	Leu	Lys	Ala	Ala	Leu	Ala	Val	
	165					170					175					
CAT	GCC	CCT	TAT	TCG	GTC	CAA	AAA	GAC	ATG	GCT	TTG	AGC	GTC	ATC	CAA	631
His	Ala	Pro	Tyr	Ser	Val	Gln	Lys	Asp	Met	Ala	Leu	Ser	Val	Ile	Gln	
180					185					190					195	
TTA	GCC	AAA	GAT	TCA	CAA	AGC	CTG	CTT	TCT	ACG	CAT	TTT	TTA	GAA	TCG	679
Leu	Ala	Lys	Asp	Ser	Gln	Ser	Leu	Leu	Ser	Thr	His	Phe	Leu	Glu	Ser	
				200					205					210		
CTT	GAA	GAA	TTA	GAA	TGG	GTA	GAA	AAC	TCT	AAA	GGG	TGG	TTT	GAA	AAT	727
Leu	Glu	Glu	Leu	Glu	Trp	Val	Glu	Asn	Ser	Lys	Gly	Trp	Phe	Glu	Asn	
			215					220					225			
TTT	TAC	CAG	CAT	TTT	TTA	AAG	GAG	TCT	CAT	TTC	AAA	TCG	CTC	TAT	AAG	775
Phe	Tyr	Gln	His	Phe	Leu	Lys	Glu	Ser	His	Phe	Lys	Ser	Leu	Tyr	Lys	
		230					235					240				
GGC	GCG	AAC	GAT	TAC	ATT	GAC	ATG	TTT	AAA	GAC	ACG	CAC	ACT	TTA	TTC	823
Gly	Ala	Asn	Asp	Tyr	Ile	Asp	Met	Phe	Lys	Asp	Thr	His	Thr	Leu	Phe	
	245					250					255					
GTG	CAT	AAC	CAG	TTC	GCT	TCT	TTA	GAA	GCG	TTA	AAA	AGG	ATT	AAA	TCT	871
Val	His	Asn	Gln	Phe	Ala	Ser	Leu	Glu	Ala	Leu	Lys					

50		55		60	
Ser Met Pro Phe Val Leu	Asn Ile Leu Leu Thr	Gln Ala Ile Tyr Pro			
65	70	75	80		
Ile Glu Thr Arg Ile Leu	His Ala Asn Pro Leu	Ser Tyr Ser Asn Ala			
	85	90	95		
Phe Ser Leu Gln Val Gly	Val Lys Asn His Ser	Lys Phe Thr Leu Asn			
	100	105	110		
Lys Cys Val Leu Arg Leu	Glu Val Leu Lys Asn	Pro His Asn Phe Val			
	115	120	125		
Glu Glu His Ala Phe Lys	Trp Phe Val Lys Lys	Ser Tyr Glu Lys Ile			
	130	135	140		
Phe Lys Glu Lys Ile Leu	Pro Lys Glu Ser Lys	Val Phe Ser Phe Phe			
145	150	155	160		
Ile Asp Asn Tyr Pro Tyr	Ser Lys Thr Ala Pro	Tyr Gln Val Ser Leu			
	165	170	175		
Phe Cys Leu					

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...1273
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

AAAGAATGAT CTTAAAAGGG CAAACCACAT TTATTAAGGA GAATGC ATG CAA GAA	55
Met Gln Glu	
1	
ATC ATA GGA GCG TCT TTA GTT TTT TTG TGC AAT GAA AAG TGC GAA GTG	103
Ile Ile Gly Ala Ser Leu Val Phe Leu Cys Asn Glu Lys Cys Glu Val	
5 10 15	
TTA GAA GAT TAT GGC GTA GTC TTT GAT GAA AAG ATT GTT GAA ATA GGC	151
Leu Glu Asp Tyr Gly Val Val Phe Asp Glu Lys Ile Val Glu Ile Gly	
20 25 30 35	
GAT TAT CAA AGT TTA ACG CTT AAA TAC CCT CAC TTA AAG GCG CAG TTT	199
Asp Tyr Gln Ser Leu Thr Leu Lys Tyr Pro His Leu Lys Ala Gln Phe	
40 45 50	
TTT GAA AAT TCC GTT CTG TTG CCC GCT TTT ATC AAC GCG CAC ACC CAT	247
Phe Glu Asn Ser Val Leu Leu Pro Ala Phe Ile Asn Ala His Thr His	

45	50	55	
TTT TTG GGT GCG TTT TTA AGC ATG CCT TTT GTT TTG AAC ATT TTA CTC			244
Phe Leu Gly Ala Phe Leu Ser Met Pro Phe Val Leu Asn Ile Leu Leu			
60	65	70	
ACT CAA GCG ATT TAC CCC ATA GAA ACA CGC ATC TTA CAC GCT AAC CCT			292
Thr Gln Ala Ile Tyr Pro Ile Glu Thr Arg Ile Leu His Ala Asn Pro			
75	80	85	90
TTA AGT TAC AGC AAC GCC TTT TCT TTG CAA GTG GGA GTC AAA AAC CAT			340
Leu Ser Tyr Ser Asn Ala Phe Ser Leu Gln Val Gly Val Lys Asn His			
95	100	105	
TCC AAA TTT ACT CTA AAC AAA TGC GTT TTA CGC CTA GAA GTG CTT AAA			388
Ser Lys Phe Thr Leu Asn Lys Cys Val Leu Arg Leu Glu Val Leu Lys			
110	115	120	
AAC CCT CAC AAT TTT GTA GAA GAG CAT GCT TTT AAA TGG TTT GTC AAA			436
Asn Pro His Asn Phe Val Glu Glu His Ala Phe Lys Trp Phe Val Lys			
125	130	135	
AAA AGC TAT GAA AAA ATT TTT AAA GAA AAG ATT TTG CCC AAA GAA TCT			484
Lys Ser Tyr Glu Lys Ile Phe Lys Glu Lys Ile Leu Pro Lys Glu Ser			
140	145	150	
AAG GTC TTT TCA TTC TTT ATT GAC AAC TAC CCT TAT TCA AAA ACG GCC			532
Lys Val Phe Ser Phe Phe Ile Asp Asn Tyr Pro Tyr Ser Lys Thr Ala			
155	160	165	170
CCT TAT CAA GTT TCT TTG TTT TGT TTA TAAAAAACTA AAAGATAACG CCAAGA			586
Pro Tyr Gln Val Ser Leu Phe Cys Leu			
175			
TAACATTCAT TAAAAAGCGA TTAAAAACGC TTAAAGGCAT AGAT			630

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

Met	Ala	Ser	Leu	Ala	Phe	Ile	Gln	Ala	Phe	Leu	Glu	Ser	Phe	Lys	Gly
1				5					10					15	
Phe	Leu	Ser	Gln	Ala	Thr	Leu	Ile	Ser	Val	Leu	Ile	Ala	Ser	Val	Leu
			20					25					30		
Ile	Leu	Phe	Cys	Ala	Ile	Leu	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Arg	Asn
		35				40					45				
Arg	Leu	Ala	Ser	Tyr	Ile	Ala	Thr	Ala	Ala	Phe	Leu	Gly	Ala	Phe	Leu

```

      195              200              205
Glu Val Ser Lys Leu Pro Asn Thr Pro Val Glu Leu Ser Ser Ile Gln
      210              215              220
Leu Arg Glu Ile Val Leu Pro Ala Lys Ile Lys Glu Gln Ile Glu Lys
      225              230              235              240
Val Gln Ile Ala Arg Gln Glu Ser Glu Arg Val Lys Tyr Glu Val Glu
      245              250              255
Arg Ser Lys Gln Glu Ala Gln Lys Gln Ala Ala Leu Ala Lys Gly Glu
      260              265              270
Ala Asp Ala Asn Arg Ile Lys Ala Gln Gly Val Ala Asp Ala Ile Val
      275              280              285
Ile Glu Ala Lys Ala Lys Ser Gln Ala Asn Leu Ser Ile Ser Gln Ser
      290              295              300
Leu Ser Asp Lys Leu Leu Arg Leu Arg Gln Ile Glu Val Gln Gly Gln
      305              310              315              320
Phe Asn Glu Ala Leu Lys Thr Asn Asn Asn Ala Gln Ile Met Leu Thr
      325              330              335
Pro Gly Gly Ala Val Pro Asn Ile Trp Ile Asp Thr Lys Ser Lys Val
      340              345              350
Lys Ser Ser Ile Ala Glu Thr Lys Glu Pro
      355              360

```

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 23...559
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

```

GACTAAAGAG CCTTAAAAAC GC ATG GCA TCT CTT GCC TTT ATC CAA GCT TTT      52
              Met Ala Ser Leu Ala Phe Ile Gln Ala Phe
              1              5              10

TTG GAG TCT TTT AAG GGA TTT TTA AGT CAA GCG ACT CTA ATC AGC GTT      100
Leu Glu Ser Phe Lys Gly Phe Leu Ser Gln Ala Thr Leu Ile Ser Val
              15              20              25

TTA ATA GCG AGC GTT TTA ATC CTT TTT TGC GCG ATT TTG CTC CTT TTG      148
Leu Ile Ala Ser Val Leu Ile Leu Phe Cys Ala Ile Leu Leu Leu Leu
              30              35              40

GCT CTG CTT TTG AGA AAC CGC TTA GCT AGC TAT ATA GCA ACA GCA GCT      196
Ala Leu Leu Leu Arg Asn Arg Leu Ala Ser Tyr Ile Ala Thr Ala Ala

```



```

TTA AGA CTG CGC CAA ATT GAA GTT CAA GGC CAG TTT AAT GAA GCG TTA      1014
Leu Arg Leu Arg Gln Ile Glu Val Gln Gly Gln Phe Asn Glu Ala Leu
310                      315                      320                      325

AAA ACG AAC AAT AAC GCT CAA ATC ATG CTC ACT CCA GGT GGG GCT GTG      1062
Lys Thr Asn Asn Asn Ala Gln Ile Met Leu Thr Pro Gly Gly Ala Val
                      330                      335                      340

CCT AAT ATT TGG ATT GAC ACT AAA AGC AAG GTT AAA TCT AGT ATT GCC      1110
Pro Asn Ile Trp Ile Asp Thr Lys Ser Lys Val Lys Ser Ser Ile Ala
                      345                      350                      355

GAG ACT AAA GAG CCT TAAAAACGCA TGGCATCTCT TGCCTTTATC CAAGCTTTTT T  1166
Glu Thr Lys Glu Pro
                      360

GGAGTCTTTTT AAGGGATTTT TAAGTCAAGC GACTCT                                1202

```

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

```

Met Pro Ile Asp Leu Asn Glu His Leu Lys Lys Lys Asn Ser Gln Arg
 1          5          10          15
Glu Thr Pro Thr Pro Asn Thr Pro Asn Asn Gly Gly Arg Phe Ile Pro
          20          25          30
Pro Ser Asn Ser Phe Asn Ser Lys Lys Leu Ser Val Leu Ile Val Ile
          35          40          45
Val Leu Leu Gly Val Ile Ala Phe Leu Ala Lys Pro Phe Glu Val Ile
 50          55          60
Ser Ser Gly Glu Ile Gly Ile Lys Ile Thr Ala Gly Lys Tyr Glu Pro
65          70          75          80
Thr Pro Leu Gln Pro Gly Ile His Phe Phe Val Pro Ile Ile Gln Asp
          85          90          95
Ile Leu Ile Val Asp Thr Arg Ile Arg Asn Ile Asn Phe Ser Arg Thr
          100          105          110
Glu Asp Met Gly Val Ala Gly Lys Asn Gln Gly Ile Phe Arg Asn Asp
          115          120          125
Ala Ile Asn Val Met Asp Ser Arg Gly Leu Thr Val Ser Ile Glu Leu
          130          135          140
Thr Val Gln Tyr Arg Leu Asn Pro Gln Thr Thr Pro Gln Thr Ile Ala
          145          150          155          160
Thr Tyr Gly Leu Ser Trp Glu Gln Lys Ile Ile Asn Pro Val Val Arg
          165          170          175
Asp Val Val Arg Ser Val Val Gly Arg Tyr Pro Ala Glu Asp Leu Pro
          180          185          190
Ile Lys Arg Asn Glu Ile Ala Ala Leu Ile Asn Ser Gly Ile Asn Lys

```

Gly Ile His Phe Phe Val Pro Ile Ile Gln Asp Ile Leu Ile Val Asp	
90 95 100	
ACA AGG ATT AGG AAT ATC AAT TTT TCA CGC ACC GAA GAC ATG GGC GTG	390
Thr Arg Ile Arg Asn Ile Asn Phe Ser Arg Thr Glu Asp Met Gly Val	
105 110 115	
GCG GGT AAA AAC CAA GGG ATT TTT AGA AAC GAC GCT ATT AAT GTG ATG	438
Ala Gly Lys Asn Gln Gly Ile Phe Arg Asn Asp Ala Ile Asn Val Met	
120 125 130	
GAT AGT AGG GGT TTG ACC GTT TCT ATT GAA CTC ACC GTG CAA TAC CGC	486
Asp Ser Arg Gly Leu Thr Val Ser Ile Glu Leu Thr Val Gln Tyr Arg	
135 140 145	
TTA AAC CCC CAA ACC ACC CCC CAA ACG ATC GCT ACT TAT GGC TTG TCT	534
Leu Asn Pro Gln Thr Thr Pro Gln Thr Ile Ala Thr Tyr Gly Leu Ser	
150 155 160 165	
TGG GAG CAA AAA ATC ATC AAC CCT GTG GTG CGC GAT GTG GTG CGC TCT	582
Trp Glu Gln Lys Ile Ile Asn Pro Val Val Arg Asp Val Val Arg Ser	
170 175 180	
GTC GTG GGG CGC TAT CCG GCT GAA GAT TTA CCC ATT AAG CGC AAT GAA	630
Val Val Gly Arg Tyr Pro Ala Glu Asp Leu Pro Ile Lys Arg Asn Glu	
185 190 195	
ATC GCC GCT CTT ATT AAT AGC GGT ATC AAT AAA GAA GTT TCT AAG CTC	678
Ile Ala Ala Leu Ile Asn Ser Gly Ile Asn Lys Glu Val Ser Lys Leu	
200 205 210	
CCT AAC ACC CCT GTG GAA TTA AGC TCT ATC CAA TTG AGA GAA ATC GTC	726
Pro Asn Thr Pro Val Glu Leu Ser Ser Ile Gln Leu Arg Glu Ile Val	
215 220 225	
TTG CCC GCT AAG ATT AAA GAG CAA ATA GAA AAA GTC CAA ATC GCG CGC	774
Leu Pro Ala Lys Ile Lys Glu Gln Ile Glu Lys Val Gln Ile Ala Arg	
230 235 240 245	
CAA GAA TCA GAA AGG GTG AAA TAC GAG GTG GAG CGC TCC AAG CAA GAA	822
Gln Glu Ser Glu Arg Val Lys Tyr Glu Val Glu Arg Ser Lys Gln Glu	
250 255 260	
GCT CAA AAA CAA GCC GCT CTG GCT AAA GGG GAA GCG GAC GCT AAC AGG	870
Ala Gln Lys Gln Ala Ala Leu Ala Lys Gly Glu Ala Asp Ala Asn Arg	
265 270 275	
ATT AAG GCT CAG GGC GTG GCT GAT GCG ATT GTG ATT GAG GCT AAG GCA	918
Ile Lys Ala Gln Gly Val Ala Asp Ala Ile Val Ile Glu Ala Lys Ala	
280 285 290	
AAA TCT CAA GCT AAT TTA AGC ATT TCG CAA AGC TTG AGC GAC AAG CTT	966
Lys Ser Gln Ala Asn Leu Ser Ile Ser Gln Ser Leu Ser Asp Lys Leu	
295 300 305	

```

Asn Asn Ile Glu Lys Ile Leu His Asn Ala Phe Asn Thr Phe Leu His
385                      390                      395                      400
Asn Pro Thr Ile Ala Leu Lys Lys Asn Ala Gln Lys Glu Glu Ser Asp
                      405                      410                      415
Val Leu Val Gly Ala Ile Lys Asn Leu Phe Asn Leu Asp Lys Ser Asn
                      420                      425                      430
Ala Asn His Ala Gln Asn Leu Asn Leu Tyr Lys Cys Glu Tyr Tyr Glu
435                      440                      445
Glu

```

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...1125
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

```

AAAACCCAAA CGCCGTTAAA ATATTTAAAA AGGAAATTC ATG CCC ATT GAT TTG      54
                               Met Pro Ile Asp Leu
                               1                      5

AAC GAA CAT TTA AAA AAG AAA AAT TCT CAA AGA GAA ACC CCC ACG CCT      102
Asn Glu His Leu Lys Lys Lys Asn Ser Gln Arg Glu Thr Pro Thr Pro
                      10                      15                      20

AAT ACG CCT AAT AAT GGG GGG CGT TTC ATC CCG CCG TCT AAT TCT TTT      150
Asn Thr Pro Asn Asn Gly Gly Arg Phe Ile Pro Pro Ser Asn Ser Phe
                      25                      30                      35

AAT TCT AAA AAA CTA TCG GTT TTA ATT GTC ATT GTC CTT TTA GGC GTT      198
Asn Ser Lys Lys Leu Ser Val Leu Ile Val Ile Val Leu Leu Gly Val
                      40                      45                      50

ATC GCT TTT TTG GCC AAG CCT TTT GAA GTG ATT AGC TCA GGA GAA ATT      246
Ile Ala Phe Leu Ala Lys Pro Phe Glu Val Ile Ser Ser Gly Glu Ile
55.                      60                      65

GGC ATT AAA ATC ACC GCC GGG AAA TAC GAA CCC ACC CCC TTA CAG CCA      294
Gly Ile Lys Ile Thr Ala Gly Lys Tyr Glu Pro Thr Pro Leu Gln Pro
70                      75                      80                      85

GGG ATC_CAC TTC TTT GTG CCT ATC ATT CAA GAC ATT CTC ATT GTG GAT      342

```

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

```

Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr Leu Ala Phe Thr
 1           5           10           15
His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu Ala Ile Asn Ser
          20           25           30
Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys Asn His Cys Pro
          35           40           45
Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn Arg Phe Glu Ile
          50           55           60
Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu Gln Lys Asn Ala
65           70           75           80
Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser Val Ser Asp Leu
          85           90           95
Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala Val His His Val
          100          105          110
Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val Gly Glu Thr Gln
          115          120          125
Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala Phe Glu Glu Lys
          130          135          140
Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe Ala Phe Lys Cys
145          150          155          160
Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys Gln Gly Val Ser
          165          170          175
Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile Phe Glu Lys Glu
          180          185          190
Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu Gly Glu Met Ala
          195          200          205
Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe Glu Ala Leu Ile
          210          215          220
Leu Gly Arg Asn Ala Ala Lys Phe Glu Asp Phe Ile Lys Glu Leu Glu
225          230          235          240
Glu Pro Lys Lys Val Ser Phe Gln Asn Ile Glu Asn Leu Asn Ala Tyr
          245          250          255
Ile Asn Glu Tyr Glu Leu Leu Phe Cys Ala Thr Ser Ser Pro His Phe
          260          265          270
Ile Val Gln Asn Arg Met Leu Lys Glu Thr Ile Phe Arg Arg Phe Trp
          275          280          285
Phe Asp Leu Ala Val Pro Arg Asn Ile Glu Lys Pro Val Leu Asp Asn
          290          295          300
Ile Phe Leu Tyr Ser Val Asp Asp Leu Glu Pro Met Val Arg Glu Asn
305          310          315          320
Val Glu Asn Arg Gln Glu Ser Arg Met Arg Ala Tyr Glu Ile Val Gly
          325          330          335
Leu Ala Thr Met Glu Phe Tyr Gln Trp Ile Gln Ser Leu Glu Val Glu
          340          345          350
Pro Val Ile Lys Asp Leu Arg Glu Leu Ala Arg Ile Ser Ala Gln Lys
          355          360          365
Glu Leu Gln Lys Ala Leu Lys Lys Arg Tyr Val Pro Lys Glu Tyr Glu
          370          375          380

```

TCG CCG CAT TTT ATC GTG CAA AAT CGC ATG TTA AAA GAA ACG ATT TTC	867
Ser Pro His Phe Ile Val Gln Asn Arg Met Leu Lys Glu Thr Ile Phe	
270 275 280	
AGG CGT TTT TGG TTT GAT TTA GCC GTG CCA CGG AAT ATT GAA AAG CCG	915
Arg Arg Phe Trp Phe Asp Leu Ala Val Pro Arg Asn Ile Glu Lys Pro	
285 290 295 300	
GTA TTG GAT AAT ATT TTC TTA TAC AGC GTT GAT GAT TTA GAG CCT ATG	963
Val Leu Asp Asn Ile Phe Leu Tyr Ser Val Asp Asp Leu Glu Pro Met	
305 310 315	
GTG AGA GAA AAT GTG GAA AAC AGG CAA GAG AGC AGA ATG AGA GCT TAT	1011
Val Arg Glu Asn Val Glu Asn Arg Gln Glu Ser Arg Met Arg Ala Tyr	
320 325 330	
GAG ATT GTA GGG CTT GCC ACA ATG GAG TTT TAC CAA TGG ATT CAA AGT	1059
Glu Ile Val Gly Leu Ala Thr Met Glu Phe Tyr Gln Trp Ile Gln Ser	
335 340 345	
TTA GAA GTA GAG CCT GTG ATT AAG GAT TTA AGG GAA TTG GCT AGG ATT	1107
Leu Glu Val Glu Pro Val Ile Lys Asp Leu Arg Glu Leu Ala Arg Ile	
350 355 360	
TCA GCC CAA AAA GAA TTG CAA AAA GCG CTT AAA AAA CGC TAT GTG CCT	1155
Ser Ala Gln Lys Glu Leu Gln Lys Ala Leu Lys Lys Arg Tyr Val Pro	
365 370 375 380	
AAA GAA TAC GAA AAC AAC ATT GAA AAG ATC TTG CAC AAC GCT TTC AAC	1203
Lys Glu Tyr Glu Asn Asn Ile Glu Lys Ile Leu His Asn Ala Phe Asn	
385 390 395	
ACT TTT TTG CAT AAC CCT ACC ATC GCC TTA AAA AAG AAC GCT CAA AAA	1251
Thr Phe Leu His Asn Pro Thr Ile Ala Leu Lys Lys Asn Ala Gln Lys	
400 405 410	
GAA GAA TCC GAT GTG CTT GTG GGT GCG ATT AAA AAC TTG TTT AAT TTA	1299
Glu Glu Ser Asp Val Leu Val Gly Ala Ile Lys Asn Leu Phe Asn Leu	
415 420 425	
GAC AAA TCT AAC GCT AAC CAT GCC CAG AAT TTG AAT CTC TAT AAA TGC	1347
Asp Lys Ser Asn Ala Asn His Ala Gln Asn Leu Asn Leu Tyr Lys Cys	
430 435 440	
GAA TAT TAC GAG GAA TAATGCATGC TATTTTCAAA ACTCTTTGCC CCCACTCTCA A	1403
Glu Tyr Tyr Glu Glu	
445	
AGAA	1407

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
 (B) TYPE: amino acid

AAC CAT TGC CCT AAC ATC AAA GAG TGC ATG GTG TTA TCC ACA TGC AAT	195
Asn His Cys Pro Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn	
45 50 55 60	
CGC TTT GAA ATC TAT GCG AGC CTA AAA CAC GGC GCT AAT ACT AAT GAA	243
Arg Phe Glu Ile Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu	
65 70 75	
CAA AAA AAC GCA CTA TTA AAG ATT TTG GCT CAA AAT AAA AAA ATG AGC	291
Gln Lys Asn Ala Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser	
80 85 90	
GTG TCT GAT TTA GAA AAA TGC GTT TTA ATG AAC ACT GAT GAA AGC GCA	339
Val Ser Asp Leu Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala	
95 100 105	
GTC CAT CAT GTC TTT AGC GTG TGC AGC AGT TTG GAT AGC TTG GTG GTT	387
Val His His Val Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val	
110 115 120	
GGG GAA ACT CAA ATC ACA GGG CAG ATG AAA AAC GCT TAT AAA TTC GCT	435
Gly Glu Thr Gln Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala	
125 130 135 140	
TTT GAA GAG AAA TTT TGC TCT AAA GAT TTA ACC CGA TTG CTC CAT TTT	483
Phe Glu Glu Lys Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe	
145 150 155	
GCT TTC AAA TGC GCC GCT AAA GTG CGC AAT TTA ACC GGC ATT TCC AAG	531
Ala Phe Lys Cys Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys	
160 165 170	
CAA GGG GTT TCC ATC TCT TCA GTG GCG GTC AAA GAA GCG CTT AAT ATT	579
Gln Gly Val Ser Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile	
175 180 185	
TTT GAA AAA GAA AGG ATT AAG GAT AAA AAA GCC CTT GTG ATA GGG CTT	627
Phe Glu Lys Glu Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu	
190 195 200	
GGC GAG ATG GCT CAA TTA GTC ATC AAG CAC CTT TTA AAC AAG CAA TTT	675
Gly Glu Met Ala Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe	
205 210 215 220	
GAA GCG CTT ATC TTA GGG CGT AAT GCG GCT AAA TTT GAA GAT TTC ATC	723
Glu Ala Leu Ile Leu Gly Arg Asn Ala Ala Lys Phe Glu Asp Phe Ile	
225 230 235	
AAA GAA TTA GAA GAA CCT AAA AAA GTA AGC TTT CAA AAT ATA GAA AAT	771
Lys Glu Leu Glu Glu Pro Lys Lys Val Ser Phe Gln Asn Ile Glu Asn	
240 245 250	
TTA AAC GCT TAT ATC AAT GAA TAC GAA CTG CTT TTT TGC GCC ACT TCT	819
Leu Asn Ala Tyr Ile Asn Glu Tyr Glu Leu Leu Phe Cys Ala Thr Ser	
255 260 265	

```

      35              40              45
Gly Ala Phe Val Ile Leu Glu Gln Lys Asp Lys Ser Tyr Lys Val
  50              55              60
Val Glu Glu Tyr Pro Ser Ser Arg Thr His Ile Val Arg Asp Leu
  65              70              75              80
Gln Gly Asn Glu Arg Val Leu Ser Asn Glu Glu Ile Gln Lys Leu Ile
      85              90              95
Lys Glu Glu Glu Ala Lys Ile Asp Asn Gly Thr Ser Lys Leu Val Gln
      100              105              110
Pro Asn Asn Gly Gly Ser Asn Glu Gly Ser Gly Phe Gly Leu Gly Ser
      115              120              125
Ala Ile Leu Gly Ser Ala Ala Gly Ala Ile Leu Gly Ser Tyr Ile Gly
      130              135              140
Asn Lys Leu Phe Asn Asn Pro Asn Tyr Gln Gln Asn Ala Gln Arg Thr
      145              150              155              160
Tyr Lys Ser Pro Gln Ala Tyr Gln Arg Ser Gln Asn Ser Phe Ser Lys
      165              170              175
Ser Ala Pro Ser Ala Ser Ser Met Gly Gly Ala Ser Lys Gly Gln Ser
      180              185              190
Gly Phe Phe Gly Ser Ser Arg Pro Thr Ser Ser Pro Ala Val Ser Ser
      195              200              205
Gly Thr Arg Gly Phe Asn Ser
      210              215

```

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...1362
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

```

TTATAGGACT TTTTA ATG GAG TTA GAA ACT CAT TTG TCA AAA TAT TTC ACC      51
      Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr
      1              5              10

CTA GCC TTT ACG CAT AAA AGC ATG AGC TTA GAA ATG CGA GAA AAA CTC      99
Leu Ala Phe Thr His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu
      15              20              25

GCT ATT AAT TCG AAT GCA ACG CTT AAA GAA TTT TTA CAA ACC ATT AAA      147
Ala Ile Asn Ser Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys
      30              35              40

```

GTG CGC GAT TTG CAA GGC AAT GAA CGC GTG TTA AGC AAT GAA GAG ATT	291
Val Arg Asp Leu Gln Gly Asn Glu Arg Val Leu Ser Asn Glu Glu Ile	
80 85 90	
CAA AAG CTC ATC AAA GAA GAA GAA GCT AAA ATT GAT AAC GGC ACG AGC	339
Gln Lys Leu Ile Lys Glu Glu Glu Ala Lys Ile Asp Asn Gly Thr Ser	
95 100 105	
AAG CTT GTC CAG CCT AAT AAT GGA GGG AGT AAT GAA GGC TCA GGC TTT	387
Lys Leu Val Gln Pro Asn Asn Gly Gly Ser Asn Glu Gly Ser Gly Phe	
110 115 120	
GGC TTG GGG AGC GCG ATT TTA GGG AGC GCG GCG GGG GCG ATT TTA GGG	435
Gly Leu Gly Ser Ala Ile Leu Gly Ser Ala Ala Gly Ala Ile Leu Gly	
125 130 135 140	
AGT TAT ATT GGT AAT AAG CTT TTC AAT AAC CCT AAT TAC CAG CAA AAC	483
Ser Tyr Ile Gly Asn Lys Leu Phe Asn Asn Pro Asn Tyr Gln Gln Asn	
145 150 155	
GCC CAA CGG ACC TAC AAA TCC CCA CAA GCT TAC CAA CGC TCT CAA AAT	531
Ala Gln Arg Thr Tyr Lys Ser Pro Gln Ala Tyr Gln Arg Ser Gln Asn	
160 165 170	
TCC TTT TCT AAA AGT GCG CCC AGT GCT TCA AGC ATG GGC GGA GCG AGT	579
Ser Phe Ser Lys Ser Ala Pro Ser Ala Ser Ser Met Gly Gly Ala Ser	
175 180 185	
AAG GGA CAG AGC GGG TTT TTT GGC TCT AGT AGG CCT ACT AGT TCA CCG	627
Lys Gly Gln Ser Gly Phe Phe Gly Ser Ser Arg Pro Thr Ser Ser Pro	
190 195 200	
GCG GTA AGC TCT GGG ACA AGG GGC TTT AAC TCA TAATTTAATT GATTCAAGGC	680
Ala Val Ser Ser Gly Thr Arg Gly Phe Asn Ser	
205 210 215	
TAAAAA	686

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

Met	Lys	Lys	Pro	Tyr	Arg	Lys	Ile	Ser	Asp	Tyr	Ala	Ile	Val	Gly	Gly
1				5				10						15	
Leu	Ser	Ala	Leu	Val	Met	Val	Ser	Ile	Val	Gly	Cys	Lys	Ser	Asn	Ala
		20						25					30		
Asp	Asp	Lys	Pro	Lys	Glu	Gln	Ser	Ser	Leu	Ser	Gln	Ser	Val	Gln	Lys


```

Met Leu Ile Met Asp Trp Lys Leu Lys Val Val Lys Glu Ile Ile Thr
 1             5             10             15
Ile Thr Ala Thr Thr Ala Thr Met Gly Ile Leu Thr Thr Tyr Ser Leu
      20             25             30
Asn Thr Asn Met Ser Thr Ile Lys Glu Lys Pro Ala Lys Lys Val Glu
      35             40             45
Ser Leu Val Leu Ala Pro Asp Phe Ala Leu Met Ile Asp Cys Pro Thr
      50             55             60
Lys Ala His Pro Val Ile Pro Pro Lys Ser Pro Glu Met Ile Phe Pro
65             70             75             80
Lys Pro Cys Ala Leu Val Ser Leu Phe Leu Ser Leu Thr Pro Ser Phe
      85             90             95
Lys Ile Thr Ser Lys Val Leu Ala Val Asn Lys Leu Ser Ile Val Pro
      100            105            110
Thr Ser Ala Lys Glu Arg Ala
      115

```

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...660
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

```

TATAAGGTTG CTCTC ATG AAA AAA CCC TAT AGG AAG ATT TCT GAT TAT GCG      51
      Met Lys Lys Pro Tyr Arg Lys Ile Ser Asp Tyr Ala
      1             5             10

ATC GTG GGT GGT TTG AGC GCG TTA GTG ATG GTG AGC ATT GTG GGG TGT      99
Ile Val Gly Gly Leu Ser Ala Leu Val Met Val Ser Ile Val Gly Cys
      15             20             25

AAG AGC AAT GCT GAT GAC AAA CCA AAA GAG CAA AGC TCT TTA AGT CAA      147
Lys Ser Asn Ala Asp Asp Lys Pro Lys Glu Gln Ser Ser Leu Ser Gln
      30             35             40

AGC GTT CAA AAA GGC GCG TTT GTG ATT TTA GAA GAG CAA AAG GAT AAA      195
Ser Val Gln Lys Gly Ala Phe Val Ile Leu Glu Glu Gln Lys Asp Lys
      45             50             55             60

TCT TAC AAG GTT GTT GAA GAA TAC CCC AGC TCA AGA ACC CAC ATT ATA      243
Ser Tyr Lys Val Val Glu Glu Tyr Pro Ser Ser Arg Thr His Ile Ile
      65             70             75

```

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...375
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

TAGAGCTTGA TTTTTTTA ATG TTA ATA ATG GAT TGG AAA TTA AAA GTG GTG	51
Met Leu Ile Met Asp Trp Lys Leu Lys Val Val	
1 5 10	
AAA GAA ATC ATC ACC ATT ACC GCC ACA ACC GCC ACA ATG GGG ATC TTA	99
Lys Glu Ile Ile Thr Ile Thr Ala Thr Thr Ala Thr Met Gly Ile Leu	
15 20 25	
ACC ACA TAT TCA TTA AAC ACT AAT ATG AGC ACC ATT AAA GAA AAG CCG	147
Thr Thr Tyr Ser Leu Asn Thr Asn Met Ser Thr Ile Lys Glu Lys Pro	
30 35 40	
GCA AAA AAA GTA GAA AGC CTT GTT TTA GCC CCG GAT TTT GCG TTA ATG	195
Ala Lys Lys Val Glu Ser Leu Val Leu Ala Pro Asp Phe Ala Leu Met	
45 50 55	
ATA GAC TGC CCC ACT AAA GCG CAC CCT GTC ATT CCC CCC AAA AGC CCT	243
Ile Asp Cys Pro Thr Lys Ala His Pro Val Ile Pro Pro Lys Ser Pro	
60 65 70 75	
GAG ATG ATA TTC CCC AAG CCT TGC GCT TTA GTT TCT TTA TTT TTA TCG	291
Glu Met Ile Phe Pro Lys Pro Cys Ala Leu Val Ser Leu Phe Leu Ser	
80 85 90	
CTC ACG CCG TCT TTT AAA ATC ACA TCT AAA GTT TTA GCC GTC AAT AAG	339
Leu Thr Pro Ser Phe Lys Ile Thr Ser Lys Val Leu Ala Val Asn Lys	
95 100 105	
CTT TCT ATC GTT CCC ACT AGT GCT AAA GAA AGA GCG TAAGGCAACA ACTCTA	391
Leu Ser Ile Val Pro Thr Ser Ala Lys Glu Arg Ala	
110 115	
TCATTATTTT AAAATCCAAA TTT	414

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

```

Met Ala Lys His Asp Leu Val Gly Ser Val Leu Trp Asp Ala Tyr Ser
 1              5              10              15
Lys Glu Val Gln Arg Arg Met Asp Asn Pro Thr His Leu Gly Val Ile
      20              25              30
Thr Glu Glu Gln Ala Lys Ala Lys Asn Ala Lys Leu Ile Val Ala Asp
      35              40              45
Tyr Gly Ala Glu Ala Cys Gly Asp Ala Val Arg Leu Tyr Trp Leu Val
      50              55              60
Asp Glu Ser Thr Asp Arg Ile Val Asp Ala Lys Phe Lys Ser Phe Gly
      65              70              75              80
Cys Gly Thr Ala Ile Ala Ser Ser Asp Met Met Val Glu Leu Cys Leu
      85              90              95
Asn Lys Arg Val Gln Asp Ala Val Lys Ile Thr Asn Leu Asp Val Glu
      100              105              110
Arg Gly Leu Arg Asp Asp Pro Asp Thr Pro Ala Val Pro Gly Gln Lys
      115              120              125
Met His Cys Ser Val Met Ala Tyr Asp Val Ile Lys Lys Ala Ala Gly
      130              135              140
Met Tyr Leu Gly Lys Asn Ala Glu Asp Phe Glu Glu Glu Ile Ile Val
      145              150              155              160
Cys Glu Cys Ala Arg Val Ser Leu Gly Thr Ile Lys Glu Val Ile Lys
      165              170              175
Leu Asn Asp Leu Lys Ser Val Glu Glu Ile Thr Asn Tyr Thr Lys Ala
      180              185              190
Gly Ala Phe Cys Lys Ser Cys Val Arg Pro Gly Gly His Glu Lys Arg
      195              200              205
Asp Tyr Tyr Leu Val Asp Ile Leu Lys Glu Val Arg Glu Glu Met Glu
      210              215              220
Ala Glu Lys Leu Lys Ala Thr Ala Asn Lys Ser Gln Ser Gly Glu Leu
      225              230              235              240
Ala Phe Arg Glu Met Thr Met Val Gln Lys Ile Lys Ala Val Asp Lys
      245              250              255
Val Ile Asp Glu Asn Ile Arg Pro Met Leu Met Met Asp Gly Gly Asp
      260              265              270
Leu Glu Ile Leu Asp Ile Lys Glu Ser Asp Asp Tyr Ile Asp Val Tyr
      275              280              285
Ile Arg Tyr Met Gly Ala Cys Asp Gly Cys Met Ser Ala Thr Thr Gly
      290              295              300
Thr Leu Phe Ala Ile Glu Asn Ala Leu Gln Glu Leu Leu Asp Arg Ser
      305              310              315              320
Ile Arg Val Leu Pro Ile
      325

```

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

GAA GAA GAA ATC ATC GTG TGC GAG TGC GCT AGG GTG AGT TTA GGT ACG	531
Glu Glu Glu Ile Ile Val Cys Glu Cys Ala Arg Val Ser Leu Gly Thr	
155 160 165 170	
ATT AAA GAA GTG ATT AAG CTC AAT GAT TTA AAA AGC GTT GAA GAA ATC	579
Ile Lys Glu Val Ile Lys Leu Asn Asp Leu Lys Ser Val Glu Glu Ile	
175 180 185	
ACT AAC TAC ACC AAA GCC GGT GCT TTT TGT AAA AGC TGT GTG AGG CCT	627
Thr Asn Tyr Thr Lys Ala Gly Ala Phe Cys Lys Ser Cys Val Arg Pro	
190 195 200	
GGA GGG CAT GAA AAA AGG GAT TAT TAC TTG GTG GAT ATT CTT AAA GAA	675
Gly Gly His Glu Lys Arg Asp Tyr Tyr Leu Val Asp Ile Leu Lys Glu	
205 210 215	
GTG CGC GAA GAA ATG GAA GCT GAA AAA CTT AAA GCG ACC GCT AAT AAA	723
Val Arg Glu Glu Met Glu Ala Glu Lys Leu Lys Ala Thr Ala Asn Lys	
220 225 230	
TCC CAA AGC GGA GAA TTG GCT TTC AGG GAA ATG ACT ATG GTT CAA AAG	771
Ser Gln Ser Gly Glu Leu Ala Phe Arg Glu Met Thr Met Val Gln Lys	
235 240 245 250	
ATT AAA GCG GTG GAT AAA GTC ATT GAT GAA AAT ATC CGC CCG ATG CTT	819
Ile Lys Ala Val Asp Lys Val Ile Asp Glu Asn Ile Arg Pro Met Leu	
255 260 265	
ATG ATG GAT GGA GGG GAT TTA GAG ATT TTA GAC ATT AAA GAA AGC GAT	867
Met Met Asp Gly Gly Asp Leu Glu Ile Leu Asp Ile Lys Glu Ser Asp	
270 275 280	
GAT TAC ATT GAT GTG TAT ATC CGC TAC ATG GGG GCA TGT GAT GGG TGC	915
Asp Tyr Ile Asp Val Tyr Ile Arg Tyr Met Gly Ala Cys Asp Gly Cys	
285 290 295	
ATG AGC GCG ACT ACC GGG ACT TTA TTT GCC ATT GAA AAC GCT TTG CAG	963
Met Ser Ala Thr Thr Gly Thr Leu Phe Ala Ile Glu Asn Ala Leu Gln	
300 305 310	
GAA TTA TTG GAT CGC AGT ATC AGG GTG TTA CCG ATT TGAAC TTTT AGGGGG	1015
Glu Leu Leu Asp Arg Ser Ile Arg Val Leu Pro Ile	
315 320 325	
TGGAGGCCTT	1025

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 22...999
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

AAAGAATATA AAGGAATCAA A ATG GCA AAA CAT GAT TTA GTG GGT TCG GTT	51
Met Ala Lys His Asp Leu Val Gly Ser Val	
1 5 10	
CTC TGG GAC GCA TAT TCT AAA GAA GTT CAA AGG CGC ATG GAC AAC CCC	99
Leu Trp Asp Ala Tyr Ser Lys Glu Val Gln Arg Arg Met Asp Asn Pro	
15 20 25	
ACG CAT TTA GGG GTC ATC ACC GAA GAG CAG GCT AAA GCC AAA AAC GCT	147
Thr His Leu Gly Val Ile Thr Glu Glu Gln Ala Lys Ala Lys Asn Ala	
30 35 40	
AAG CTC ATT GTG GCG GAT TAT GGC GCA GAG GCA TGC GGT GAT GCG GTG	195
Lys Leu Ile Val Ala Asp Tyr Gly Ala Glu Ala Cys Gly Asp Ala Val	
45 50 55	
AGG TTG TAT TGG CTT GTA GAT GAA AGC ACG GAT AGA ATT GTT GAC GCG	243
Arg Leu Tyr Trp Leu Val Asp Glu Ser Thr Asp Arg Ile Val Asp Ala	
60 65 70	
AAG TTT AAA AGC TTT GGT TGC GGA ACA GCG ATC GCA AGC TCA GAC ATG	291
Lys Phe Lys Ser Phe Gly Cys Gly Thr Ala Ile Ala Ser Ser Asp Met	
75 80 85 90	
ATG GTA GAG TTG TGC TTG AAT AAA AGA GTC CAA GAT GCG GTA AAA ATC	339
Met Val Glu Leu Cys Leu Asn Lys Arg Val Gln Asp Ala Val Lys Ile	
95 100 105	
ACG AAT TTA GAT GTG GAA AGA GGC TTG AGA GAC GAT CCG GAC ACG CCG	387
Thr Asn Leu Asp Val Glu Arg Gly Leu Arg Asp Asp Pro Asp Thr Pro	
110 115 120	
GCG GTG CCT GGG CAA AAA ATG CAC TGC TCG GTG ATG GCG TAT GAT GTG	435
Ala Val Pro Gly Gln Lys Met His Cys Ser Val Met Ala Tyr Asp Val	
125 130 135	
ATC AAA AAA GCT GCC GGC ATG TAT TTG GGG AAA AAC GCT GAA GAT TTT	483
Ile Lys Lys Ala Ala Gly Met Tyr Leu Gly Lys Asn Ala Glu Asp Phe	
140 145 150	

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

```

Met Val Val Leu Gly Ser Thr Gly Ser Ile Gly Lys Asn Ala Leu Lys
 1           5           10           15
Ile Ala Lys Lys Phe Gly Ile Glu Ile Glu Ala Leu Ser Cys Gly Lys
 20           25           30
Asn Ile Ala Leu Ile Asn Glu Gln Ile Gln Val Phe Lys Pro Lys Lys
 35           40           45
Val Ala Ile Leu Asp Pro Ser Asp Leu Asn Asp Leu Glu Pro Leu Gly
 50           55           60
Ala Glu Val Phe Val Gly Leu Glu Gly Ile Asp Ala Met Ile Glu Glu
 65           70           75           80
Cys Thr Ser Asn Leu Val Leu Asn Ala Ile Val Gly Val Ala Gly Leu
 85           90           95
Lys Ala Ser Phe Lys Ser Leu Gln Arg Asn Lys Lys Leu Ala Leu Ala
100           105           110
Asn Lys Glu Ser Leu Val Ser Ala Gly His Leu Leu Asp Ile Ser Gln
115           120           125
Ile Thr Pro Ile Asp Ser Glu His Phe Gly Leu Trp Ala Leu Leu Gln
130           135           140
Asn Lys Thr Leu Lys Pro Lys Ser Leu Ile Ile Ser Ala Ser Gly Gly
145           150           155           160
Ala Phe Arg Asp Thr Pro Leu Glu Phe Ile Pro Ile Gln Asn Ala Gln
165           170           175
Asn Ala Leu Lys His Pro Asn Trp Ser Met Gly Ser Lys Ile Thr Ile
180           185           190
Asp Ser Ala Ser Met Val Asn Lys Leu Phe Glu Ile Leu Glu Thr Tyr
195           200           205
Trp Leu Phe Gly Ala Ser Leu Lys Ile Asp Ala Leu Ile Glu Arg Ser
210           215           220
Ser Ile Val His Ala Leu Val Glu Phe Glu Asp Asn Ser Ile Ile Ala
225           230           235           240
His Leu Ala Ser Ala Asp Met Gln Leu Pro Ile Ser Tyr Ala Ile Asp
245           250           255
Pro Lys Leu Ala Ser Leu Ser Ala Ser Ile Lys Pro Leu Asp Leu Tyr
260           265           270
Ala Leu Ser Ala Ile Lys Phe Glu Pro Ile Ser Met Glu Arg Tyr Thr
275           280           285
Leu Trp Cys Tyr Lys Asp Leu Leu Leu Glu Asn Pro Lys Leu Gly Val
290           295           300
Val Leu Asn Ala Ser Asn Glu Val Ala Met Glu Lys Phe Leu Asn Lys
305           310           315           320
Glu Ile Ala Phe Gly Gly Leu Ile Gln Thr Ile Ser Gln Ala Leu Glu
325           330           335
Ser Tyr Asp Lys Met Pro Phe Lys Leu Ser Ser Leu Glu Glu Val Leu
340           345           350
Glu Leu Asp Lys Glu Val Arg Glu Arg Phe Lys Asn Val Ala Gly Val
355           360           365

```

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1025 base pairs

Ile Thr Ile Asp Ser Ala Ser Met Val Asn Lys Leu Phe Glu Ile Leu	
190 195 200 205	
GAA ACT TAT TGG CTT TTT GGC GCG TCT TTA AAG ATT GAT GCG CTG ATT	674
Glu Thr Tyr Trp Leu Phe Gly Ala Ser Leu Lys Ile Asp Ala Leu Ile	
210 215 220	
GAA AGG AGT TCT ATC GTG CAT GCT TTG GTG GAG TTT GAA GAC AAC TCT	722
Glu Arg Ser Ser Ile Val His Ala Leu Val Glu Phe Glu Asp Asn Ser	
225 230 235	
ATC ATC GCG CAT TTA GCG AGC GCA GAT ATG CAA TTA CCC ATA AGC TAT	770
Ile Ile Ala His Leu Ala Ser Ala Asp Met Gln Leu Pro Ile Ser Tyr	
240 245 250	
GCG ATC GAT CCG AAG TTG GCC TCT TTG AGC GCG TCT ATC AAG CCC TTA	818
Ala Ile Asp Pro Lys Leu Ala Ser Leu Ser Ala Ser Ile Lys Pro Leu	
255 260 265	
GAT CTA TAC GCT TTA AGC GCG ATT AAA TTT GAA CCC ATT AGC ATG GAG	866
Asp Leu Tyr Ala Leu Ser Ala Ile Lys Phe Glu Pro Ile Ser Met Glu	
270 275 280 285	
CGC TAC ACT TTG TGG TGT TAT AAA GAC TTA CTG CTA GAA AAC CCT AAG	914
Arg Tyr Thr Leu Trp Cys Tyr Lys Asp Leu Leu Leu Glu Asn Pro Lys	
290 295 300	
CTT GGC GTG GTG CTG AAT GCG AGC AAT GAA GTG GCG ATG GAG AAG TTT	962
Leu Gly Val Val Leu Asn Ala Ser Asn Glu Val Ala Met Glu Lys Phe	
305 310 315	
TTA AAC AAA GAG ATC GCT TTT GGT GGC CTT ATC CAA ACC ATT TCT CAA	1010
Leu Asn Lys Glu Ile Ala Phe Gly Gly Leu Ile Gln Thr Ile Ser Gln	
320 325 330	
GCC TTA GAA TCA TAC GAT AAA ATG CCT TTC AAG CTC TCT AGT TTA GAA	1058
Ala Leu Glu Ser Tyr Asp Lys Met Pro Phe Lys Leu Ser Ser Leu Glu	
335 340 345	
GAA GTG CTG GAA TTA GAC AAA GAA GTT AGG GAG CGT TTT AAA AAT GTA	1106
Glu Val Leu Glu Leu Asp Lys Glu Val Arg Glu Arg Phe Lys Asn Val	
350 355 360 365	
GCG GGA GTG TAGTATAATA AGATTTTGCT TCTAATAGCG TTTTATTTC A T	1157
Ala Gly Val	

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

TAGGGGATTG A ATG GTT GTT TTA GGA AGC ACC GGC TCT ATT GGG AAA AAC	50
Met Val Val Leu Gly Ser Thr Gly Ser Ile Gly Lys Asn	
1 5 10	
GCC CTA AAA ATC GCA AAA AAA TTT GGC ATA GAA ATA GAG GCC TTA AGC	98
Ala Leu Lys Ile Ala Lys Lys Phe Gly Ile Glu Ile Glu Ala Leu Ser	
15 20 25	
TGT GGG AAA AAT ATC GCT TTA ATC AAT GAA CAA ATC CAA GTT TTC AAA	146
Cys Gly Lys Asn Ile Ala Leu Ile Asn Glu Gln Ile Gln Val Phe Lys	
30 35 40 45	
CCC AAG AAA GTG GCG ATT TTA GAT CCT AGC GAT TTG AAT GAT TTA GAG	194
Pro Lys Lys Val Ala Ile Leu Asp Pro Ser Asp Leu Asn Asp Leu Glu	
50 55 60	
CCT TTG GGT GCG GAA GTG TTT GTG GGG TTA GAG GGC ATT GAT GCG ATG	242
Pro Leu Gly Ala Glu Val Phe Val Gly Leu Glu Gly Ile Asp Ala Met	
65 70 75	
ATA GAA GAG TGC ACC TCA AAT TTA GTC CTT AAC GCC ATT GTG GGC GTG	290
Ile Glu Glu Cys Thr Ser Asn Leu Val Leu Asn Ala Ile Val Gly Val	
80 85 90	
GCA GGA TTG AAA GCG AGC TTT AAA AGC TTA CAA AGG AAT AAA AAA CTG	338
Ala Gly Leu Lys Ala Ser Phe Lys Ser Leu Gln Arg Asn Lys Lys Leu	
95 100 105	
GCC CTA GCG AAT AAA GAA AGC TTA GTG AGC GCG GGG CAT TTA TTA GAC	386
Ala Leu Ala Asn Lys Glu Ser Leu Val Ser Ala Gly His Leu Leu Asp	
110 115 120 125	
ATT TCA CAA ATC ACG CCC ATT GAT AGC GAG CAT TTT GGT TTG TGG GCG	434
Ile Ser Gln Ile Thr Pro Ile Asp Ser Glu His Phe Gly Leu Trp Ala	
130 135 140	
TTG TTG CAA AAC AAG ACT TTA AAG CCT AAA TCC TTA ATC ATT AGC GCG	482
Leu Leu Gln Asn Lys Thr Leu Lys Pro Lys Ser Leu Ile Ile Ser Ala	
145 150 155	
AGT GGG GGG GCT TTC AGG GAC ACG CCT TTA GAA TTT ATT CCT ATT CAA	530
Ser Gly Gly Ala Phe Arg Asp Thr Pro Leu Glu Phe Ile Pro Ile Gln	
160 165 170	
AAC GCG CAA AAT GCG CTC AAG CAC CCT AAT TGG AGC ATG GGA TCT AAA	578
Asn Ala Gln Asn Ala Leu Lys His Pro Asn Trp Ser Met Gly Ser Lys	
175 180 185	
ATC ACC ATT GAT TCA GCG AGC ATG GTC AAT AAG CTT TTT GAA ATC CTA	626

Gly Asp
180

TCGCAAAAAA ATTTGGC

661

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

Met	Val	Met	Ala	Ser	Val	Ile	Ala	Tyr	Gln	Lys	Ala	His	His	Ser	Glu
1				5					10					15	
Ala	Ile	Leu	Pro	Phe	Leu	Tyr	Pro	Gly	Val	Gly	Phe	Phe	Ala	Leu	Phe
			20					25					30		
Gly	Val	Tyr	Lys	Asp	Phe	Gly	Ala	Val	Ala	Ile	Ile	Trp	Leu	Leu	Val
		35				40						45			
Val	Val	Val	Ala	Ser	Asp	Val	Gly	Ala	Phe	Phe	Gly	Gly	Lys	Leu	Leu
		50				55					60				
Gly	Lys	Thr	Pro	Phe	Thr	Pro	Thr	Ser	Pro	Asn	Lys	Thr	Leu	Glu	Gly
65					70					75				80	
Ala	Leu	Ile	Gly	Val	Val	Leu	Ala	Ser	Val	Leu	Gly	Ser	Phe	Val	Gly
				85					90					95	
Met	Gly	Lys	Leu	Ser	Gly	Gly	Phe	Phe	Met	Ala	Leu	Phe	Phe	Ser	Phe
			100					105					110		
Leu	Ile	Ala	Leu	Val	Ala	Val	Phe	Gly	Asp	Leu	Tyr	Glu	Ser	Tyr	Leu
		115					120					125			
Lys	Arg	Lys	Val	Gly	Ile	Lys	Asp	Ser	Gly	Lys	Ile	Leu	Pro	Gly	His
		130				135					140				
Gly	Gly	Val	Leu	Asp	Arg	Leu	Asp	Ser	Met	Leu	Phe	Gly	Ala	Leu	Gly
145					150					155				160	
Leu	His	Ala	Leu	Leu	Tyr	Phe	Leu	Glu	Ile	Trp	Lys	Glu	Thr	Ala	Val
				165					170					175	
Phe	Leu	Gly	Asp												
			180												

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 12...1115

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

```

GGTGGCGGCG TATTTTAACG GGCGTCCTAT AGAATGCGCT CTTATTAGCG CC ATG GTC      58
                                   Met Val
                                   1

ATG GCT AGT GTT ATC GCT TAT CAA AAA GCG CAC CAT AGC GAA GCC ATT      106
Met Ala Ser Val Ile Ala Tyr Gln Lys Ala His His Ser Glu Ala Ile
      5                      10                      15

TTA CCC TTT TTG TAT CCG GGC GTT GGG TTT TTT GCG CTT TTT GGG GTT      154
Leu Pro Phe Leu Tyr Pro Gly Val Gly Phe Phe Ala Leu Phe Gly Val
      20                      25                      30

TAT AAG GAT TTT GGT GCA GTA GCG ATC ATT TGG CTT TTA GTC GTG GTG      202
Tyr Lys Asp Phe Gly Ala Val Ala Ile Ile Trp Leu Leu Val Val Val
      35                      40                      45                      50

GTT GCA AGC GAT GTG GGG GCG TTT TTT GGA GGC AAG CTT TTA GGC AAA      250
Val Ala Ser Asp Val Gly Ala Phe Phe Gly Gly Lys Leu Leu Gly Lys
                        55                      60                      65

ACC CCT TTC ACG CCC ACT TCG CCG AAT AAA ACC TTA GAG GGC GCG TTG      298
Thr Pro Phe Thr Pro Thr Ser Pro Asn Lys Thr Leu Glu Gly Ala Leu
                        70                      75                      80

ATT GGC GTG GTT TTG GCG AGC GTT TTA GGA TCG TTT GTG GGC ATG GGG      346
Ile Gly Val Val Leu Ala Ser Val Leu Gly Ser Phe Val Gly Met Gly
      85                      90                      95

AAA TTG AGC GGA GGC TTT TTT ATG GCG CTC TTT TTT AGT TTT TTA ATC      394
Lys Leu Ser Gly Gly Phe Phe Met Ala Leu Phe Phe Ser Phe Leu Ile
      100                      105                      110

GCT CTT GTG GCG GTG TTT GGG GAT TTG TAT GAA AGC TAT TTG AAA AGA      442
Ala Leu Val Ala Val Phe Gly Asp Leu Tyr Glu Ser Tyr Leu Lys Arg
      115                      120                      125                      130

AAG GTC GGT ATC AAA GAT AGC GGT AAG ATT TTA CCC GGG CAT GGG GGC      490
Lys Val Gly Ile Lys Asp Ser Gly Lys Ile Leu Pro Gly His Gly Gly
                        135                      140                      145

GTT TTA GAC CGG TTG GAT TCC ATG CTT TTT GGG GCT TTA GGC TTG CAT      538
Val Leu Asp Arg Leu Asp Ser Met Leu Phe Gly Ala Leu Gly Leu His
                        150                      155                      160

GCG CTG TTG TAT TTT TTA GAA ATT TGG AAA GAA ACG GCG GTG TTT TTA      586
Ala Leu Leu Tyr Phe Leu Glu Ile Trp Lys Glu Thr Ala Val Phe Leu
      165                      170                      175

GGG GAT TGAATGGTTG TTTTAGGAAG CACCGGCTCT ATTGGGAAAA ACGCCCTAAA AA      644

```

225		230		235		240
Ser Ile Cys Leu Met Leu Gly Ile Ala Tyr Ala Ala Ser Ile Gly Ser						
	245		250			255
Leu Gly Thr Leu Ile Gly Thr Pro Pro Asn Ala Leu Leu Ala Gly Tyr						
	260		265			270
Met Lys Thr Ala Phe Asn Ile Glu Ile Asp Phe Ala Gln Trp Met Val						
	275		280			285
Phe Gly Thr Pro Leu Ala Phe Ile Met Leu Ile Leu Ala Trp Leu Leu						
	290		295			300
Leu Thr Tyr Val Ile Phe Pro Leu Lys Ile Lys Glu Ile Pro Gly Gly						
305		310		315		320
Lys Glu Val Ile Arg Val Glu Leu Lys Lys Leu Gly Arg Leu Ser Gln						
	325		330			335
Ala Glu Ile Ser Val Gly Ile Ile Phe Ile Leu Ala Ser Leu Gly Trp						
	340		345			350
Ile Phe Leu Gly Val Met Leu Lys Ser Trp Gly Val Lys Ile Asp Lys						
	355		360			365
Ile Asp Ser Val Ile Ala Met Gly Val Ser Ala Leu Leu Phe Ile Leu						
	370		375			380
Pro Ala Asn His Gln Gly Asp Arg Leu Ile Asp Trp Gly Val Ala Lys						
385		390		395		400
Lys Leu Pro Trp Asp Val Leu Leu Leu Phe Gly Gly Gly Leu Ala Leu						
	405		410			415
Ser Ala Gln Phe Ser Lys Thr Gly Leu Ser Leu Trp Ile Gly His Leu						
	420		425			430
Val Ser Gly Phe Ser His Leu Pro Ile Leu Phe Ile Ile Val Met Val						
	435		440			445
Thr Leu Met Val Ile Phe Leu Thr Glu Ile Thr Ser Asn Thr Ala Thr						
	450		455			460
Ala Ala Ala Phe Leu Pro Val Ile Gly Gly Val Ala Met Gly Met Gly						
465		470		475		480
Tyr Glu Asn His Gln Ser Leu Leu Leu Thr Ile Pro Val Ala Leu Ser						
	485		490			495
Ala Thr Cys Ala Phe Met Leu Pro Val Val Thr Pro Pro Asn Ala Ile						
	500		505			510
Ala Tyr Gly Ser Gly Tyr Val Lys Ile Thr Asp Met Ile Lys Ala Gly						
	515		520			525
Leu Trp Leu Asn Leu Val Gly Val Val Leu Ile Ser Thr Phe Ser Tyr						
	530		535			540
Phe Leu Val Ser Leu Ile Phe Asn						
545		550				

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...592

AAA ATA ACG GAC ATG ATT AAA GCC GGT TTG TGG CTT AAT CTG GTA GGA 1637
 Lys Ile Thr Asp Met Ile Lys Ala Gly Leu Trp Leu Asn Leu Val Gly
 520 525 530 535

GTT GTT TTG ATT AGC ACG TTT AGC TAT TTT TTG GTT TCG TTA ATA TTT 1685
 Val Val Leu Ile Ser Thr Phe Ser Tyr Phe Leu Val Ser Leu Ile Phe
 540 545 550

AAT TGATTAAGGA AAAAAGTGAA AGAAGAGTTA TTAAAGAAA AATCTCGTTA CATTAC 1744
 Asn

AGGGTTTGTT TTAATC 1760

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

Met Glu Asn His Ser His Ala Asn Thr His Thr Asp Thr Arg Thr Asp
 1 5 10 15
 Asp Lys Ser Thr Lys Ile Val Arg Leu Leu Gly Leu Ile Gly Gly Ala
 20 25 30
 Leu Ile Ala Leu Val Ile Tyr Tyr Ala Leu Asn Ser Gln Met Pro His
 35 40 45
 Ile Val Glu Glu Ile Pro Lys Leu Ser Ser Leu Asn Tyr Lys Ala Met
 50 55 60
 Pro Val Val Ala Gly Val Ala Val Leu Met Gly Ile Trp Trp Met Thr
 65 70 75 80
 Glu Ala Ile Asp Leu Pro Ala Thr Ala Leu Leu Pro Leu Val Leu Phe
 85 90 95
 Ser Val Phe Ser Val Asp Gln Phe Ala Ser Val Ser Ser Ser Tyr Ala
 100 105 110
 Ser Pro Ile Ile Phe Leu Phe Met Gly Gly Phe Ile Leu Ala Leu Ser
 115 120 125
 Met Gln Lys Trp Asn Leu His Thr Arg Ile Ala Leu Ser Ile Ile Leu
 130 135 140
 Leu Val Gly Thr Ser Pro Arg Arg Leu Ile Leu Gly Phe Met Met Ala
 145 150 155 160
 Thr Gly Phe Leu Ser Met Trp Val Ser Asn Thr Ala Thr Ala Val Met
 165 170 175
 Met Leu Pro Val Gly Met Ser Val Leu Gln Leu Val Ala Lys Leu Val
 180 185 190
 Gly Lys Glu Asp Ala Ser Asn Ser Trp His Gln Lys Glu Glu Ile Thr
 195 200 205
 Lys Ala His Gly Gly Ile Met Ser Asn Ile Val His Lys Gly Lys Asp
 210 215 220
 Ile Thr Gln Val Ile Gln Glu Lys Thr Thr Ile Tyr Arg Thr Asn Phe

ATC ATG CTC ATT TTA GCG TGG CTC TTG CTC ACT TAT GTG ATT TTC CCT	965
Ile Met Leu Ile Leu Ala Trp Leu Leu Leu Thr Tyr Val Ile Phe Pro	
300 305 310	
TTA AAG ATT AAA GAA ATC CCA GGG GGT AAG GAA GTC ATT AGG GTA GAG	1013
Leu Lys Ile Lys Glu Ile Pro Gly Gly Lys Glu Val Ile Arg Val Glu	
315 320 325	
TTA AAA AAA TTA GGC CGT TTG AGT CAG GCG GAA ATC TCT GTG GGG ATT	1061
Leu Lys Lys Leu Gly Arg Leu Ser Gln Ala Glu Ile Ser Val Gly Ile	
330 335 340	
ATT TTT ATT TTA GCG TCT TTA GGG TGG ATT TTT TTA GGC GTA ATG TTA	1109
Ile Phe Ile Leu Ala Ser Leu Gly Trp Ile Phe Leu Gly Val Met Leu	
345 350 355	
AAA TCT TGG GGC GTT AAG ATA GAT AAA ATT GAT TCA GTG ATC GCT ATG	1157
Lys Ser Trp Gly Val Lys Ile Asp Lys Ile Asp Ser Val Ile Ala Met	
360 365 370 375	
GGG GTT TCT GCG CTT TTA TTC ATT TTG CCC GCT AAC CAT CAG GGC GAT	1205
Gly Val Ser Ala Leu Leu Phe Ile Leu Pro Ala Asn His Gln Gly Asp	
380 385 390	
AGG CTC ATT GAT TGG GGT GTT GCT AAA AAA CTC CCT TGG GAT GTG TTG	1253
Arg Leu Ile Asp Trp Gly Val Ala Lys Lys Leu Pro Trp Asp Val Leu	
395 400 405	
CTT TTA TTT GGC GGC GGG TTA GCC TTG AGC GCG CAA TTT TCT AAA ACC	1301
Leu Leu Phe Gly Gly Gly Leu Ala Leu Ser Ala Gln Phe Ser Lys Thr	
410 415 420	
GGG TTG AGT TTG TGG ATC GGG CAT TTA GTC TCT GGC TTT TCG CAT TTA	1349
Gly Leu Ser Leu Trp Ile Gly His Leu Val Ser Gly Phe Ser His Leu	
425 430 435	
CCG ATT TTA TTC ATC ATT GTC ATG GTT ACT TTA ATG GTC ATT TTC TTA	1397
Pro Ile Leu Phe Ile Ile Val Met Val Thr Leu Met Val Ile Phe Leu	
440 445 450 455	
ACC GAA ATC ACT TCT AAC ACC GCC ACC GCT GCC GCA TTT TTA CCG GTG	1445
Thr Glu Ile Thr Ser Asn Thr Ala Thr Ala Ala Ala Phe Leu Pro Val	
460 465 470	
ATT GGA GGG GTT GCG ATG GGC ATG GGT TAT GAA AAC CAT CAG AGC TTG	1493
Ile Gly Gly Val Ala Met Gly Met Gly Tyr Glu Asn His Gln Ser Leu	
475 480 485	
TTA TTG ACC ATT CCT GTA GCC TTG AGT GCG ACT TGC GCG TTC ATG CTC	1541
Leu Leu Thr Ile Pro Val Ala Leu Ser Ala Thr Cys Ala Phe Met Leu	
490 495 500	
CCT GTG GTC ACC CCA CCG AAT GCA ATA GCT TAT GGC TCT GGG TAT GTT	1589
Pro Val Val Thr Pro Pro Asn Ala Ile Ala Tyr Gly Ser Gly Tyr Val	
505 510 515	

Val	Leu	Met	Gly	Ile	Trp	Trp	Met	Thr	Glu	Ala	Ile	Asp	Leu	Pro	Ala		
			75					80					85				
ACC	GCG	CTT	TTA	CCT	TTG	GTG	CTT	TTT	AGC	GTC	TTT	AGC	GTG	GAT	CAA	341	
Thr	Ala	Leu	Leu	Pro	Leu	Val	Leu	Phe	Ser	Val	Phe	Ser	Val	Asp	Gln		
		90					95					100					
TTC	GCT	AGC	GTC	AGC	TCT	TCT	TAC	GCA	TCG	CCG	ATC	ATC	TTT	CTT	TTT	389	
Phe	Ala	Ser	Val	Ser	Ser	Ser	Tyr	Ala	Ser	Pro	Ile	Ile	Phe	Leu	Phe		
	105					110					115						
ATG	GGA	GGG	TTT	ATT	TTA	GCC	CTA	AGC	ATG	CAA	AAA	TGG	AAT	TTG	CAC	437	
Met	Gly	Gly	Phe	Ile	Leu	Ala	Leu	Ser	Met	Gln	Lys	Trp	Asn	Leu	His		
120					125					130				135			
ACG	CGC	ATC	GCT	TTA	AGC	ATT	ATT	TTA	TTA	GTA	GGC	ACA	AGC	CCT	AGG	485	
Thr	Arg	Ile	Ala	Leu	Ser	Ile	Ile	Leu	Leu	Val	Gly	Thr	Ser	Pro	Arg		
				140						145				150			
AGG	TTG	ATT	TTA	GGT	TTC	ATG	ATG	GCT	ACA	GGC	TTT	CTG	TCT	ATG	TGG	533	
Arg	Leu	Ile	Leu	Gly	Phe	Met	Met	Ala	Thr	Gly	Phe	Leu	Ser	Met	Trp		
			155					160						165			
GTG	AGC	AAT	ACC	GCA	ACG	GCG	GTG	ATG	ATG	CTC	CCT	GTT	GGC	ATG	AGC	581	
Val	Ser	Asn	Thr	Ala	Thr	Ala	Val	Met	Met	Leu	Pro	Val	Gly	Met	Ser		
		170					175						180				
GTT	TTG	CAA	TTA	GTC	GCT	AAA	CTG	GTG	GGC	AAA	GAA	GAC	GCC	TCT	AAT	629	
Val	Leu	Gln	Leu	Val	Ala	Lys	Leu	Val	Gly	Lys	Glu	Asp	Ala	Ser	Asn		
	185					190					195						
TCA	TGG	CAT	CAA	AAA	GAA	GAA	ATC	ACC	AAA	GCG	CAT	GGG	GGT	ATT	ATG	677	
Ser	Trp	His	Gln	Lys	Glu	Glu	Ile	Thr	Lys	Ala	His	Gly	Gly	Ile	Met		
200					205					210				215			
AGT	AAT	ATC	GTG	CAT	AAG	GGT	AAA	GAT	ATT	ACT	CAA	GTC	ATT	CAA	GAA	725	
Ser	Asn	Ile	Val	His	Lys	Gly	Lys	Asp	Ile	Thr	Gln	Val	Ile	Gln	Glu		
				220					225					230			
AAG	ACT	ACT	ATC	TAT	CGC	ACG	AAT	TTC	AGT	ATT	TGC	TTG	ATG	CTT	GGC	773	
Lys	Thr	Thr	Ile	Tyr	Arg	Thr	Asn	Phe	Ser	Ile	Cys	Leu	Met	Leu	Gly		
			235					240						245			
ATC	GCT	TAT	GCG	GCT	TCT	ATT	GGC	TCT	TTA	GGC	ACT	TTG	ATT	GGC	ACG	821	
Ile	Ala	Tyr	Ala	Ala	Ser	Ile	Gly	Ser	Leu	Gly	Thr	Leu	Ile	Gly	Thr		
		250					255							260			
CCG	CCT	AAC	GCT	TTA	TTG	GCC	GGC	TAT	ATG	AAA	ACC	GCT	TTC	AAT	ATT	869	
Pro	Pro	Asn	Ala	Leu	Leu	Ala	Gly	Tyr	Met	Lys	Thr	Ala	Phe	Asn	Ile		
		265				270					275						
GAA	ATT	GAT	TTC	GCT	CAG	TGG	ATG	GTG	TTT	GGG	ACG	CCG	TTA	GCC	TTT	917	
Glu	Ile	Asp	Phe	Ala	Gln	Trp	Met	Val	Phe	Gly	Thr	Pro	Leu	Ala	Phe		
280					285					290					295		

```

Gly Lys His His Ile Arg Val Asn Ala Leu Ser Ala Gly Pro Ile Arg
      180      185      190
Thr Leu Ala Ser Ser Gly Ile Ala Asp Phe Arg Met Ile Leu Lys Trp
      195      200      205
Asn Glu Ile Asn Ala Pro Leu Arg Lys Asn Val Ser Leu Glu Glu Val
      210      215      220
Gly Asn Ala Gly Met Tyr Leu Leu Ser Ser Leu Ser Ser Gly Val Ser
      225      230      235      240
Gly Glu Val His Phe Val Asp Ala Gly Tyr His Val Met Gly Met Gly
      245      250      255
Ala Val Glu Glu Lys Asp Asn Lys Ala Thr Leu Leu Trp Asp Leu His
      260      265      270
Lys Glu Gln
      275

```

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...1688
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

```

TGGAGGTTAG TAATTTTAAA GGGTAAAATA AA ATG GAA AAT CAT TCG CAT GCC      53
      Met Glu Asn His Ser His Ala
      1      5

AAT ACG CAT ACC GAT ACG CGC ACC GAT GAT AAA AGC ACT AAG ATC GTG      101
Asn Thr His Thr Asp Thr Arg Thr Asp Asp Lys Ser Thr Lys Ile Val
      10      15      20

CGC TTG TTG GGG TTA ATA GGG GGA GCG TTA ATC GCG CTT GTT ATC TAC      149
Arg Leu Leu Gly Leu Ile Gly Gly Ala Leu Ile Ala Leu Val Ile Tyr
      25      30      35

TAT GCG CTC AAT TCT CAA ATG CCT CAT ATT GTA GAA GAA ATC CCC AAG      197
Tyr Ala Leu Asn Ser Gln Met Pro His Ile Val Glu Glu Ile Pro Lys
      40      45      50      55

CTC AGT TCT TTG AAT TAT AAG GCG ATG CCT GTT GTG GCA GGG GTG GCT      245
Leu Ser Ser Leu Asn Tyr Lys Ala Met Pro Val Val Ala Gly Val Ala
      60      65      70

GTT TTA ATG GGG ATA TGG TGG ATG ACT GAA GCC ATT GAC TTG CCC GCA      293

```

```

Ile Leu Lys Trp Asn Glu Ile Asn Ala Pro Leu Arg Lys Asn Val Ser
205                210                215                220

TTA GAA GAA GTG GGC AAT GCC GGG ATG TAT TTG CTC TCT AGT TTG TCT      723
Leu Glu Glu Val Gly Asn Ala Gly Met Tyr Leu Leu Ser Ser Leu Ser
                225                230                235

AGC GGG GTG AGT GGG GAA GTG CAT TTT GTG GAT GCT GGC TAT CAT GTT      771
Ser Gly Val Ser Gly Glu Val His Phe Val Asp Ala Gly Tyr His Val
                240                245                250

ATG GGC ATG GGG GCT GTG GAA GAA AAA GAT AAT AAA GCT ACG CTA CTG      819
Met Gly Met Gly Ala Val Glu Glu Lys Asp Asn Lys Ala Thr Leu Leu
                255                260                265

TGG GAT TTG CAT AAA GAA CAA TAAGGGGTAT TGATGAAATT AAGCGAATTG TTAA      874
Trp Asp Leu His Lys Glu Gln
                270                275

ACGCCTATTC TATTG                                                    889

```

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

```

Met Gly Phe Leu Lys Gly Lys Lys Gly Leu Ile Val Gly Val Ala Asn
 1                5                10                15
Asn Lys Ser Ile Ala Tyr Gly Ile Ala Gln Ser Cys Phe Asn Gln Gly
 20                25                30
Ala Thr Leu Ala Phe Thr Tyr Leu Asn Glu Ser Leu Glu Lys Arg Val
 35                40                45
Arg Pro Ile Ala Gln Glu Leu Asn Ser Pro Tyr Val Tyr Glu Leu Asp
 50                55                60
Val Ser Lys Glu Glu His Phe Lys Ser Leu Tyr Asn Ser Val Lys Lys
 65                70                75                80
Asp Leu Gly Ser Leu Asp Phe Ile Val His Ser Val Ala Phe Ala Pro
 85                90                95
Lys Glu Ala Leu Glu Gly Ser Leu Leu Glu Thr Ser Lys Ser Ala Phe
100                105                110
Asn Thr Ala Met Glu Ile Ser Val Tyr Ser Leu Ile Glu Leu Thr Asn
115                120                125
Thr Leu Lys Pro Leu Leu Asn Asn Gly Ala Ser Val Leu Thr Leu Ser
130                135                140
Tyr Leu Gly Ser Thr Lys Tyr Met Ala His Tyr Asn Val Met Gly Leu
145                150                155                160
Ala Lys Ala Ala Leu Glu Ser Ala Val Arg Tyr Leu Ala Val Asp Leu
165                170                175

```


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

TTATAAAGGA AAATC ATG GGA TTT TTA AAA GGT AAA AAA GGG CTT ATT GTA	51
Met Gly Phe Leu Lys Gly Lys Lys Gly Leu Ile Val	
1 5 10	
GGG GTG GCG AAC AAT AAA TCC ATC GCT TAT GGG ATC GCT CAA TCT TGT	99
Gly Val Ala Asn Asn Lys Ser Ile Ala Tyr Gly Ile Ala Gln Ser Cys	
15 20 25	
TTC AAT CAA GGG GCT ACT TTG GCT TTC ACT TAT TTG AAT GAG AGT TTA	147
Phe Asn Gln Gly Ala Thr Leu Ala Phe Thr Tyr Leu Asn Glu Ser Leu	
30 35 40	
GAA AAG CGC GTA AGG CCT ATC GCG CAG GAA TTG AAT AGC CCC TAT GTG	195
Glu Lys Arg Val Arg Pro Ile Ala Gln Glu Leu Asn Ser Pro Tyr Val	
45 50 55 60	
TAT GAA TTG GAT GTG AGC AAA GAA GAG CAT TTC AAG TCG CTA TAC AAT	243
Tyr Glu Leu Asp Val Ser Lys Glu Glu His Phe Lys Ser Leu Tyr Asn	
65 70 75	
AGC GTT AAA AAG GAT TTA GGC TCA TTG GAT TTT ATT GTT CAT AGC GTG	291
Ser Val Lys Lys Asp Leu Gly Ser Leu Asp Phe Ile Val His Ser Val	
80 85 90	
GCC TTT GCC CCT AAA GAG GCT TTA GAG GGG AGC TTG TTG GAA ACT TCT	339
Ala Phe Ala Pro Lys Glu Ala Leu Glu Gly Ser Leu Leu Glu Thr Ser	
95 100 105	
AAA AGC GCG TTT AAC ACC GCT ATG GAA ATT TCT GTT TAT TCT TTA ATA	387
Lys Ser Ala Phe Asn Thr Ala Met Glu Ile Ser Val Tyr Ser Leu Ile	
110 115 120	
GAG CTG ACA AAC ACC CTA AAA CCT TTA TTG AAT AAC GGA GCG TCT GTT	435
Glu Leu Thr Asn Thr Leu Lys Pro Leu Leu Asn Asn Gly Ala Ser Val	
125 130 135 140	
TTG ACT CTA AGC TAT TTG GGT AGC ACC AAA TAC ATG GCG CAT TAC AAT	483
Leu Thr Leu Ser Tyr Leu Gly Ser Thr Lys Tyr Met Ala His Tyr Asn	
145 150 155	
GTG ATG GGG TTG GCT AAA GCG GCC CTA GAG AGT GCG GTG CGT TAT TTA	531
Val Met Gly Leu Ala Lys Ala Ala Leu Glu Ser Ala Val Arg Tyr Leu	
160 165 170	
GCG GTG GAT TTA GGC AAA CAC CAT ATA AGA GTG AAT GCC CTA TCG GCC	579
Ala Val Asp Leu Gly Lys His His Ile Arg Val Asn Ala Leu Ser Ala	
175 180 185	
GGG CCT ATT AGG ACG CTC GCT TCT AGC GGG ATC GCT GAT TTT AGA ATG	627
Gly Pro Ile Arg Thr Leu Ala Ser Ser Gly Ile Ala Asp Phe Arg Met	
190 195 200	
ATT TTA AAA TGG AAT GAA ATC AAC GCC CCT TTA AGA AAA AAT GTG AGT	675

			100					105				110					
Thr	Tyr	Glu	Lys	Leu	Lys	Asp	Glu	Leu	Lys	Lys	Ile	Lys	Lys	Ser	Lys		
		115					120					125					
Leu	Lys	Ser	Phe	Ile	Gln	Ser	Tyr	Val	Ser	Asp	Leu	Lys	Asn	Phe	Tyr		
		130				135					140						
Gln	Ala	Phe	Leu	Asp	Leu	Ser	Glu	Ile	Asp	Thr	Asn	Pro	Thr	Thr			
145				150					155					160			
Phe	Lys	Val	Met	Leu	Ile	Asn	Lys	Ile	Asp	Ser	Ser	Phe	Phe	Asn	Ser		
			165					170					175				
Leu	Ile	Arg	Leu	Lys	Ile	Asn	Asn	Glu	Leu	Asp	Asp	Glu	Thr	Leu	Lys		
		180						185					190				
Leu	Phe	Ala	Lys	Thr	Asp	Ile	Val	Leu	Phe	Lys	Ala	Thr	Arg	Asp	Arg		
	195					200					205						
Pro	Gly	Thr	Asp	Asn	Leu	Ile	Asn	Ala	Tyr	Leu	Lys	Lys	Gly	Lys	Glu		
	210				215					220							
Gly	Leu	Lys	Ser	Glu	Met	Ile	Ala	Gln	Cys	Arg	Asn	Asp	Ile	Gly	Leu		
225				230				235					240				
Ala	Phe	Trp	Gln	Ser	Val	Asn	Asn	Ala	Ser	Asn	Ser	Ser	Cys	Phe	His		
			245					250					255				
Tyr	Ile	Phe	Phe	Glu	Lys	Asn	Cys	Gln	Glu	Met	Gly	Leu	Ala	Asp	Leu		
		260						265					270				
Lys	Lys	Leu	Ile	Pro	Arg	Lys	Gln	Phe	Ser	Gln	Glu	Lys	Glu	His	Ile		
	275					280						285					
Ile	Pro	Ile	Asn	Leu	Leu	Lys	Gln	Glu	Ser	Asn	Asn	Lys	Ile	Arg	Asp		
	290				295					300							
Leu	Gly	Phe	Glu	Asp	Lys	Lys	Asp	Leu	Glu	Asp	Tyr	Ile	Asp	Thr	Tyr		
305				310						315				320			
Gly	Asn	Leu	Ile	Ser	Leu	Glu	Lys	Ser	Leu	Asn	Arg	Lys	Ala	Ser	Asp		
			325					330					335				
Lys	Asp	Leu	Tyr	Gly	Lys	Asp	Glu	Ile	Tyr	Lys	Ser	Ser	Glu	Ile	Pro		
		340						345					350				
Phe	Asn	Arg	Arg	Phe	Asp	Thr	Lys	Asn	Phe	Asn	Lys	Lys	Ala	Leu	Val		
	355					360						365					
Lys	Arg	Asn	Glu	Glu	Met	Arg	Glu	Trp	Leu	Ile	Asp	Thr	Phe	Phe	Lys		
	370					375					380						
Asp	Phe	Ala	Ala	His													
385																	

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...840
- (D) OTHER INFORMATION:

```

TTC TCC CAA GAA AAA GAA CAC ATC ATC CCC ATC AAT TTA TTA AAA CAG      918
Phe Ser Gln Glu Lys Glu His Ile Ile Pro Ile Asn Leu Leu Lys Gln
                285                      290                      295

GAA TCC AAC AAT AAG ATC AGA GAT CTT GGT TTT GAA GAC AAA AAA GAT      966
Glu Ser Asn Asn Lys Ile Arg Asp Leu Gly Phe Glu Asp Lys Lys Asp
                300                      305                      310

CTT GAA GAC TAC ATT GAC ACA TAC GGC AAC CTC ATC TCC CTG GAA AAA      1014
Leu Glu Asp Tyr Ile Asp Thr Tyr Gly Asn Leu Ile Ser Leu Glu Lys
                315                      320                      325

TCG CTC AAT CGT AAG GCA AGC GAT AAG GAT CTG TAT GGA AAA GAT GAA      1062
Ser Leu Asn Arg Lys Ala Ser Asp Lys Asp Leu Tyr Gly Lys Asp Glu
                330                      335                      340

ATC TAT AAA AGT AGT GAG ATC CCT TTC AAC AGG CGC TTT GAT ACA AAA      1110
Ile Tyr Lys Ser Ser Glu Ile Pro Phe Asn Arg Arg Phe Asp Thr Lys
                345                      350                      355                      360

AAC TTC AAT AAG AAG GCA TTG GTA AAA AGA AAT GAA GAA ATG CGA GAA      1158
Asn Phe Asn Lys Lys Ala Leu Val Lys Arg Asn Glu Glu Met Arg Glu
                365                      370                      375

TGG CTG ATC GAC ACC TTT TTT AAG GAT TTC GCC GCC CAC TAAAGAGAGT GA      1209
Trp Leu Ile Asp Thr Phe Phe Lys Asp Phe Ala Ala His
                380                      385

GATTAAAGA GAGTGATCGC ACTCA                                          1234

```

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

```

Met Val Leu Met Arg Phe Glu Glu Pro Asp Pro Gly Arg Ala Ile Arg
 1          5          10          15
Thr Phe Gln Ser Val Asn Asp Arg Gly Val Pro Leu Leu Leu Asp
 20          25          30
Lys Leu Lys Ser Leu Leu Ile Tyr Ser Asn Ile Phe Cys Asp Gly
 35          40          45
Lys Arg Gly Leu Asp Gln Phe Ile Ile Asp His Phe Gly Glu Ile Phe
 50          55          60
Lys Ile Phe Ala Lys Ile Lys Lys Ser Asp His Ile Ser Ser Val Gly
 65          70          75          80
Gly Phe Asp Glu Gly Asp Ile Phe Arg Tyr His Ala Gly Ser Gln Lys
 85          90          95
Phe Asp Gly Ile Glu Phe Leu Gly His Tyr Glu Ala Ser Thr Asp Lys

```

ATC GAT CAT TTT GGG GAG ATC TTT AAG ATC TTT GCC AAG ATT AAA AAG	246
Ile Asp His Phe Gly Glu Ile Phe Lys Ile Phe Ala Lys Ile Lys Lys	
60 65 70	
AGC GAC CAC ATC TCC AGC GTT GGA GGC TTT GAT GAA GGC GAT ATC TTC	294
Ser Asp His Ile Ser Ser Val Gly Gly Phe Asp Glu Gly Asp Ile Phe	
75 80 85	
CGC TAC CAC GCA GGG AGC CAA AAA TTT GAT GGA ATC GAG TTT TTA GGG	342
Arg Tyr His Ala Gly Ser Gln Lys Phe Asp Gly Ile Glu Phe Leu Gly	
90 95 100	
CAC TAC GAA GCA AGC ACG GAC AAA ACC TAC GAG AAA CTC AAA GAT GAA	390
His Tyr Glu Ala Ser Thr Asp Lys Thr Tyr Glu Lys Leu Lys Asp Glu	
105 110 115 120	
CTA AAA AAA ATC AAA AAA AGC AAA TTG AAA AGT TTC ATC CAA TCC TAT	438
Leu Lys Lys Ile Lys Lys Ser Lys Leu Lys Ser Phe Ile Gln Ser Tyr	
125 130 135	
GTC AGC GAT TTG AAA AAT TTC TAT CAG GCT TTT CTT GAT CTA TTG AGC	486
Val Ser Asp Leu Lys Asn Phe Tyr Gln Ala Phe Leu Asp Leu Leu Ser	
140 145 150	
GAG ATT GAC ACC AAC CCA ACC ACC TTT AAG GTC ATG CTC ATC AAC AAG	534
Glu Ile Asp Thr Asn Pro Thr Thr Phe Lys Val Met Leu Ile Asn Lys	
155 160 165	
ATC GAC TCG TCT TTT TTC AAT TCG CTC ATC CGC CTG AAA ATC AAC AAC	582
Ile Asp Ser Ser Phe Phe Asn Ser Leu Ile Arg Leu Lys Ile Asn Asn	
170 175 180	
GAA CTA GAC GAT GAA ACG CTG AAA CTC TTT GCC AAA ACC GAT ATT GTG	630
Glu Leu Asp Asp Glu Thr Leu Lys Leu Phe Ala Lys Thr Asp Ile Val	
185 190 195 200	
CTT TTC AAA GCT ACT AGA GAT AGG CCA GGA ACG GAC AAC CTG ATT AAT	678
Leu Phe Lys Ala Thr Arg Asp Arg Pro Gly Thr Asp Asn Leu Ile Asn	
205 210 215	
GCG TAT CTT AAA AAG GGC AAA GAG GGA TTG AAG AGC GAG ATG ATT GCT	726
Ala Tyr Leu Lys Lys Gly Lys Glu Gly Leu Lys Ser Glu Met Ile Ala	
220 225 230	
CAA TGC AGA AAT GAT ATA GGG CTG GCT TTT TGG CAG TCT GTA AAC AAC	774
Gln Cys Arg Asn Asp Ile Gly Leu Ala Phe Trp Gln Ser Val Asn Asn	
235 240 245	
GCA TCC AAC TCA TCA TGC TTC CAC TAT ATC TTC TTT GAA AAG AAC TGC	822
Ala Ser Asn Ser Ser Cys Phe His Tyr Ile Phe Phe Glu Lys Asn Cys	
250 255 260	
CAG GAG ATG GGT CTT GCC GAT CTC AAA AAA TTG ATC CCT AGG AAG CAA	870
Gln Glu Met Gly Leu Ala Asp Leu Lys Lys Leu Ile Pro Arg Lys Gln	
265 270 275 280	

```

      195              200              205
Leu Cys Pro Ile Leu Ala Thr Thr Leu Gly Ala Ser Met Ile Glu Lys
  210              215              220
His Phe Ile Leu Asn Lys Ser Leu Gln Thr Pro Asp Ser Ala Phe Ser
  225              230              235              240
Met Asp Phe Asn Gly Phe Lys Ser Met Val Glu Ala Ile Lys Gln Ser
      245              250              255
Val Leu Ala Leu Gly Glu Glu Glu Pro Arg Ile Asn Pro Lys Thr Leu
      260              265              270
Glu Lys Arg Arg Phe Phe Ala Arg Ser Leu Phe Val Ile Lys Asp Ile
      275              280              285
Gln Lys Gly Glu Ala Leu Thr Glu Asn Asn Ile Lys Ala Leu Arg Pro
      290              295              300
Asn Leu Gly Leu His Pro Lys Phe Tyr Lys Glu Ile Leu Gly Gln Lys
  305              310              315              320
Ala Ser Lys Phe Leu Lys Ala Asn Thr Pro Leu Ser Ala Asp Asp Ile
      325              330              335
Glu Arg Ser Leu
      340

```

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1197
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

```

GTGAATGAGC GTTTGGAGGT GCTGTTGGAA  ATG GTT TTG ATG CGG TTT GAA GAG      54
                               Met Val Leu Met Arg Phe Glu Glu
                               1              5

CCC GAT CCT GGA AGA GCT ATC AGA ACC TTT CAG AGC GTG AAT GAC AGA      102
Pro Asp Pro Gly Arg Ala Ile Arg Thr Phe Gln Ser Val Asn Asp Arg
  10              15              20

GGC GTG CCT CTC CTC TTG CTA GAC AAA CTA AAA TCC CTT CTC ATC TAT      150
Gly Val Pro Leu Leu Leu Leu Asp Lys Leu Lys Ser Leu Leu Ile Tyr
  25              30              35              40

TAC TCC AAC ATT TTT TGC GAT GGG AAA AGG GGG CTA GAC CAA TTT ATC      198
Tyr Ser Asn Ile Phe Cys Asp Gly Lys Arg Gly Leu Asp Gln Phe Ile
      45              50              55

```

```

GTT ATT AAG GAT ATT CAA AAA GGC GAA GCA TTG ACT GAA AAC AAT ATC      915
Val Ile Lys Asp Ile Gln Lys Gly Glu Ala Leu Thr Glu Asn Asn Ile
    285                      290                      295

AAA GCC TTA CGC CCC AAC CTT GGC TTA CAC CCT AAA TTT TAT AAA GAA      963
Lys Ala Leu Arg Pro Asn Leu Gly Leu His Pro Lys Phe Tyr Lys Glu
    300                      305                      310                      315

ATT TTA GGC CAA AAA GCA TCA AAA TTC TTA AAA GCC AAC ACC CCC TTA      1011
Ile Leu Gly Gln Lys Ala Ser Lys Phe Leu Lys Ala Asn Thr Pro Leu
                320                      325                      330

AGC GCT GAT GAT ATA GAA CGC TCA TTG TAGGTTTCGTT TTGATCAAAA AATGGGG      1065
Ser Ala Asp Asp Ile Glu Arg Ser Leu
                335                      340

TTTTTAATTT TGTTTTATGG TTTTAGATTT GATTTTAAAC TCATTTTCTT TATTTTAA      1123

```

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

```

Met Leu Gln Pro Pro Lys Ile Val Ala Glu Leu Ser Ala Asn His Asn
  1                      5                      10                      15
Gln Asp Leu Asn Leu Ala Lys Glu Ser Leu His Ala Ile Lys Glu Ser
                20                      25                      30
Gly Ala Asp Phe Val Lys Leu Gln Thr Tyr Thr Pro Ser Cys Met Thr
                35                      40                      45
Leu Asn Ser Lys Glu Asp Pro Phe Ile Ile Gln Gly Thr Leu Trp Asp
    50                      55                      60
Lys Glu Asn Leu Tyr Glu Leu Tyr Gln Lys Ala Ser Thr Pro Leu Glu
    65                      70                      75                      80
Trp His Ala Glu Leu Phe Glu Leu Ala Arg Lys Leu Asp Leu Gly Ile
                85                      90                      95
Phe Ser Ser Pro Phe Ser Ser Gln Ala Leu Glu Leu Leu Glu Ser Leu
                100                      105                      110
Asn Cys Pro Met Tyr Lys Ile Ala Ser Phe Glu Ile Val Asp Leu Asp
                115                      120                      125
Leu Ile Glu Lys Ala Ala Arg Thr Gln Lys Pro Ile Ile Leu Ser Ser
    130                      135                      140
Gly Ile Ala Thr His Thr Glu Leu Gln Asp Ala Ile Ser Leu Cys Arg
    145                      150                      155                      160
Arg Val Asn Asn Phe Asp Ile Thr Leu Leu Lys Cys Val Ser Ala Tyr
                165                      170                      175
Pro Ser Lys Ile Glu Asp Ala Asn Leu Leu Ser Met Val Lys Leu Gly
                180                      185                      190
Glu Ile Phe Gly Val Lys Phe Gly Leu Ser Asp His Thr Ile Gly Ser

```

Gly	Thr	Leu	Trp	Asp	Lys	Glu	Asn	Leu	Tyr	Glu	Leu	Tyr	Gln	Lys	Ala	
60					65					70					75	
TCT	ACC	CCC	CTA	GAA	TGG	CAT	GCT	GAA	TTG	TTT	GAG	TTG	GCT	AGA	AAG	291
Ser	Thr	Pro	Leu	Glu	Trp	His	Ala	Glu	Leu	Phe	Glu	Leu	Ala	Arg	Lys	
				80					85					90		
CTT	GAT	TTA	GGC	ATT	TTT	AGC	TCG	CCT	TTT	AGT	TCA	CAA	GCT	TTA	GAG	339
Leu	Asp	Leu	Gly	Ile	Phe	Ser	Ser	Pro	Phe	Ser	Ser	Gln	Ala	Leu	Glu	
			95					100					105			
CTT	TTA	GAG	AGC	CTA	AAT	TGC	CCC	ATG	TAT	AAA	ATC	GCT	AGT	TTT	GAA	387
Leu	Leu	Glu	Ser	Leu	Asn	Cys	Pro	Met	Tyr	Lys	Ile	Ala	Ser	Phe	Glu	
		110					115					120				
ATC	GTT	GAT	TTG	GAC	TTG	ATT	GAA	AAG	GCC	GCT	CGC	ACA	CAA	AAG	CCC	435
Ile	Val	Asp	Leu	Asp	Leu	Ile	Glu	Lys	Ala	Ala	Arg	Thr	Gln	Lys	Pro	
	125					130					135					
ATT	ATC	CTT	TCT	AGC	GGT	ATC	GCT	ACA	CAC	ACC	GAA	TTG	CAA	GAC	GCT	483
Ile	Ile	Leu	Ser	Ser	Gly	Ile	Ala	Thr	His	Thr	Glu	Leu	Gln	Asp	Ala	
140					145					150					155	
ATC	TCA	TTG	TGC	AGA	AGA	GTG	AAT	AAT	TTT	GAC	ATC	ACC	CTT	TTA	AAA	531
Ile	Ser	Leu	Cys	Arg	Arg	Val	Asn	Asn	Phe	Asp	Ile	Thr	Leu	Leu	Lys	
				160					165					170		
TGC	GTG	AGC	GCT	TAT	CCC	AGT	AAA	ATA	GAA	GAC	GCT	AAC	TTG	TTG	AGC	579
Cys	Val	Ser	Ala	Tyr	Pro	Ser	Lys	Ile	Glu	Asp	Ala	Asn	Leu	Leu	Ser	
			175					180					185			
ATG	GTT	AAA	TTA	GGC	GAA	ATC	TTT	GGC	GTT	AAA	TTT	GGC	TTG	AGC	GAT	627
Met	Val	Lys	Leu	Gly	Glu	Ile	Phe	Gly	Val	Lys	Phe	Gly	Leu	Ser	Asp	
		190					195					200				
CAC	ACG	ATT	GGC	TCT	CTT	TGC	CCC	ATT	TTA	GCC	ACC	ACT	TTA	GGA	GCG	675
His	Thr	Ile	Gly	Ser	Leu	Cys	Pro	Ile	Leu	Ala	Thr	Thr	Leu	Gly	Ala	
	205					210					215					
AGC	ATG	ATA	GAA	AAG	CAT	TTC	ATT	TTA	AAC	AAA	TCC	TTA	CAA	ACC	CCA	723
Ser	Met	Ile	Glu	Lys	His	Phe	Ile	Leu	Asn	Lys	Ser	Leu	Gln	Thr	Pro	
220					225					230					235	
GAC	AGC	GCT	TTT	AGC	ATG	GAT	TTT	AAC	GGA	TTT	AAA	AGC	ATG	GTT	GAA	771
Asp	Ser	Ala	Phe	Ser	Met	Asp	Phe	Asn	Gly	Phe	Lys	Ser	Met	Val	Glu	
				240					245					250		
GCC	ATC	AAG	CAA	AGC	GTT	TTA	GCC	TTA	GGC	GAA	GAA	GAG	CCA	AGA	ATC	819
Ala	Ile	Lys	Gln	Ser	Val	Leu	Ala	Leu	Gly	Glu	Glu	Glu	Pro	Arg	Ile	
		255						260					265			
AAT	CCA	AAG	ACT	TTA	GAA	AAG	CGA	AGA	TTT	TTT	GCA	CGC	TCT	TTA	TTT	867
Asn	Pro	Lys	Thr	Leu	Glu	Lys	Arg	Arg	Phe	Phe	Ala	Arg	Ser	Leu	Phe	
		270					275					280				

```

Leu Lys Asn Arg Gly Phe Thr Asp Gly Tyr Leu Met Arg Arg Pro Phe
  210                      215                      220
Glu Arg Leu Asp Thr Gln Asn His Gln Thr Ala Ile Ser Glu Gly Asp
  225                      230                      235                      240
Phe Gln Val Asn Gly Glu Ile Thr Glu Asp Gly Arg Phe Phe Ala Cys
                      245                      250                      255
Lys Phe Thr Thr Thr Thr Asn Thr Ala Tyr Glu Ile Ile Ala Pro Lys
                      260                      265                      270
Asn Ala Ala Ile Thr Pro Ile Val Asn Glu Ile Gly Lys Ile Tyr Thr
                      275                      280                      285
Phe Glu Lys Arg Ser Tyr Leu Val Leu Tyr Lys Ile Leu Leu Glu Asn
                      290                      295                      300
Asn Thr Glu Leu Glu Thr Ile His Ser Gly Asn Val Asn Leu Val Arg
  305                      310                      315                      320
Leu Pro Ala Pro Leu Pro Ala Phe Ser Phe Leu Arg Thr Gln Val Arg
                      325                      330                      335
Val

```

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1038
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

```

ATTAAGGAGA AATAAGAA ATG TTA CAA CCC CCT AAA ATT GTC GCT GAA TTG      51
      Met Leu Gln Pro Pro Lys Ile Val Ala Glu Leu
      1                      5                      10

AGC GCT AAT CAT AAC CAG GAT TTA AAC CTA GCC AAA GAA AGC CTT CAT      99
Ser Ala Asn His Asn Gln Asp Leu Asn Leu Ala Lys Glu Ser Leu His
      15                      20                      25

GCC ATT AAG GAA AGC GGT GCG GAT TTT GTC AAG CTC CAA ACC TAC ACG      147
Ala Ile Lys Glu Ser Gly Ala Asp Phe Val Lys Leu Gln Thr Tyr Thr
      30                      35                      40

CCA AGC TGC ATG ACT TTA AAC TCT AAA GAA GAT CCT TTC ATC ATT CAA      195
Pro Ser Cys Met Thr Leu Asn Ser Lys Glu Asp Pro Phe Ile Ile Gln
      45                      50                      55

GGC ACT TTA TGG GAT AAA GAA AAT TTG TAT GAA TTG TAT CAA AAG GCT      243

```



```

Ile Tyr Thr Phe Glu Lys Arg Ser Tyr Leu Val Leu Tyr Lys Ile Leu
                290                      295                      300

TTA GAA AAT AAC ACC GAG CTA GAA ACT ATC CAT AGC GGG AAC GTG AAT      1022
Leu Glu Asn Asn Thr Glu Leu Glu Thr Ile His Ser Gly Asn Val Asn
                305                      310                      315

TTA GTG CGA CTG CCC GCA CCC TTA CCG GCT TTT AGT TTT TTA CGC ACC      1070
Leu Val Arg Leu Pro Ala Pro Leu Pro Ala Phe Ser Phe Leu Arg Thr
                320                      325                      330

CAA GTC AGA GTC TAAAAATGGC GTTTAGAGAT TAGGTATTGA AAATGATTAA GAGAA  1127
Gln Val Arg Val
                335

ACGCATG                                                              1134

```

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

```

Met Ala Glu Leu Glu Pro Asp Ala Phe Ile Ile Ala Ala Pro Gly Val
 1           5           10           15
Val Lys Leu Ala Leu Lys Ile Ala Pro His Ile Pro Ile His Leu Ser
          20           25           30
Thr Gln Ala Asn Val Leu Asn Leu Leu Asp Ala Gln Val Phe Tyr Asp
          35           40           45
Leu Gly Val Lys Arg Ile Val Cys Ala Arg Glu Leu Ser Leu Asn Asp
          50           55           60
Ala Ile Glu Ile Lys Lys Ala Leu Pro Asn Leu Glu Leu Glu Ile Phe
          65           70           75           80
Val His Gly Ser Met Cys Phe Ala Phe Ser Gly Arg Cys Leu Ile Ser
          85           90           95
Ala Leu Gln Lys Gly Arg Val Pro Asn Arg Gly Ser Cys Ala Asn Asp
          100          105          110
Cys Arg Phe Asp Tyr Glu Tyr Tyr Val Lys Asn Pro Asp Asn Gly Val
          115          120          125
Met Met Arg Leu Val Glu Glu Gly Val Gly Thr His Ile Phe Asn
          130          135          140
Ala Lys Asp Leu Asn Leu Ser Gly His Ile Ala Glu Ile Leu Ser Ser
          145          150          155          160
Asn Ala Ile Ser Ala Leu Lys Ile Glu Gly Arg Thr Lys Ser Ser Tyr
          165          170          175
Tyr Ala Ala Gln Thr Thr Arg Ile Tyr Arg Leu Ala Val Asp Asp Phe
          180          185          190
Tyr His Asn Thr Leu Lys Pro Ser Phe Tyr Ala Ser Glu Leu Asn Thr
          195          200          205

```

65					70					75							
GAA ATC TTT GTG CAT GGG AGC ATG TGC TTT GCC TTT TCA GGG CGC TGC																350	
Glu Ile Phe Val His Gly Ser Met Cys Phe Ala Phe Ser Gly Arg Cys																	
80						85						90					
TTG ATT TCG GCC TTA CAA AAG GGG CGC GTG CCT AAT AGA GGG AGT TGC																398	
Leu Ile Ser Ala Leu Gln Lys Gly Arg Val Pro Asn Arg Gly Ser Cys																	
95						100						105					
GCG AAT GAT TGC CGG TTT GAT TAT GAA TAT TAC GTG AAA AAC CCT GAT																446	
Ala Asn Asp Cys Arg Phe Asp Tyr Glu Tyr Tyr Val Lys Asn Pro Asp																	
110						115						120					
AAT GGC GTG ATG ATG AGA CTG GTT GAA GAA GAG GGC GTA GGC ACG CAT																494	
Asn Gly Val Met Met Arg Leu Val Glu Glu Glu Gly Val Gly Thr His																	
130						135						140					
ATT TTT AAC GCT AAG GAT TTG AAC CTC TCT GGC CAT ATC GCT GAA ATT																542	
Ile Phe Asn Ala Lys Asp Leu Asn Leu Ser Gly His Ile Ala Glu Ile																	
145						150						155					
TTA AGT TCC AAC GCC ATT AGC GCG CTT AAG ATT GAA GGG CGC ACC AAG																590	
Leu Ser Ser Asn Ala Ile Ser Ala Leu Lys Ile Glu Gly Arg Thr Lys																	
160						165						170					
TCC AGT TAC TAC GCC GCG CAA ACC ACG CGC ATC TAT CGT TTA GCG GTT																638	
Ser Ser Tyr Tyr Ala Ala Gln Thr Thr Arg Ile Tyr Arg Leu Ala Val																	
175						180						185					
GAT GAT TTT TAC CAT AAC ACC TTA AAG CCG AGT TTT TAT GCC AGC GAA																686	
Asp Asp Phe Tyr His Asn Thr Leu Lys Pro Ser Phe Tyr Ala Ser Glu																	
190						195						200					
TTG AAC ACG CTT AAA AAC AGG GGT TTT ACG GAC GGC TAT TTG ATG CGA																734	
Leu Asn Thr Leu Lys Asn Arg Gly Phe Thr Asp Gly Tyr Leu Met Arg																	
210						215						220					
AGG CCT TTT GAA AGG TTG GAT ACT CAA AAC CAC CAA ACA GCC ATT AGC																782	
Arg Pro Phe Glu Arg Leu Asp Thr Gln Asn His Gln Thr Ala Ile Ser																	
225						230						235					
GAA GGG GAT TTT CAA GTC AAT GGC GAA ATA ACC GAA GAC GGG CGT TTT																830	
Glu Gly Asp Phe Gln Val Asn Gly Glu Ile Thr Glu Asp Gly Arg Phe																	
240						245						250					
TTT GCA TGC AAA TTC ACC ACT ACC ACT AAC ACC GCT TAT GAA ATC ATC																878	
Phe Ala Cys Lys Phe Thr Thr Thr Thr Asn Thr Ala Tyr Glu Ile Ile																	
255						260						265					
GCT CCC AAA AAT GCG GCT ATC ACG CCC ATA GTC AAT GAA ATT GGC AAG																926	
Ala Pro Lys Asn Ala Ala Ile Thr Pro Ile Val Asn Glu Ile Gly Lys																	
270						275						280					
ATT TAC ACC TTT GAA AAA CGC TCT TAT TTA GTG CTG TAT AAA ATC CTT																974	

```

Gln Ser Leu Leu Arg Arg Ser His Lys Lys Glu Glu Val Ser Glu Pro
      115                      120                      125
Gly Asp Ala Asn Ile Phe Arg Val Asp Lys Asp Ser Arg Glu Val Tyr
      130                      135                      140
Met His Glu Lys Lys Leu Asp Leu Thr Arg Ala Glu Tyr Glu Ile Leu
      145                      150                      155                      160
Ser Leu Leu Ile Ser Lys Lys Gly Tyr Val Phe Ser Arg Glu Ser Ile
      165                      170                      175
Ala Ile Glu Ser Glu Ser Ile Asn Pro Glu Ser Ser Asn Lys Ser Ile
      180                      185                      190
Asp Val Ile Ile Gly Arg Leu Arg Ser Lys Ile Glu Lys Asn Pro Lys
      195                      200                      205
Gln Pro Gln Tyr Ile Ile Ser Val Arg Gly Ile Gly Tyr Lys Leu Glu
      210                      215                      220
Tyr
225

```

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 72...1082
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

```

AAGTCTATGC CACGATCAAT GGTTCCTT TCAATTCACA GCTCAAACCTT TTAGAAGAAC      60
ATATTGATAA A ATG GCA GAA TTA GAG CCG GAC GCT TTT ATT ATC GCT GCG      110
      Met Ala Glu Leu Glu Pro Asp Ala Phe Ile Ile Ala Ala
              1              5              10

CCT GGT GTG GTG AAA CTC GCT TTA AAA ATC GCC CCG CAT ATC CCT ATC      158
Pro Gly Val Val Lys Leu Ala Leu Lys Ile Ala Pro His Ile Pro Ile
      15              20              25

CAT TTA TCC ACG CAA GCG AAT GTC TTA AAT TTG CTA GAT GCA CAA GTG      206
His Leu Ser Thr Gln Ala Asn Val Leu Asn Leu Leu Asp Ala Gln Val
      30              35              40              45

TTT TAT GAT TTA GGG GTT AAA CGC ATC GTG TGC GCG AGG GAA TTG AGC      254
Phe Tyr Asp Leu Gly Val Lys Arg Ile Val Cys Ala Arg Glu Leu Ser
              50              55              60

CTG AAT GAT GCG ATT GAG ATT AAA AAA GCC TTA CCT AAT TTA GAA TTA      302
Leu Asn Asp Ala Ile Glu Ile Lys Lys Ala Leu Pro Asn Leu Glu Leu

```

```

GGC GAT GCG AAT ATC TTT AGG GTG GAT AAG GAT AGC CGA GAA GTG TAT      432
Gly Asp Ala Asn Ile Phe Arg Val Asp Lys Asp Ser Arg Glu Val Tyr
   130                               135                               140

ATG CAT GAA AAA AAG CTG GAC TTA ACT AGG GCT GAA TAT GAA ATC CTT      480
Met His Glu Lys Lys Leu Asp Leu Thr Arg Ala Glu Tyr Glu Ile Leu
   145                               150                               155                               160

TCG CTT CTC ATT AGC AAA AAA GGT TAT GTG TTT AGC CGT GAA AGC ATT      528
Ser Leu Leu Ile Ser Lys Lys Gly Tyr Val Phe Ser Arg Glu Ser Ile
                   165                               170                               175

GCG ATT GAG AGC GAG AGC ATC AAC CCT GAA AGC TCT AAT AAA AGC ATT      576
Ala Ile Glu Ser Glu Ser Ile Asn Pro Glu Ser Ser Asn Lys Ser Ile
                   180                               185                               190

GAT GTG ATC ATT GGC CGT TTG CGA TCT AAG ATT GAA AAA AAT CCT AAA      624
Asp Val Ile Ile Gly Arg Leu Arg Ser Lys Ile Glu Lys Asn Pro Lys
                   195                               200                               205

CAA CCG CAA TAC ATC ATC TCT GTT AGA GGG ATT GGT TAT AAA TTA GAA      672
Gln Pro Gln Tyr Ile Ile Ser Val Arg Gly Ile Gly Tyr Lys Leu Glu
                   210                               215                               220

TAC TGA                                                                678
Tyr
225

```

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

```

Met Ile Glu Val Leu Met Ile Glu Asp Asp Ile Glu Leu Ala Glu Phe
 1                               5                               10                               15
Leu Ser Glu Phe Leu Leu Gln His Gly Ile His Val Thr Asn Tyr Asp
                   20                               25                               30
Glu Pro Tyr Thr Gly Ile Ser Ala Ala Asn Thr Gln Asn Tyr Asp Leu
                   35                               40                               45
Leu Leu Leu Asp Leu Thr Leu Pro Asn Leu Asp Gly Leu Glu Val Cys
                   50                               55                               60
Arg Arg Ile Ser Lys Gln Lys His Ile Pro Ile Ile Ile Ser Ser Ala
65                               70                               75                               80
Arg Ser Asp Val Glu Asp Lys Ile Lys Ala Leu Asp Tyr Gly Ala Asp
                   85                               90                               95
Asp Tyr Leu Pro Lys Pro Tyr Asp Pro Lys Glu Leu Leu Ala Arg Ile
                   100                               105                               110

```

(2) INFORMATION FOR SEQ ID NO:1219:

(A) LENGTH: 678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...675
(D) OTHER INFORMATION:

ATG	ATA	GAA	GTT	TTA	ATG	ATA	GAA	GAT	GAT	ATA	GAA	TTA	GCC	GAG	TTT	48
Met	Ile	Glu	Val	Leu	Met	Ile	Glu	Asp	Asp	Ile	Glu	Leu	Ala	Glu	Phe	
1				5				10						15		
TTG	AGC	GAG	TTT	TTG	CTC	CAA	CAT	GGC	ATT	CAT	GTA	ACC	AAT	TAC	GAT	96
Leu	Ser	Glu	Phe	Leu	Leu	Gln	His	Gly	Ile	His	Val	Thr	Asn	Tyr	Asp	
			20					25					30			
GAG	CCA	TAT	ACC	GGC	ATT	AGT	GCG	GCT	AAC	ACA	CAA	AAT	TAT	GAT	TTG	144
Glu	Pro	Tyr	Thr	Gly	Ile	Ser	Ala	Ala	Asn	Thr	Gln	Asn	Tyr	Asp	Leu	
		35					40					45				
TTG	TTG	TTG	GAT	TTG	ACT	TTG	CCT	AAT	TTA	GAC	GGG	CTT	GAA	GTG	TGT	192
Leu	Leu	Leu	Asp	Leu	Thr	Leu	Pro	Asn	Leu	Asp	Gly	Leu	Glu	Val	Cys	
	50					55					60					
AGG	CGC	ATC	TCC	AAA	CAA	AAA	CAT	ATC	CCT	ATT	ATT	ATT	TCT	TCA	GCG	240
Arg	Arg	Ile	Ser	Lys	Gln	Lys	His	Ile	Pro	Ile	Ile	Ile	Ser	Ser	Ala	
65				70						75					80	
AGA	AGT	GAT	GTG	GAA	GAT	AAG	ATT	AAA	GCA	CTA	GAT	TAT	GGG	GCT	GAT	288
Arg	Ser	Asp	Val	Glu	Asp	Lys	Ile	Lys	Ala	Leu	Asp	Tyr	Gly	Ala	Asp	
			85						90					95		
GAT	TAC	CTC	CCT	AAA	CCC	TAT	GAT	CCT	AAA	GAA	TTA	TTA	GCT	CGC	ATC	336
Asp	Tyr	Leu	Pro	Lys	Pro	Tyr	Asp	Pro	Lys	Glu	Leu	Leu	Ala	Arg	Ile	
			100					105					110			
CAA	TCG	CTA	CTC	AGG	CGT	TCT	CAT	AAA	AAA	GAA	GAA	GTG	AGT	GAG	CCA	384
Gln	Ser	Leu	Leu	Arg	Arg	Ser	His	Lys	Lys	Glu	Glu	Val	Ser	Glu	Pro	
		115					120					125				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

```

AAGGGGGGAT TTATATCGGT AAAGAGTTGT TTAAGC ATG GCT AGT GGC CTT TTT      54
                               Met Ala Ser Gly Leu Phe
                               1           5

GAA AAC GAT GGA ATC AAA GAC AAC AAA GCG CGA GAT TTT TTC TAT AGC      102
Glu Asn Asp Gly Ile Lys Asp Asn Lys Ala Arg Asp Phe Phe Tyr Ser
          10           15           20

CAT AGC TCC CTA ATT GTC TTT TTC CTT TTA CTG CTT GGG TTT GGG TAT      150
His Ser Ser Leu Ile Val Phe Phe Leu Leu Leu Leu Gly Phe Gly Tyr
          25           30           35

TAT TTA GGG AAG TTG CTT TTT GGG GGC TCT TCT TTA GAA GTT TAT TTG      198
Tyr Leu Gly Lys Leu Leu Phe Gly Gly Ser Ser Leu Glu Val Tyr Leu
          40           45           50

GAT TTA AGA GAC AAG CAT GAA CGA TTG CAG CAA GAA ATC ACC GAA TTG      246
Asp Leu Arg Asp Lys His Glu Arg Leu Gln Gln Glu Ile Thr Glu Leu
          55           60           65           70

CAA AGC AAG AAT GTG CGC TTG CAA AAG CGT TTG TTT GAG TTG AAG GAA      294
Gln Ser Lys Asn Val Arg Leu Gln Lys Arg Leu Phe Glu Leu Lys Glu
          75           80           85

TTA CGG CCT AGA GAT TAGATTTAAG GAAAATGGTA GTGTTAAAAA AGATGATAGG T      350
Leu Arg Pro Arg Asp
          90

TTGGTGG      357

```

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

```

Met Ala Ser Gly Leu Phe Glu Asn Asp Gly Ile Lys Asp Asn Lys Ala
 1           5           10           15
Arg Asp Phe Phe Tyr Ser His Ser Ser Leu Ile Val Phe Phe Leu Leu
          20           25           30
Leu Leu Gly Phe Gly Tyr Tyr Leu Gly Lys Leu Leu Phe Gly Gly Ser
          35           40           45
Ser Leu Glu Val Tyr Leu Asp Leu Arg Asp Lys His Glu Arg Leu Gln
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

```

Met Gly Arg Phe Ser Leu Lys Glu Ile Leu Met Leu Ser Leu Thr Leu
 1           5           10           15
Leu Ala Leu Leu Gly Trp Ile Phe Gly Lys Pro Leu Gly Leu His Ala
 20           25           30
Ser Ala Thr Ala Leu Ile Val Met Val Leu Met Ala Phe Cys Lys Ile
 35           40           45
Val Ser Tyr Glu Asp Ile Ile Lys Asn Lys Ser Ala Phe Asn Ile Phe
 50           55           60
Leu Leu Leu Gly Ser Leu Leu Thr Met Ala Gly Gly Leu Lys Asn Val
 65           70           75           80
Gly Phe Leu Asn Phe Ile Gly Asn Ala Ala Gln Asn Phe Leu Glu His
 85           90           95
Ala His Leu Asp Pro Leu Ile Ala Val Leu Phe Ile Val Ala Leu Phe
100          105          110
Tyr Leu Ser His Tyr Phe Phe Ala Ser Ile Thr Ala His Val Ser Ala
115          120          125
Leu Phe Ala Leu Phe Val Gly Ile Gly Ser His Ile Gln Gly Val Asn
130          135          140
Leu Gln Glu Leu Ser Leu Phe Leu Met Phe Ser Leu Gly Ile Met Gly
145          150          155          160
Ile Leu Thr Pro Tyr Gly Thr Gly Pro Ser Thr Ile Tyr Tyr Gly Ser
165          170          175
Gly Tyr Ile Gln Ser Lys Asp Phe Trp Lys Trp Gly Phe Ile Phe Gly
180          185          190
Phe Leu Tyr Leu Ile Val Phe Leu Ser Val Cys Thr Pro Trp Val Lys
195          200          205
Phe Ile Ala Tyr Arg Trp Leu
210          215

```

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...309
- (D) OTHER INFORMATION:

1	5	10	
ACC TTA TTG GCT TTA CTG GGT TGG ATT TTT GGC AAA CCT TTA GGC TTG			159
Thr Leu Leu Ala Leu Leu Gly Trp Ile Phe Gly Lys Pro Leu Gly Leu			
15	20	25	30
CAT GCG AGT GCG ACG GCT TTG ATT GTC ATG GTT TTA ATG GCG TTT TGT			207
His Ala Ser Ala Thr Ala Leu Ile Val Met Val Leu Met Ala Phe Cys			
	35	40	45
AAG ATT GTA AGC TAT GAA GAC ATC ATT AAA AAC AAG AGC GCG TTC AAT			255
Lys Ile Val Ser Tyr Glu Asp Ile Ile Lys Asn Lys Ser Ala Phe Asn			
	50	55	60
ATT TTT TTA TTG CTT GGA TCG CTG CTC ACG ATG GCT GGC GGG CTT AAA			303
Ile Phe Leu Leu Leu Gly Ser Leu Leu Thr Met Ala Gly Gly Leu Lys			
	65	70	75
AAT GTA GGG TTT TTA AAT TTT ATC GGC AAT GCG GCT CAA AAT TTT TTA			351
Asn Val Gly Phe Leu Asn Phe Ile Gly Asn Ala Ala Gln Asn Phe Leu			
	80	85	90
GAG CAT GCT CAC TTG GAT CCG TTA ATA GCG GTC TTG TTT ATT GTA GCC			399
Glu His Ala His Leu Asp Pro Leu Ile Ala Val Leu Phe Ile Val Ala			
	95	100	105
CTC TTT TAT CTG TCG CAT TAT TTT TTC GCA AGC ATC ACC GCT CAT GTG			447
Leu Phe Tyr Leu Ser His Tyr Phe Phe Ala Ser Ile Thr Ala His Val			
	115	120	125
AGC GCG TTA TTC GCG CTT TTT GTA GGG ATT GGT TCG CAC ATT CAA GGG			495
Ser Ala Leu Phe Ala Leu Phe Val Gly Ile Gly Ser His Ile Gln Gly			
	130	135	140
GTC AAT TTG CAA GAA TTG AGC TTG TTT TTA ATG TTT TCT TTA GGG ATT			543
Val Asn Leu Gln Glu Leu Ser Leu Phe Leu Met Phe Ser Leu Gly Ile			
	145	150	155
ATG GGG ATT TTA ACG CCC TAT GGC ACA GGC CCA TCC ACC ATT TAT TAC			591
Met Gly Ile Leu Thr Pro Tyr Gly Thr Gly Pro Ser Thr Ile Tyr Tyr			
	160	165	170
GGG AGC GGG TAT ATT CAA AGC AAG GAT TTT TGG AAA TGG GGG TTT ATT			639
Gly Ser Gly Tyr Ile Gln Ser Lys Asp Phe Trp Lys Trp Gly Phe Ile			
	175	180	185
TTT GGC TTT TTG TAT TTA ATC GTG TTT TTA AGC GTG TGC ACA CCT TGG			687
Phe Gly Phe Leu Tyr Leu Ile Val Phe Leu Ser Val Cys Thr Pro Trp			
	195	200	205
GTC AAA TTC ATC GCT TAT AGG TGG TTG TAGCTGGAAA CTTTACACAA CGCCCTT			741
Val Lys Phe Ile Ala Tyr Arg Trp Leu			
	210	215	
TTAAAATGGT ATGAAGAA			759

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

```

Met Met Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe
 1             5             10             15
Asn Met Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe
      20             25             30
Leu Asp Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu
      35             40             45
Lys Ile Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val
 50             55             60
Ile Asp Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu
65             70             75             80
Ile Glu Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe
      85             90             95
Ser Val Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile
      100            105            110
Lys Asn Ile Glu Ser Arg Gln Val Asp Val Ile Val Ser Ala Asp Ala
      115            120            125
Gly Cys Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu
      130            135            140
Thr Lys Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu
145            150            155            160

```

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...714
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

```

AACCTGCAAA CCCACCTTAA AAGGCTCAAA AGAAGTGAGT TTGTGGGCCA AAAAAAGGAA      60
TTAGAGGGC ATG GGG AGG TTT TCT TTA AAA GAA ATT TTA ATG CTC AGC CTT      111
--Met Gly Arg Phe Ser Leu Lys Glu Ile Leu Met Leu Ser Leu

```

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 52...531
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

TATTCCAATA ACGACTACCC TATTATTTTG CCTAGCGGTT CATGCACAGG G ATG ATG	57
Met Met	
1	
CGG CAT GAT TAT TTG GAA TTG TTT GAA GGG CAT GCG GAA TTC AAC ATG	105
Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe Asn Met	
5 10 15	
GTT AAA GAT TTT TGC TCT AGG GTG TAT GAA TTG AGC GAA TTT TTG GAT	153
Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe Leu Asp	
20 25 30	
AAA AAA TTG CAA GTC AAA TAT GAA GAT AAG GGC GAA CCC CTT AAA ATC	201
Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu Lys Ile	
35 40 45 50	
ACA TGG CAT TCT AAT TGC CAT GCC TTA AGG GTG GCT AAA GTG ATT GAC	249
Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val Ile Asp	
55 60 65	
TCG GCG AAA AAC CTC ATC AGA CAG CTT AAA AAT GTG GAA CTC ATT GAA	297
Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu Ile Glu	
70 75 80	
TTG GAA AAA GAA GAA GAA TGC TGC GGG TTT GGG GGG ACT TTT TCG GTT	345
Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe Ser Val	
85 90 95	
AAA GAG CCT GAA ATT TCA GCG GTT ATG GTT AAA GAA AAG ATT AAA AAC	393
Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile Lys Asn	
100 105 110	
ATA GAA AGC CGT CAA GTG GAT GTG ATT GTT TCA GCG GAT GCT GGG TGT	441
Ile Glu Ser Arg Gln Val Asp Val Ile Val Ser Ala Asp Ala Gly Cys	
115 120 125 130	
TTG ATG AAT ATC AGC ACC GCT ATG CAA AAA ATG GGC TCT TTG ACA AAA	489
Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu Thr Lys	
135 140 145	
CCC ATG CAT TTT TAT GAC TTT TTA GCC TCA AGA CTT GGG CTT TAACATTAA	540
Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu	
150 155 160	
AGAATTATTT TAAGGAATGA TCATGGAAAA A	571

Gln Lys Val Ala Ile Ile Leu Tyr
205 210

GGGCAATTAG CCCCTGATT

700

(2) INFORMATION FOR SEO ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

ACTTAGAAGG GGTGATTT ATG AGT AAA GAG CTT ATT TTA AAG CGC ATT AAA	51
Met Ser Lys Glu Leu Ile Leu Lys Arg Ile Lys	
1 5 10	
GAA GCC AGA GCC AAG CAT GCC ATT CAG GGA GCG AAC CCT ATT TAT AGG	99
Glu Ala Arg Ala Lys His Ala Ile Gln Gly Ala Asn Pro Ile Tyr Arg	
15 20 25	
AAT ATC ATT AAA GTG GAG TTT GAG GAC TTG GTG GAA GAA TAC AAG CAT	147
Asn Ile Ile Lys Val Glu Phe Glu Asp Leu Val Glu Glu Tyr Lys His	
30 35 40	
TTC CAA GTG TTG AAT AAA GCT GAA GTC ATT GAA AGC GCT AAA GAA AAT	195
Phe Gln Val Leu Asn Lys Ala Glu Val Ile Glu Ser Ala Lys Glu Asn	
45 50 55	
TTA GAG CAA GCC ATT TTA AAG GCT TTA GAA AAT TTT AAA AGC AAA AAA	243
Leu Glu Gln Ala Ile Leu Lys Ala Leu Glu Asn Phe Lys Ser Lys Lys	
60 65 70 75	
ATC TTA CAC TCC ACA GAT TTG AAT TTG AAT TTT GAA GCG TTT AAG GAT	291
Ile Leu His Ser Thr Asp Leu Asn Leu Asn Phe Glu Ala Phe Lys Asp	
80 85 90	
TTT ACT TTA CAG CCT TAT GAT AAA GAA ATT GAA GCG ATG CGT GAA GAG	339
Phe Thr Leu Gln Pro Tyr Asp Lys Glu Ile Glu Ala Met Arg Glu Glu	
95 100 105	
TTG TTT GAG ATT GAT ACG GCT TTA TTG CAT GGG GTT TGT GGG ATT TCA	387
Leu Phe Glu Ile Asp Thr Ala Leu Leu His Gly Val Cys Gly Ile Ser	
110 115 120	
AGC TTG GGC ATG ATT GGG GCG GTC TCT TCG CAT GCA AGC CCG CGA TTG	435
Ser Leu Gly Met Ile Gly Ala Val Ser Ser His Ala Ser Pro Arg Leu	
125 130 135	
CTT TCG CTC ATC ACC CTT AAT TGC ATC ATC TTA TTG AAA AAA GAA TCC	483
Leu Ser Leu Ile Thr Leu Asn Cys Ile Ile Leu Leu Lys Lys Glu Ser	
140 145 150 155	
ATT GTG CGC AAT TTG AGT GAA GGC ATG CAA GCT TTA AAA AAC CAA AGC	531
Ile Val Arg Asn Leu Ser Glu Gly Met Gln Ala Leu Lys Asn Gln Ser	
160 165 170	
CAA AAC GGT GCA TTA CCC ACA AAC ATG CTC CTT ATT GGC GGG CCT AGC	579
Gln Asn Gly Ala Leu Pro Thr Asn Met Leu Leu Ile Gly Gly Pro Ser	
175 180 185	
CGG ACA GCT GAC ATT GAA TTA AAA ACC GTT TTT GGG GTG CAT GGG CCT	627
Arg Thr Ala Asp Ile Glu Leu Lys Thr Val Phe Gly Val His Gly Pro	
190 195 200	
CAA AAA GTC GCT ATC ATT CTC TAC TAAAGGATAA GAATGGAAAA ATTAGAAGTA	681

AAG GTT TTA GAG AGT TTG TAGTTTAACT TTCTAACTTT CGCCCATTTT AATTTGAG 544
 Lys Val Leu Glu Ser Leu
 150

ATTTTTTAGC CATT 558

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

Met	Glu	Lys	Leu	Glu	Val	Gly	Gln	Leu	Ala	Pro	Asp	Phe	Arg	Leu	Lys	1	5	10	15
Asn	Ser	Asp	Gly	Val	Glu	Ile	Ser	Leu	Lys	Asp	Leu	Leu	His	Lys	Lys	20	25	30	
Val	Val	Leu	Tyr	Phe	Tyr	Pro	Lys	Asp	Asn	Thr	Pro	Gly	Cys	Thr	Leu	35	40	45	
Glu	Ala	Lys	Asp	Phe	Ser	Ala	Leu	Phe	Ser	Glu	Phe	Glu	Lys	Lys	Asn	50	55	60	
Ala	Val	Val	Val	Gly	Ile	Ser	Pro	Asp	Asn	Ala	Gln	Ser	His	Gln	Lys	65	70	75	80
Phe	Ile	Ser	Gln	Cys	Ser	Leu	Asn	Val	Ile	Leu	Leu	Cys	Asp	Glu	Asp	85	90	95	
Lys	Lys	Ala	Ala	Asn	Leu	Tyr	Lys	Ala	Tyr	Gly	Lys	Arg	Met	Leu	Tyr	100	105	110	
Gly	Lys	Glu	His	Leu	Gly	Ile	Ile	Arg	Ser	Thr	Phe	Ile	Ile	Asn	Thr	115	120	125	
Gln	Gly	Val	Leu	Glu	Lys	Cys	Phe	Tyr	Asn	Val	Lys	Ala	Lys	Gly	His	130	135	140	
Ala	Gln	Lys	Val	Leu	Glu	Ser	Leu									145	150		

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...651
- (D) OTHER INFORMATION:

(A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...506
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

GGGTGCATGG GCCTCAAAAA GTCGCTATCA TTCTCTACTA AAGGATAAGA	ATG GAA	56
	Met Glu	
	1	
AAA TTA GAA GTA GGG CAA TTA GCC CCT GAT TTT AGA TTG AAA AAC AGC		104
Lys Leu Glu Val Gly Gln Leu Ala Pro Asp Phe Arg Leu Lys Asn Ser		
5 10 15		
GAT GGC GTG GAA ATT TCT TTA AAA GAT TTG CTC CAT AAA AAA GTG GTG		152
Asp Gly Val Glu Ile Ser Leu Lys Asp Leu Leu His Lys Lys Val Val		
20 25 30		
CTG TAT TTC TAC CCT AAA GAC AAC ACC CCC GGA TGC ACT CTA GAA GCC		200
Leu Tyr Phe Tyr Pro Lys Asp Asn Thr Pro Gly Cys Thr Leu Glu Ala		
35 40 45 50		
AAA GAC TTT AGC GCT CTA TTT AGT GAA TTT GAA AAG AAA AAC GCT GTT		248
Lys Asp Phe Ser Ala Leu Phe Ser Glu Phe Glu Lys Lys Asn Ala Val		
55 60 65		
GTC GTA GGC ATA AGC CCT GAT AAC GCG CAA TCG CAT CAA AAA TTT ATC		296
Val Val Gly Ile Ser Pro Asp Asn Ala Gln Ser His Gln Lys Phe Ile		
70 75 80		
AGC CAA TGC TCT TTG AAT GTG ATT TTG CTC TGC GAT GAA GAT AAA AAA		344
Ser Gln Cys Ser Leu Asn Val Ile Leu Leu Cys Asp Glu Asp Lys Lys		
85 90 95		
GCC GCC AAT CTT TAC AAA GCT TAT GGC AAA CGC ATG CTT TAT GGG AAG		392
Ala Ala Asn Leu Tyr Lys Ala Tyr Gly Lys Arg Met Leu Tyr Gly Lys		
100 105 110		
GAG CAT TTG GGG ATT ATC CGC TCC ACC TTC ATT ATC AAC ACG CAA GGC		440
Glu His Leu Gly Ile Ile Arg Ser Thr Phe Ile Ile Asn Thr Gln Gly		
115 120 125 130		
GTT TTA GAA AAA TGT TTC TAC AAT GTC AAA GCG AAA GGC CAT GCT CAA		488
Val Leu Glu Lys Cys Phe Tyr Asn Val Lys Ala Lys Gly His Ala Gln		
135 140 145		

65	70	75	80	
TTA AGC CAA GAA GAT CGC AAC AAG CGT AAA AAA GAA ATT CTT GAA GCG				348
Leu Ser Gln Glu Asp Arg Asn Lys Arg Lys Lys Glu Ile Leu Glu Ala				
	85	90	95	
ATT GCT AAC AAA AAG AAA ACA ATG ACC ATG AAA GAA TAT CGT GAA GAA				396
Ile Ala Asn Lys Lys Lys Thr Met Thr Met Lys Glu Tyr Arg Glu Glu				
	100	105	110	
GGG TTG GAT TTG CAT GAT TGC GCA TGC GAA GGC CCT TTT CAT GAT CAT				444
Gly Leu Asp Leu His Asp Cys Ala Cys Glu Gly Pro Phe His Asp His				
	115	120	125	
GAG AGA AAA AAA GGG AAA AAA CCA AGC CAT CAT AAG CAT TAGCGCTTAG GG				495
Glu Arg Lys Lys Gly Lys Lys Pro Ser His His Lys His				
	130	135	140	
TGTGCTAACT TTTTTTGATT TTTGTGAAAC CACGCCGTAA GTCCCTAGCT TTTGGCTGTG				555
GGGATTAAGG				565

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

Met	Lys	Lys	Leu	Ala	Val	Ser	Leu	Leu	Phe	Thr	Gly	Thr	Phe	Leu	Gly
1				5					10					15	
Leu	Phe	Leu	Asn	Ala	Ser	Asp	Phe	Lys	Ser	Met	Asp	Asp	Lys	Gln	Leu
			20					25					30		
Leu	Glu	Gln	Ala	Gly	Lys	Val	Ala	Pro	Ser	Glu	Val	Pro	Glu	Phe	Arg
		35					40					45			
Ala	Glu	Val	Asn	Lys	Arg	Leu	Ala	Val	Met	Lys	Glu	Glu	Asp	Arg	Lys
	50					55					60				
Asn	Tyr	Lys	Ala	Asp	Phe	Lys	Lys	Ala	Met	Asp	Lys	Asn	Leu	Ala	Ser
65					70					75				80	
Leu	Ser	Gln	Glu	Asp	Arg	Asn	Lys	Arg	Lys	Lys	Glu	Ile	Leu	Glu	Ala
			85					90						95	
Ile	Ala	Asn	Lys	Lys	Lys	Thr	Met	Thr	Met	Lys	Glu	Tyr	Arg	Glu	Glu
		100					105						110		
Gly	Leu	Asp	Leu	His	Asp	Cys	Ala	Cys	Glu	Gly	Pro	Phe	His	Asp	His
		115				120					125				
Glu	Arg	Lys	Lys	Gly	Lys	Lys	Pro	Ser	His	His	Lys	His			
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

```

Asp Phe Leu Ser Leu Phe Asp Gly Phe Ser Ile Gly Ser Asn Asp Leu
    675                      680                      685
Thr Gln Leu Thr Leu Gly Val Asp Arg Asp Ser Glu Leu Val Ser His
    690                      695                      700
Val Phe Asp Glu Arg Asn Glu Ala Met Leu Lys Met Phe Lys Lys Ala
    705                      710                      715                      720
Ile Glu Ala Cys Lys Arg His Asn Lys Tyr Cys Gly Ile Cys Gly Gln
    725                      730                      735
Ala Pro Ser Asp Tyr Pro Glu Val Thr Glu Phe Leu Val Lys Glu Gly
    740                      745                      750
Ile Thr Ser Ile Ser Leu Asn Pro Asp Ser Val Ile Pro Thr Trp Asn
    755                      760                      765
Ala Val Ala Lys Leu Glu Lys Glu Leu Lys Glu His Gly Leu Thr Glu
    770                      775                      780
His
785

```

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 61...483
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

```

GTTATCTTTA ATCAATCAGA TGATAGAATT TATCTTTTAT TTTTGAATTG GGAGCATTTG      60
ATG AAA AAA TTA GCG GTT TCT TTA TTA TTT ACA GGG ACT TTT TTG GGG      108
Met Lys Lys Leu Ala Val Ser Leu Leu Phe Thr Gly Thr Phe Leu Gly
  1                      5                      10                      15

CTT TTT TTG AAT GCG AGC GAT TTT AAG AGC ATG GAT GAC AAG CAA CTA      156
Leu Phe Leu Asn Ala Ser Asp Phe Lys Ser Met Asp Asp Lys Gln Leu
    20                      25                      30

TTA GAG CAA GCA GGG AAA GTT GCT CCT AGC GAA GTC CCT GAG TTT CGC      204
Leu Glu Gln Ala Gly Lys Val Ala Pro Ser Glu Val Pro Glu Phe Arg
    35                      40                      45

GCG GAA GTC AAT AAG CGA TTA GCA GTG ATG AAA GAA GAA GAT CGT AAA      252
Ala Glu Val Asn Lys Arg Leu Ala Val Met Lys Glu Glu Asp Arg Lys
    50                      55                      60

AAT TAT AAA GCG GAT TTT AAG AAA GCG ATG GAT AAG AAT TTA GCT TCT      300
Asn Tyr Lys Ala Asp Phe Lys Lys Ala Met Asp Lys Asn Leu Ala Ser

```


225		230		235		240
Arg Gly Ser Glu His	Pro Thr Arg Asn Ile	Lys Thr Thr Lys Lys	Glu			
	245	250	255			
Trp Gln Ser Phe Ser	Leu Ser Asp Glu Asp	Val Leu Ile Leu Ala	Lys			
	260	265	270			
Tyr Ala Ile Glu Ile	Glu Lys His Tyr Ser	Lys Glu Ala Lys Gln	Tyr			
	275	280	285			
Arg Pro Met Asp Ile	Glu Trp Ala Lys Asp	Gly Glu Ser Gly Glu	Ile			
	290	295	300			
Phe Ile Val Gln Ala	Arg Pro Glu Thr Val	Gln Ser Gln Lys Ser	Lys			
305	310	315	320			
Glu Glu Ser Gln Val	Phe Glu Lys Phe Lys	Phe Lys Asn Pro Asn	Glu			
	325	330	335			
Lys Lys Glu Ile Ile	Leu Gln Gly Arg Ala	Ile Gly Ser Lys Ile	Gly			
	340	345	350			
Ser Gly Lys Val Arg	Ile Ile Asn Asp Leu	Glu His Met Asn Ser	Phe			
	355	360	365			
Lys Glu Gly Glu Ile	Leu Val Thr Asp Asn	Thr Asp Pro Asp Trp	Glu			
	370	375	380			
Pro Cys Met Lys Lys	Ala Ser Ala Val Ile	Thr Asn Arg Gly Gly	Arg			
385	390	395	400			
Thr Cys His Ala Ala	Ile Val Ala Arg Glu	Ile Gly Val Pro Ala	Ile			
	405	410	415			
Val Gly Val Ser Gly	Ala Thr Asp Ser Leu	Tyr Thr Gly Met Glu	Ile			
	420	425	430			
Thr Val Ser Cys Ala	Glu Gly Glu Gly Tyr	Val Tyr Ala Gly Ile				
	435	440	445			
Tyr Glu His Glu Ile	Glu Arg Val Glu Leu	Ser Asn Met Gln Glu	Thr			
	450	455	460			
Gln Thr Lys Ile Tyr	Ile Asn Ile Gly Asn	Pro Glu Lys Ala Phe	Gly			
465	470	475	480			
Phe Ser Gln Leu Pro	Asn His Gly Val Gly	Leu Ala Arg Met Glu	Met			
	485	490	495			
Ile Ile Leu Asn Gln	Ile Lys Ala His Pro	Leu Ala Leu Val Asp	Leu			
	500	505	510			
His His Lys Lys Ser	Val Lys Glu Lys Asn	Glu Ile Glu Asn Leu	Met			
	515	520	525			
Ala Gly Tyr Ala Asn	Pro Lys Asp Phe Phe	Val Lys Lys Ile Ala	Glu			
	530	535	540			
Gly Ile Gly Met Ile	Ser Ala Ala Phe Tyr	Pro Lys Pro Val Ile	Val			
545	550	555	560			
Arg Thr Ser Asp Phe	Lys Ser Asn Glu Tyr	Met Arg Met Leu Gly	Gly			
	565	570	575			
Ser Ser Tyr Glu Pro	Asn Glu Glu Asn Pro	Met Leu Gly Tyr Arg	Gly			
	580	585	590			
Ala Ser Arg Tyr Tyr	Ser Glu Ser Tyr Asn	Glu Ala Phe Ser Trp	Glu			
	595	600	605			
Cys Glu Ala Leu Ala	Leu Val Arg Glu Glu	Met Gly Leu Thr Asn	Met			
	610	615	620			
Lys Val Met Ile Pro	Phe Leu Arg Thr Ile	Glu Glu Gly Lys Lys	Val			
625	630	635	640			
Leu Glu Ile Leu Arg	Lys Asn Asn Leu Glu	Ser Gly Lys Asn Gly	Leu			
	645	650	655			
Glu Ile Tyr Ile Met	Cys Glu Leu Pro Val	Asn Val Ile Leu Ala	Asp			
	660	665	670			

ACA GAG TTT TTA GTC AAA GAG GGC ATC ACT TCC ATT TCT TTA AAC CCT 2370
 Thr Glu Phe Leu Val Lys Glu Gly Ile Thr Ser Ile Ser Leu Asn Pro
 745 750 755 760

GAT AGC GTG ATC CCC ACT TGG AAC GCT GTA GCC AAG TTA GAA AAA GAA 2418
 Asp Ser Val Ile Pro Thr Trp Asn Ala Val Ala Lys Leu Glu Lys Glu
 765 770 775

CTA AAA GAA CAT GGC TTA ACT GAA CAT TGATAATAAA TAAATCAATC TAACTTG 2472
 Leu Lys Glu His Gly Leu Thr Glu His
 780 785

AGTGGATTTT TCGTATTAGT TTCCAT 2498

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

Met Phe Gln Glu Leu Val Pro Ile Gly Ile Lys Val Pro Asp Gly Phe
 1 5 10 15
 Ala Ile Thr Ser Glu Ala Tyr Trp Tyr Leu Leu Glu Gln Gly Gly Ala
 20 25 30
 Lys Gln Lys Ile Ile Glu Leu Leu Glu Asn Val Asp Ala Thr Glu Ile
 35 40 45
 Asp Val Leu Lys Ile Arg Ser Lys Gln Ile Arg Glu Leu Ile Phe Gly
 50 55 60
 Thr Pro Phe Pro Ser Asp Leu Arg Asp Glu Ile Phe Gln Ala Tyr Glu
 65 70 75 80
 Ile Leu Ser Gln Gln Tyr His Met Lys Glu Ala Asp Val Ala Val Arg
 85 90 95
 Ser Ser Ala Thr Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln
 100 105 110
 Gln Asp Thr Tyr Leu Asn Ile Lys Gly Lys Thr Glu Leu Ile His Tyr
 115 120 125
 Ile Lys Ser Cys Leu Ala Ser Leu Phe Thr Asp Arg Ala Ile Ser Tyr
 130 135 140
 Arg Ala Ser Arg Gly Phe Asp His Leu Lys Val Ala Leu Ser Val Gly
 145 150 155 160
 Val Gln Lys Met Val Arg Ala Asp Lys Gly Ser Ala Gly Val Met Phe
 165 170 175
 Ser Ile Asp Thr Glu Thr Gly Phe Lys Asp Ala Val Phe Ile Thr Ser
 180 185 190
 Ala Trp Gly Leu Gly Glu Asn Val Val Gly Gly Thr Ile Asn Pro Asp
 195 200 205
 Glu Phe Tyr Val Phe Lys Pro Thr Leu Glu Gln Asn Lys Arg Pro Ile
 210 215 220
 Ile Lys Arg Gln Leu Gly Asn Lys Thr Gln Lys Met Val Tyr Ala Pro

AAA AAT GAA ATT GAA AAC CTC ATG GCA GGC TAT GCT AAC CCT AAA GAT	1698
Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn Pro Lys Asp	
525 530 535	
TTT TTT GTG AAA AAA ATC GCT GAA GGC ATT GGC ATG ATC AGT GCA GCG	1746
Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile Ser Ala Ala	
540 545 550	
TTT TAC CCT AAA CCT GTC ATT GTG AGA ACG AGC GAT TTC AAA TCC AAT	1794
Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe Lys Ser Asn	
555 560 565	
GAA TAC ATG CGC ATG CTT GGC GGC TCT AGC TAT GAG CCT AAT GAA GAA	1842
Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro Asn Glu Glu	
570 575 580	
AAC CCC ATG CTT GGC TAT AGG GGG GCT AGT CGG TAT TAT TCA GAG AGC	1890
Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr Ser Glu Ser	
585 590 595 600	
TAT AAT GAA GCG TTT TCG TGG GAG TGT GAA GCC TTA GCG TTA GTG AGG	1938
Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala Leu Val Arg	
605 610 615	
GAA GAA ATG GGA TTA ACC AAC ATG AAA GTG ATG ATC CCT TTT TTG CGA	1986
Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro Phe Leu Arg	
620 625 630	
ACC ATT GAA GAG GGT AAA AAA GTC CTA GAA ATC TTA AGA AAA AAC AAT	2034
Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg Lys Asn Asn	
635 640 645	
TTA GAA TCC GGT AAA AAC GGG CTT GAA ATT TAT ATC ATG TGC GAA TTG	2082
Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met Cys Glu Leu	
650 655 660	
CCG GTG AAT GTC ATT TTG GCT GAT GAT TTC TTG AGC TTG TTT GAT GGC	2130
Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu Phe Asp Gly	
665 670 675 680	
TTT TCT ATT GGA TCA AAC GAT TTA ACC CAG CTC ACT TTA GGC GTG GAT	2178
Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu Gly Val Asp	
685 690 695	
AGA GAC AGC GAA TTG GTC AGC CAT GTC TTT GAT GAA AGG AAT GAA GCG	2226
Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg Asn Glu Ala	
700 705 710	
ATG CTA AAG ATG TTT AAA AAA GCG ATT GAA GCT TGC AAA AGG CAC AAC	2274
Met Leu Lys Met Phe Lys Lys Ala Ile Glu Ala Cys Lys Arg His Asn	
715 720 725	
AAA TAT TGC GGG ATT TGC GGG CAA GCC CCA AGC GAT TAC CCT GAA GTA	2322
Lys Tyr Cys Gly Ile Cys Gly Gln Ala Pro Ser Asp Tyr Pro Glu Val	
730 735 740	

AAA GAT GGC GAG AGC GGG GAA ATC TTT ATC GTT CAA GCG CGC CCA GAA	1026
Lys Asp Gly Glu Ser Gly Glu Ile Phe Ile Val Gln Ala Arg Pro Glu	
300 305 310	
ACC GTT CAA AGC CAA AAA AGT AAA GAA GAA AGT CAA GTC TTT GAA AAA	1074
Thr Val Gln Ser Gln Lys Ser Lys Glu Glu Ser Gln Val Phe Glu Lys	
315 320 325	
TTC AAA TTC AAA AAC CCT AAC GAA AAG AAA GAG ATT ATC TTA CAA GGC	1122
Phe Lys Phe Lys Asn Pro Asn Glu Lys Lys Glu Ile Ile Leu Gln Gly	
330 335 340	
AGA GCG ATT GGG AGT AAA ATT GGC TCA GGA AAA GTG CGC ATC ATC AAT	1170
Arg Ala Ile Gly Ser Lys Ile Gly Ser Gly Lys Val Arg Ile Ile Asn	
345 350 355 360	
GAT TTG GAG CAC ATG AAT TCT TTT AAA GAG GGC GAA ATT TTA GTT ACG	1218
Asp Leu Glu His Met Asn Ser Phe Lys Glu Gly Glu Ile Leu Val Thr	
365 370 375	
GAT AAC ACC GAT CCG GAC TGG GAG CCT TGC ATG AAA AAA GCG AGC GCG	1266
Asp Asn Thr Asp Pro Asp Trp Glu Pro Cys Met Lys Lys Ala Ser Ala	
380 385 390	
GTT ATC ACT AAT CGT GGA GGG CGC ACT TGC CAT GCC GCT ATT GTG GCG	1314
Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala Ile Val Ala	
395 400 405	
AGA GAA ATT GGC GTG CCA GCT ATC GTT GGG GTG AGC GGG GCG ACT GAT	1362
Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly Ala Thr Asp	
410 415 420	
AGC CTT TAT ACC GGC ATG GAA ATC ACG GTT TCT TGC GCT GAG GGC GAA	1410
Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala Glu Gly Glu	
425 430 435 440	
GAG GGC TAT GTG TAT GCG GGC ATT TAT GAG CAT GAA ATT GAA AGG GTG	1458
Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile Glu Arg Val	
445 450 455	
GAG CTT TCT AAC ATG CAA GAA ACT CAA ACA AAA ATT TAC ATC AAT ATT	1506
Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr Ile Asn Ile	
460 465 470	
GGA AAC CCT GAA AAA GCC TTT GGC TTT TCT CAA CTC CCT AAT CAC GGC	1554
Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro Asn His Gly	
475 480 485	
GTA GGG CTA GCC AGG ATG GAA ATG ATT ATT TTA AAT CAA ATC AAA GCC	1602
Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln Ile Lys Ala	
490 495 500	
CAC CCT TTA GCT TTA GTG GAT TTG CAC CAC AAA AAA AGC GTG AAA GAA	1650
His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser Val Lys Glu	
505 510 515 520	

GAT GAG ATT TTT CAA GCT TAT GAG ATT TTA AGC CAG CAA TAC CAC ATG	354
Asp Glu Ile Phe Gln Ala Tyr Glu Ile Leu Ser Gln Gln Tyr His Met	
75 80 85	
AAA GAA GCC GAT GTG GCT GTA AGG AGT TCC GCT ACT GCA GAA GAT TTG	402
Lys Glu Ala Asp Val Ala Val Arg Ser Ser Ala Thr Ala Glu Asp Leu	
90 95 100	
CCG GAC GCT TCT TTT GCC GGG CAG CAA GAC ACT TAT TTA AAC ATT AAG	450
Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr Leu Asn Ile Lys	
105 110 115 120	
GGT AAA ACC GAA TTG ATC CAC TAT ATC AAA TCC TGT TTA GCG TCG CTT	498
Gly Lys Thr Glu Leu Ile His Tyr Ile Lys Ser Cys Leu Ala Ser Leu	
125 130 135	
TTT ACC GAT AGA GCG ATT AGC TAT AGG GCG AGT CGT GGG TTT GAT CAT	546
Phe Thr Asp Arg Ala Ile Ser Tyr Arg Ala Ser Arg Gly Phe Asp His	
140 145 150	
TTA AAA GTC GCG CTC AGC GTG GGG GTG CAA AAA ATG GTG CGA GCG GAT	594
Leu Lys Val Ala Leu Ser Val Gly Val Gln Lys Met Val Arg Ala Asp	
155 160 165	
AAA GGC AGC GCG GGC GTG ATG TTT TCT ATT GAC ACC GAA ACC GGT TTT	642
Lys Gly Ser Ala Gly Val Met Phe Ser Ile Asp Thr Glu Thr Gly Phe	
170 175 180	
AAA GAC GCG GTG TTT ATC ACT TCA GCG TGG GGG TTA GGC GAA AAT GTG	690
Lys Asp Ala Val Phe Ile Thr Ser Ala Trp Gly Leu Gly Glu Asn Val	
185 190 195 200	
GTG GGT GGC ACG ATA AAC CCT GAT GAA TTT TAT GTG TTT AAG CCC ACT	738
Val Gly Gly Thr Ile Asn Pro Asp Glu Phe Tyr Val Phe Lys Pro Thr	
205 210 215	
TTA GAG CAA AAC AAA CGC CCC ATT ATC AAA CGC CAA CTC GGC AAT AAA	786
Leu Glu Gln Asn Lys Arg Pro Ile Ile Lys Arg Gln Leu Gly Asn Lys	
220 225 230	
ACG CAA AAA ATG GTC TAT GCC CCA AGG GGT AGC GAA CAC CCC ACC AGA	834
Thr Gln Lys Met Val Tyr Ala Pro Arg Gly Ser Glu His Pro Thr Arg	
235 240 245	
AAC ATT AAA ACC ACC AAA AAA GAA TGG CAA TCC TTT TCA TTG AGC GAT	882
Asn Ile Lys Thr Thr Lys Lys Glu Trp Gln Ser Phe Ser Leu Ser Asp	
250 255 260	
GAA GAC GTG CTG ATT TTA GCC AAA TAC GCC ATT GAA ATT GAA AAA CAC	930
Glu Asp Val Leu Ile Leu Ala Lys Tyr Ala Ile Glu Ile Glu Lys His	
265 270 275 280	
TAC TCT AAA GAA GCC AAA CAA TAC CGC CCT ATG GAT ATA GAA TGG GCT	978
Tyr Ser Lys Glu Ala Lys Gln Tyr Arg Pro Met Asp Ile Glu Trp Ala	
285 290 295	

```

Arg His Asn Arg Leu Leu Pro Arg Asp Tyr Leu Gly Tyr Arg Ser Leu
    115          120          125
Gly Glu Glu Ile Ser Ile Phe Asn Pro Lys Asp Tyr Asp Ser Trp Gln
    130          135          140
Glu Arg Ala Asp Thr Glu Ile Leu Arg Gln Leu Gln Glu Ser Lys Lys
    145          150          155          160
Tyr Phe Val Phe Ile Lys Gly Cys Gly Ile Phe Ala Tyr His Arg Glu
    165          170          175
Leu Ser Lys Leu Met Glu Val Phe Asp Leu Ile Glu Asn Ser Cys Lys
    180          185          190
Val Leu Arg Leu Gly Asp Leu Met Asp Tyr Cys Tyr Asn Asp Asp Pro
    195          200          205
Arg Leu Ser Val
    210

```

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 91...2445
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

```

GGGAGTTTTG TGCGATATAT CAAGTTTTTC AAAGAGTTGA ACAATAAAAA TGTGAATCTG      60
GTTGGGGGCA AGAACGCTAG TATTGGTGAA  ATG TTT CAA GAA TTA GTG CCT ATT      114
                               Met Phe Gln Glu Leu Val Pro Ile
                               1              5

GGT ATT AAA GTG CCT GAT GGC TTT GCG ATC ACC AGC GAA GCG TAT TGG      162
Gly Ile Lys Val Pro Asp Gly Phe Ala Ile Thr Ser Glu Ala Tyr Trp
    10              15              20

TAT CTT TTA GAG CAA GGA GGG GCT AAA CAA AAA ATC ATA GAG CTT TTA      210
Tyr Leu Leu Glu Gln Gly Gly Ala Lys Gln Lys Ile Ile Glu Leu Leu
    25              30              35              40

GAA AAT GTT GAT GCC ACC GAA ATT GAT GTG TTA AAA ATC CGC TCC AAA      258
Glu Asn Val Asp Ala Thr Glu Ile Asp Val Leu Lys Ile Arg Ser Lys
    45              50              55

CAA ATC AGA GAG CTT ATT TTT GGC ACG CCT TTT CCT AGC GAT TTG AGA      306
Gln Ile Arg Glu Leu Ile Phe Gly Thr Pro Phe Pro Ser Asp Leu Arg
    60              65              70

```

CGA TTG CTC CCT AGA GAT TAT TTA GGG TAT CGT TCT TTG GGC GAA GAA	442
Arg Leu Leu Pro Arg Asp Tyr Leu Gly Tyr Arg Ser Leu Gly Glu Glu	
120 125 130	
ATT TCC ATT TTT AAC CCC AAA GAC TAT GAC AGC TGG CAA GAA AGA GCG	490
Ile Ser Ile Phe Asn Pro Lys Asp Tyr Asp Ser Trp Gln Glu Arg Ala	
135 140 145	
GAT ACA GAA ATT TTA CGC CAA CTG CAA GAG AGC AAA AAA TAT TTT GTT	538
Asp Thr Glu Ile Leu Arg Gln Leu Gln Glu Ser Lys Lys Tyr Phe Val	
150 155 160	
TTC ATT AAG GGG TGT GGG ATT TTT GCC TAC CAC AGA GAG CTT TCT AAA	586
Phe Ile Lys Gly Cys Gly Ile Phe Ala Tyr His Arg Glu Leu Ser Lys	
165 170 175	
CTC ATG GAA GTT TTT GAT TTG ATT GAA AAC TCA TGC AAG GTT TTA CGA	634
Leu Met Glu Val Phe Asp Leu Ile Glu Asn Ser Cys Lys Val Leu Arg	
180 185 190 195	
TTG GGC GAT TTA ATG GAT TAT TGC TAT AAT GAT GAT CCA CGA TTG AGC	682
Leu Gly Asp Leu Met Asp Tyr Cys Tyr Asn Asp Asp Pro Arg Leu Ser	
200 205 210	
GTG TAAAAAGCTA AAAAGGATAA AACATGACCA TCAAC	720
Val	

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

Met	Ile	Asn	Met	Asn	Thr	His	Thr	Arg	Gly	Ile	Asp	Ser	Asn	Leu	Ile
1				5					10					15	
His	Ser	Leu	Gln	Ser	Ile	Ser	Leu	Ser	Met	Phe	Arg	Lys	Gly	Phe	Phe
			20					25					30		
Gly	Leu	Tyr	Gln	Gly	Ser	Ile	Ser	Ala	Arg	Ile	Gly	Ala	Asn	Gln	Phe
			35				40					45			
Val	Ile	Asn	Lys	Arg	Asn	Ala	Val	Phe	Asp	Gln	Leu	Asn	Glu	Asn	Thr
			50			55					60				
Leu	Leu	Val	Leu	His	Asp	Lys	Ile	Asp	Tyr	Arg	Trp	Lys	Glu	Ala	Ser
65					70				75					80	
Leu	Asp	Ser	Pro	Ile	His	Ala	Ser	Val	Tyr	Arg	Glu	Phe	Leu	Asp	Ala
				85					90				95		
Lys	Phe	Ile	Ala	Tyr	Ala	Arg	Pro	Pro	Tyr	Ser	Leu	Ala	Tyr	Ser	Leu
			100					105					110		

260
 Ser Glu Glu Glu
 275
 265
 270

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...685
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

```

AGCTCTTTAC TATTTTATTA TCTATCTTTT ATTAAAAAAA CTTGTTATC ATG ATA AAC      58
                                     Met Ile Asn
                                     1

ATG AAC ACA CAC ACA AGA GGC ATT GAC AGC AAT CTG ATT CAT TCG CTC      106
Met Asn Thr His Thr Arg Gly Ile Asp Ser Asn Leu Ile His Ser Leu
   5                10                15

CAA AGC ATT TCA TTA TCC ATG TTT AGA AAG GGT TTT TTT GGG CTT TAT      154
Gln Ser Ile Ser Leu Ser Met Phe Arg Lys Gly Phe Phe Gly Leu Tyr
  20                25                30                35

CAA GGC TCT ATT TCA GCA CGC ATT GGC GCA AAT CAA TTT GTG ATC AAC      202
Gln Gly Ser Ile Ser Ala Arg Ile Gly Ala Asn Gln Phe Val Ile Asn
                40                45                50

AAA AGA AAC GCT GTT TTT GAT CAA TTG AAT GAA AAC ACC TTA CTG GTT      250
Lys Arg Asn Ala Val Phe Asp Gln Leu Asn Glu Asn Thr Leu Leu Val
                55                60                65

TTG CAT GAC AAA ATA GAT TAC CGC TGG AAA GAA GCG AGC TTG GAT TCG      298
Leu His Asp Lys Ile Asp Tyr Arg Trp Lys Glu Ala Ser Leu Asp Ser
                70                75                80

CCC ATT CAT GCG AGC GTG TAT AGG GAG TTT TTG GAC GCT AAA TTC ATC      346
Pro Ile His Ala Ser Val Tyr Arg Glu Phe Leu Asp Ala Lys Phe Ile
   85                90                95

GCT TAC GCG CGC CCT CCT TAT AGT TTG GCG TAT TCC TTG CGC CAC AAC      394
Ala Tyr Ala Arg Pro Pro Tyr Ser Leu Ala Tyr Ser Leu Arg His Asn
 100                105                110                115

```


CCT GTA GAA TTT CAA AAC AAG CGG ATG CAA CTG CTT TGC GTG GGG AAA 825
 Pro Val Glu Phe Gln Asn Lys Arg Met Gln Leu Leu Cys Val Gly Lys
 245 250 255 260

CTA GAA TGC GAT TAT GAA GGG TTT TTT CAA ACG ATT TCT GAG GAG GAA T 874
 Leu Glu Cys Asp Tyr Glu Gly Phe Phe Gln Thr Ile Ser Glu Glu Glu
 265 270 275

AATGAAAGAT GAACACAACC AAGAACACGA TCATTAA 912

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

Met	Val	Ile	Asp	Glu	Ile	Phe	Gln	Ile	Met	Met	Leu	Arg	Arg	Ile	Lys	1	5	10	15
Val	Gly	Ser	Asn	Leu	Asn	Lys	Lys	Glu	Ser	Leu	Leu	Asp	Ala	Phe	Val	20	25	30	
Lys	Thr	Tyr	Leu	Gln	Ile	Leu	Glu	Pro	Ile	Ser	Ser	Lys	Arg	Leu	Lys	35	40	45	
Glu	Leu	Ala	Asp	Leu	Lys	Ile	Ser	Cys	Ala	Thr	Ile	Arg	Asn	Tyr	Phe	50	55	60	
Gln	Ile	Leu	Ser	Lys	Glu	Gly	Met	Leu	Tyr	Gln	Ala	His	Ser	Ser	Gly	65	70	75	80
Ala	Arg	Leu	Pro	Thr	Phe	Lys	Ala	Phe	Glu	Asn	Tyr	Trp	Gln	Lys	Ser	85	90	95	
Leu	Arg	Phe	Glu	Thr	Leu	Lys	Val	Asn	Glu	Lys	Arg	Leu	Lys	Ser	Ala	100	105	110	
Ser	Glu	Asn	Phe	Gly	Leu	Phe	Thr	Leu	Leu	Lys	Lys	Pro	Ser	Leu	Glu	115	120	125	
Arg	Leu	Glu	Arg	Val	Ile	Glu	Cys	Glu	Lys	Arg	Phe	Leu	Ile	Leu	Asp	130	135	140	
Phe	Leu	Ala	Phe	Ser	Cys	Ala	Leu	Gly	Tyr	Ser	Val	Lys	Met	Glu	Lys	145	150	155	160
Phe	Leu	Leu	Glu	Leu	Val	Gly	Arg	Ser	Val	Lys	Glu	Val	Arg	Ser	Ile	165	170	175	
Ala	Ala	Ser	Phe	Asn	Ala	Leu	Ser	Leu	Ala	Arg	Gln	Leu	Glu	Arg	Leu	180	185	190	
Glu	Tyr	Ser	Asn	Thr	Gln	Ile	Thr	Arg	Phe	Asn	Leu	Met	Gly	Leu	Lys	195	200	205	
Thr	Leu	Leu	Asn	Ser	Pro	Leu	Phe	Phe	Asp	Ile	Leu	Gly	Gly	Lys	Val	210	215	220	
Leu	Glu	Arg	Leu	Ser	Lys	Gly	Leu	His	Phe	Ile	Glu	Pro	Asp	Cys	Met	225	230	235	240
Leu	Val	Thr	Arg	Pro	Val	Glu	Phe	Gln	Asn	Lys	Arg	Met	Gln	Leu	Leu	245	250	255	
Cys	Val	Gly	Lys	Leu	Glu	Cys	Asp	Tyr	Glu	Gly	Phe	Phe	Gln	Thr	Ile				

Leu Asn Lys Lys Glu Ser Leu Leu Asp Ala Phe Val Lys Thr Tyr Leu	
25 30 35	
CAG ATT TTA GAA CCC ATT AGT TCT AAA CGC TTA AAA GAG TTG GCG GAC	201
Gln Ile Leu Glu Pro Ile Ser Ser Lys Arg Leu Lys Glu Leu Ala Asp	
40 45 50	
TTG AAA ATA TCT TGC GCG ACG ATC AGG AAT TAT TTT CAA ATC CTT TCT	249
Leu Lys Ile Ser Cys Ala Thr Ile Arg Asn Tyr Phe Gln Ile Leu Ser	
55 60 65	
AAA GAG GGC ATG CTT TAT CAA GCC CAT TCT AGT GGC GCT AGA TTG CCC	297
Lys Glu Gly Met Leu Tyr Gln Ala His Ser Ser Gly Ala Arg Leu Pro	
70 75 80	
ACT TTT AAG GCG TTT GAA AAC TAT TGG CAA AAG TCG TTG CGC TTT GAA	345
Thr Phe Lys Ala Phe Glu Asn Tyr Trp Gln Lys Ser Leu Arg Phe Glu	
85 90 95 100	
ACT TTA AAG GTG AAT GAA AAA CGC CTA AAA AGC GCG AGT GAA AAT TTT	393
Thr Leu Lys Val Asn Glu Lys Arg Leu Lys Ser Ala Ser Glu Asn Phe	
105 110 115	
GGG CTT TTC ACG CTG TTA AAA AAA CCC AGT TTG GAG CGT TTA GAA AGA	441
Gly Leu Phe Thr Leu Leu Lys Lys Pro Ser Leu Glu Arg Leu Glu Arg	
120 125 130	
GTC ATT GAG TGC GAA AAA CGC TTT TTG ATT TTG GAC TTT TTG GCG TTT	489
Val Ile Glu Cys Glu Lys Arg Phe Leu Ile Leu Asp Phe Leu Ala Phe	
135 140 145	
TCT TGC GCA CTG GGT TAC AGC GTT AAA ATG GAA AAG TTT TTA TTA GAG	537
Ser Cys Ala Leu Gly Tyr Ser Val Lys Met Glu Lys Phe Leu Leu Glu	
150 155 160	
CTT GTG GGC AGA AGC GTT AAA GAA GTG CGC TCA ATC GCT GCT TCT TTC	585
Leu Val Gly Arg Ser Val Lys Glu Val Arg Ser Ile Ala Ala Ser Phe	
165 170 175 180	
AAT GCG TTG AGT TTG GCC AGG CAA TTA GAG CGT TTG GAG TAT TCC AAC	633
Asn Ala Leu Ser Leu Ala Arg Gln Leu Glu Arg Leu Glu Tyr Ser Asn	
185 190 195	
ACA CAA ATC ACA CGC TTT AAT CTG ATG GGG TTA AAA ACG CTT TTA AAC	681
Thr Gln Ile Thr Arg Phe Asn Leu Met Gly Leu Lys Thr Leu Leu Asn	
200 205 210	
AGC CCT TTA TTT TTT GAC ATT TTA GGG GGT AAG GTT TTA GAG CGT TTG	729
Ser Pro Leu Phe Phe Asp Ile Leu Gly Gly Lys Val Leu Glu Arg Leu	
215 220 225	
AGT AAG GGT TTG CAT TTT ATA GAG CCT GAT TGC ATG CTA GTA ACA CGC	777
Ser Lys Gly Leu His Phe Ile Glu Pro Asp Cys Met Leu Val Thr Arg	
230 235 240	

```

Tyr Tyr Gln Asn Pro Leu Leu Leu Gly Ala Asp Ile Val Ala His Ser
    180                                185                                190
Gly Thr Lys Tyr Leu Gly Gly His Ser Asp Val Val Ala Gly Leu Val
    195                                200                                205
Thr Thr Asn Asn Glu Ala Leu Ala Gln Glu Ile Ala Phe Phe Gln Asn
    210                                215                                220
Ala Ile Gly Gly Val Leu Gly Pro Gln Asp Ser Trp Leu Leu Gln Arg
    225                                230                                235                                240
Gly Ile Lys Thr Leu Gly Leu Arg Met Glu Ala His Gln Lys Asn Ala
    245                                250                                255
Leu Cys Val Ala Glu Phe Leu Glu Lys His Pro Lys Val Glu Arg Val
    260                                265                                270
Tyr Tyr Pro Gly Leu Pro Thr His Pro Asn Tyr Glu Leu Ala Lys Lys
    275                                280                                285
Gln Met Arg Gly Phe Ser Gly Met Leu Ser Phe Thr Leu Lys Asn Asp
    290                                295                                300
Ser Glu Ala Val Ala Phe Val Glu Ser Leu Lys Leu Phe Ile Leu Gly
    305                                310                                315                                320
Glu Ser Leu Gly Gly Val Glu Ser Leu Val Gly Ile Pro Ala Phe Met
    325                                330                                335
Thr His Ala Cys Ile Pro Lys Thr Gln Arg Glu Ala Ala Gly Ile Arg
    340                                345                                350
Asp Gly Leu Val Arg Leu Ser Val Gly Ile Glu His Glu Gln Asp Leu
    355                                360                                365
Leu Glu Asp Leu Glu Gln Ala Phe Ala Lys Ile Gly
    370                                375                                380

```

(2) INFORMATION FOR SEQ ID NO:1201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...873
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

```

ATTATTAAC TTTTATGCTA TAATGCGAGG GTTCTTTCAT CAAGA ATG GTG ATT GAC      57
                                   Met Val Ile Asp
                                   1

GAG ATT TTT CAA ATA ATG ATG TTA AGA AGA ATT AAA GTA GGT TCT AAT      105
Glu Ile Phe Gln Ile Met Met Leu Arg Arg Ile Lys Val Gly Ser Asn
  5                                10                                15                                20

TTG AAT AAA AAA GAG AGT TTG TTA GAT GCG TTT GTT AAA ACC TAT CTG      153

```

```

CTT AAA CTA TTC ATT TTA GGC GAG AGT TTG GGC GGG GTG GAA AGT TTG      1011
Leu Lys Leu Phe Ile Leu Gly Glu Ser Leu Gly Gly Val Glu Ser Leu
    315                      320                      325

GTG GGG ATT CCG GCA TTT ATG ACC CAT GCG TGC ATC CCT AAA ACG CAA      1059
Val Gly Ile Pro Ala Phe Met Thr His Ala Cys Ile Pro Lys Thr Gln
    330                      335                      340                      345

CGA GAA GCT GCT GGG ATT AGA GAT GGC CTG GTG CGC TTG TCT GTA GGG      1107
Arg Glu Ala Ala Gly Ile Arg Asp Gly Leu Val Arg Leu Ser Val Gly
                350                      355                      360

ATT GAG CAT GAA CAG GAT TTG TTA GAA GAT TTA GAG CAA GCG TTC GCT      1155
Ile Glu His Glu Gln Asp Leu Leu Glu Asp Leu Glu Gln Ala Phe Ala
                365                      370                      375

AAA ATA GGC TAAAGTTTCA TTACAATTTA TGAATAAAGG AGTTAAAAAC ATGAA      1209
Lys Ile Gly
    380

```

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

```

Met Arg Met Gln Thr Lys Leu Ile His Gly Gly Ile Ser Glu Asp Ala
 1          5          10          15
Thr Thr Gly Ala Val Ser Val Pro Ile Tyr Gln Thr Ser Thr Tyr Arg
    20          25          30
Gln Asp Ala Ile Gly Arg His Lys Gly Tyr Glu Tyr Ser Arg Ser Gly
    35          40          45
Asn Pro Thr Arg Phe Ala Leu Glu Glu Leu Ile Ala Asp Leu Glu Gly
    50          55          60
Gly Val Lys Gly Phe Ala Phe Ala Ser Gly Leu Ala Gly Ile His Ala
    65          70          75          80
Val Phe Ser Leu Leu Gln Ser Gly Asp His Val Leu Leu Gly Asp Asp
                85          90          95
Val Tyr Gly Gly Thr Phe Arg Leu Phe Asn Gln Val Leu Val Lys Asn
    100          105          110
Gly Leu Ser Cys Thr Ile Ile Asp Thr Ser Asp Ile Ser Gln Ile Lys
    115          120          125
Lys Ala Ile Lys Pro Asn Thr Lys Ala Leu Tyr Leu Glu Thr Pro Ser
    130          135          140
Asn Pro Leu Leu Lys Ile Thr Asp Leu Ala Gln Cys Ala Ser Val Ala
    145          150          155          160
Lys Asp His Gly Leu Leu Thr Ile Val Asp Asn Thr Phe Ala Thr Pro
                165          170          175

```

CAT GTG TTA TTG GGC GAT GAT GTT TAT GGG GGG ACT TTC CGC TTG TTT	339
His Val Leu Leu Gly Asp Asp Val Tyr Gly Gly Thr Phe Arg Leu Phe	
90 95 100 105	
AAT CAA GTG CTT GTC AAA AAC GGG CTT TCT TGC ACC ATT ATA GAC ACT	387
Asn Gln Val Leu Val Lys Asn Gly Leu Ser Cys Thr Ile Ile Asp Thr	
110 115 120	
AGC GAT ATA TCC CAA ATT AAA AAG GCT ATC AAG CCC AAC ACC AAA GCC	435
Ser Asp Ile Ser Gln Ile Lys Lys Ala Ile Lys Pro Asn Thr Lys Ala	
125 130 135	
CTT TAT TTA GAA ACC CCT AGT AAC CCC TTG CTT AAA ATC ACG GAT TTA	483
Leu Tyr Leu Glu Thr Pro Ser Asn Pro Leu Leu Lys Ile Thr Asp Leu	
140 145 150	
GCG CAA TGC GCT AGT GTC GCT AAA GAT CAT GGT TTG CTC ACT ATC GTG	531
Ala Gln Cys Ala Ser Val Ala Lys Asp His Gly Leu Leu Thr Ile Val	
155 160 165	
GAT AAC ACC TTT GCC ACC CCC TAT TAT CAA AAC CCG CTT CTT TTG GGA	579
Asp Asn Thr Phe Ala Thr Pro Tyr Tyr Gln Asn Pro Leu Leu Leu Gly	
170 175 180 185	
GCG GAC ATT GTG GCA CAT AGC GGC ACC AAA TAC TTA GGC GGG CAT AGC	627
Ala Asp Ile Val Ala His Ser Gly Thr Lys Tyr Leu Gly Gly His Ser	
190 195 200	
GAT GTG GTC GCC GGG CTT GTA ACC ACT AAT AAT GAA GCG CTA GCC CAA	675
Asp Val Val Ala Gly Leu Val Thr Thr Asn Asn Glu Ala Leu Ala Gln	
205 210 215	
GAG ATC GCT TTT TTC CAA AAC GCT ATC GGT GGG GTT TTA GGC CCT CAA	723
Glu Ile Ala Phe Phe Gln Asn Ala Ile Gly Gly Val Leu Gly Pro Gln	
220 225 230	
GAC AGC TGG CTG TTG CAA AGA GGG ATT AAA ACG CTG GGA TTG CGC ATG	771
Asp Ser Trp Leu Leu Gln Arg Gly Ile Lys Thr Leu Gly Leu Arg Met	
235 240 245	
GAA GCC CAT CAA AAA AAC GCT CTT TGT GTG GCT GAG TTT TTA GAA AAA	819
Glu Ala His Gln Lys Asn Ala Leu Cys Val Ala Glu Phe Leu Glu Lys	
250 255 260 265	
CAC CCT AAA GTG GAA AGG GTT TAT TAC CCG GGC CTT CCC ACT CAC CCT	867
His Pro Lys Val Glu Arg Val Tyr Tyr Pro Gly Leu Pro Thr His Pro	
270 275 280	
AAT TAC GAA CTA GCT AAA AAA CAG ATG CGT GGC TTT AGC GGG ATG CTC	915
Asn Tyr Glu Leu Ala Lys Lys Gln Met Arg Gly Phe Ser Gly Met Leu	
285 290 295	
TCT TTC ACT CTC AAA AAT GAT AGC GAG GCG GTT GCT TTT GTA GAA AGC	963
Ser Phe Thr Leu Lys Asn Asp Ser Glu Ala Val Ala Phe Val Glu Ser	
300 305 310	

```

65          70          75          80
Ile Leu Ala Leu Lys Ser Leu Ser Pro Arg Leu Lys Ala Leu Ile Leu
          85          90          95
Arg Thr Ser Ser Ser Met Arg Phe Thr Ile Leu Asn Leu Ala Tyr Met
          100         105         110
Ser Val Lys Thr Thr Ser Ala Ile Val Ala Val Ser Ile Gln Arg Asn
          115         120         125
Asn Phe Val Val Phe Ser Ser Lys Thr Leu Phe Thr Pro Ser Leu Ile
          130         135         140
Ala Leu Phe Ser Val Leu Met Ser Val
145          150

```

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1164
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

```

AAATTCAATA AAAAAGGAAA AACC ATG CGC ATG CAA ACC AAA TTA ATC CAT      51
                Met Arg Met Gln Thr Lys Leu Ile His
                1                5

GGG GGC ATT AGT GAG GAC GCA ACA ACG GGG GCG GTG AGC GTG CCT ATT      99
Gly Gly Ile Ser Glu Asp Ala Thr Thr Gly Ala Val Ser Val Pro Ile
10                15                20                25

TAT CAA ACT TCC ACC TAC CGC CAA GAC GCC ATA GGC CGC CAT AAG GGC      147
Tyr Gln Thr Ser Thr Tyr Arg Gln Asp Ala Ile Gly Arg His Lys Gly
                30                35                40

TAT GAA TAC TCT CGC TCA GGC AAC CCC ACG CGC TTT GCT TTA GAA GAA      195
Tyr Glu Tyr Ser Arg Ser Gly Asn Pro Thr Arg Phe Ala Leu Glu Glu
                45                50                55

CTC ATC GCT GAT TTA GAA GGG GGG GTT AAG GGG TTT GCT TTT GCC TCT      243
Leu Ile Ala Asp Leu Glu Gly Gly Val Lys Gly Phe Ala Phe Ala Ser
        60                65                70

GGA TTA GCT GGA ATC CAC GCC GTT TTT TCC CTC TTG CAA TCA GGC GAT      291
Gly Leu Ala Gly Ile His Ala Val Phe Ser Leu Leu Gln Ser Gly Asp
        75                80                85

```

TGG GTT TCT TGC GTG ATT TGG ACT AAT TTA TCC ATT GAA GTT TTA TTG	147
Trp Val Ser Cys Val Ile Trp Thr Asn Leu Ser Ile Glu Val Leu Leu	
30 35 40	
AGG GTG GAA ATC CCT TTA ATC TCT TCC ATA ATC AAG CGG GCG TTT TCC	195
Arg Val Glu Ile Pro Leu Ile Ser Ser Ile Ile Lys Arg Ala Phe Ser	
45 50 55 60	
ACA AAC AAA TTG ATC CCA CGG CCC ACT TGC GAG ATT TCA TCG TTG CGA	243
Thr Asn Lys Leu Ile Pro Arg Pro Thr Cys Glu Ile Ser Ser Leu Arg	
65 70 75	
TCA CCC ACA TCA ATT TTG GCT CTC AAA TCC TTA TCC CCA CGG CTA AAA	291
Ser Pro Thr Ser Ile Leu Ala Leu Lys Ser Leu Ser Pro Arg Leu Lys	
80 85 90	
GCG TTG ATT TTA AGG ACC AGT TCA TCA ATG CGT TTC ACG ATC CTT AAT	339
Ala Leu Ile Leu Arg Thr Ser Ser Ser Met Arg Phe Thr Ile Leu Asn	
95 100 105	
TTA GCG TAT ATG AGC GTC AAA ACC ACT AGC GCT ATC GTC GCT GTC AGT	387
Leu Ala Tyr Met Ser Val Lys Thr Thr Ser Ala Ile Val Ala Val Ser	
110 115 120	
ATC CAA AGG AAT AAT TTC GTG GTG TTT TCA TCA AAA ACC TTA TTC ACG	435
Ile Gln Arg Asn Asn Phe Val Val Phe Ser Ser Lys Thr Leu Phe Thr	
125 130 135 140	
CCT TCT TTG ATC GCT TTA TTT TCT GTG TTA ATG TCA GTG TAATAGGAAG TC	486
Pro Ser Leu Ile Ala Leu Phe Ser Val Leu Met Ser Val	
145 150	
GTTGCGATCA CCATTGAGA AACTTCATCA TAATGCGAG	525

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

Met Glu Ala Phe Ile Met Leu Ala Ile Ser Val Ala Leu Phe Phe Thr	
1 5 10 15	
Glu Phe Arg Val Val Glu Glu Ser Phe Met Leu Phe Trp Val Ser Cys	
20 25 30	
Val Ile Trp Thr Asn Leu Ser Ile Glu Val Leu Leu Arg Val Glu Ile	
35 40 45	
Pro Leu Ile Ser Ser Ile Ile Lys Arg Ala Phe Ser Thr Asn Lys Leu	
50 55 60	
Ile Pro Arg Pro Thr Cys Glu Ile Ser Ser Leu Arg Ser Pro Thr Ser	

```

          355          360          365
Ser Gln Ile Thr Glu Ser Ala His Thr Glu Glu Glu Leu Ser Ser Lys
  370          375          380
Val Glu Gln Leu Ser Arg Asn Ala Asp Asp Val Lys Ser Ile Leu Asp
385          390          395          400
Ile Ile Asn Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu Asn Ala
          405          410          415
Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe Ala Val
          420          425          430
Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser Leu
          435          440          445
Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn Ala
          450          455          460
Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu Ser
465          470          475          480
Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser Asn
          485          490          495
Leu Ser Ser Val Val Ser Asp Ser Asn Gln Ser Met Asp Asp Tyr Ala
          500          505          510
Lys Ser Gly His Gln Ile Glu Val Met Val Ser Asp Phe Ala Glu Val
          515          520          525
Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile Leu Asn
          530          535          540
Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Asp Lys Gln Val
545          550          555          560
Asn Leu Phe Lys Thr
          565

```

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...474
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

```

CCTTGAGATT GCTCT ATG GAA GCA TTC ATC ATG CTC GCT ATA TCA GTG GCT      51
      Met Glu Ala Phe Ile Met Leu Ala Ile Ser Val Ala
          1              5              10

TTA TTT TTC ACG GAA TTT AGG GTG GTT GAG GAA TCT TTC ATG CTC TTT      99
Leu Phe Phe Thr Glu Phe Arg Val Val Glu Glu Ser Phe Met Leu Phe
      15              20              25

```


(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

```

Met Met Phe Ser Ser Met Phe Ala Ser Leu Gly Thr Arg Ile Met Leu
 1             5             10             15
Val Val Leu Ala Ala Leu Leu Gly Leu Gly Gly Leu Phe Ile Gly Phe
      20             25             30
Val Lys Val Met Gln Lys Asp Val Leu Ala Gln Leu Met Glu His Leu
      35             40             45
Glu Thr Gly Gln Tyr Lys Lys Arg Glu Lys Thr Leu Ala Tyr Met Thr
      50             55             60
Lys Ile Ile Glu Gln Gly Ile His Glu Tyr Tyr Lys Asn Phe Asp Asn
65             70             75             80
Ala Thr Ala Arg Lys Met Ala Leu Asp Tyr Phe Lys Arg Ile Asn Asp
      85             90             95
Asp Lys Gly Met Ile Tyr Met Val Val Val Asp Lys Asn Gly Val Val
      100            105            110
Leu Phe Asp Pro Val Asn Pro Lys Thr Val Xaa Gln Ser Gly Leu Asp
      115            120            125
Ala Gln Ser Val Asp Gly Val Tyr Tyr Val Arg Gly Tyr Leu Glu Ala
      130            135            140
Ala Lys Lys Gly Gly Gly Tyr Thr Tyr Tyr Lys Met Pro Lys Tyr Asp
145            150            155            160
Gly Gly Val Pro Glu Lys Lys Phe Ala Tyr Ser His Tyr Asp Glu Val
      165            170            175
Ser Gln Met Val Ile Ala Thr Thr Ser Tyr Tyr Thr Asp Ile Asn Thr
      180            185            190
Glu Asn Lys Ala Ile Lys Glu Gly Val Asn Lys Val Phe Asp Glu Asn
      195            200            205
Thr Thr Lys Leu Phe Leu Trp Ile Leu Thr Ala Thr Ile Ala Leu Val
      210            215            220
Val Leu Thr Leu Ile Tyr Ala Lys Leu Arg Ile Val Lys Arg Ile Asp
225            230            235            240
Glu Leu Val Leu Lys Ile Asn Ala Phe Ser Arg Gly Asp Lys Asp Leu
      245            250            255
Arg Ala Lys Ile Asp Val Gly Asp Arg Asn Asp Glu Ile Ser Gln Val
      260            265            270
Gly Arg Gly Ile Asn Leu Phe Val Glu Asn Ala Arg Leu Ile Met Glu
      275            280            285
Glu Ile Lys Gly Ile Ser Thr Leu Asn Lys Thr Ser Met Asp Lys Leu
      290            295            300
Val Gln Ile Thr Gln Glu Thr Gln Lys Ser Met Lys Asp Ser Ser Thr
305            310            315            320
Thr Leu Asn Ser Val Lys Asn Lys Ala Thr Asp Ile Ala Ser Met Met
      325            330            335
Asn Ala Ser Ile Glu Gln Ser Gln Gly Leu Arg Lys Arg Leu Ile Glu
      340            345            350
Thr Gln Gly Leu Val Lys Glu Ser Lys Asp Ala Ile Gly Asp Leu Phe

```

TTA TTT TCT CAA ATC ACA GAG AGC GCG CAC ACT GAA GAG GAA CTC TCT	1153
Leu Phe Ser Gln Ile Thr Glu Ser Ala His Thr Glu Glu Glu Leu Ser	
370 375 380	
AGC AAA GTG GAG CAG CTA AGC CGT AAC GCT GAT GAT GTC AAA TCC ATT	1201
Ser Lys Val Glu Gln Leu Ser Arg Asn Ala Asp Asp Val Lys Ser Ile	
385 390 395	
CTG GAT ATT ATC AAT GAT ATT GCC GAT CAA ACG AAT TTA TTA GCC CTA	1249
Leu Asp Ile Ile Asn Asp Ile Ala Asp Gln Thr Asn Leu Leu Ala Leu	
400 405 410	
AAC GCT GCT ATT GAA GCC GCA AGG GCT GGC GAG CAT GGC AGA GGC TTT	1297
Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly Glu His Gly Arg Gly Phe	
415 420 425 430	
GCG GTG GTG GCT GAT GAA GTT AGG AAT TTA GCC GGG CGC ACT CAA AAG	1345
Ala Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys	
435 440 445	
TCT TTA GCC GAA ATC AAT TCC ACT ATC ATG GTG ATT GTC CAA GAA ATC	1393
Ser Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile	
450 455 460	
AAT GCC GTG AGT TCG CAA ATG AAT CTC AAT TCG CAA AAA ATG GAG CGT	1441
Asn Ala Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg	
465 470 475	
TTG AGC GAT ATG AGT AAA AGC GTG CAA GAA ACT TAC GAA AAA ATG AGT	1489
Leu Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser	
480 485 490	
TCT AAT TTA AGC TCA GTC GTG TCA GAC AGC AAT CAA AGC ATG GAC GAT	1537
Ser Asn Leu Ser Ser Val Val Ser Asp Ser Asn Gln Ser Met Asp Asp	
495 500 505 510	
TAC GCC AAA TCC GGA CAC CAA ATT GAA GTT ATG GTA AGC GAT TTT GCA	1585
Tyr Ala Lys Ser Gly His Gln Ile Glu Val Met Val Ser Asp Phe Ala	
515 520 525	
GAG GTG GAA AAA GTG GCT TCT AAG ACT TTA GCG GAT TCT TCA GAT ATT	1633
Glu Val Glu Lys Val Ala Ser Lys Thr Leu Ala Asp Ser Ser Asp Ile	
530 535 540	
TTA AAC ATC GCT ACG CAT GTG AGT GGA ACG ACC ATG AAT TTA GAC AAA	1681
Leu Asn Ile Ala Thr His Val Ser Gly Thr Thr Met Asn Leu Asp Lys	
545 550 555	
CAA GTG AAT TTG TTT AAA ACT TAATCAGGGG GAGTTTATTA AAAAAGGGTT GGAT	1736
Gln Val Asn Leu Phe Lys Thr	
560 565	
TGTTAAAAGT TTCTGTGATC AC	1758

(2) INFORMATION FOR SEQ ID NO:1196:

GAG GCG GCC AAA AAA GGG GGA GGC TAC ACT TAT TAT AAA ATG CCT AAA	481
Glu Ala Ala Lys Lys Gly Gly Gly Tyr Thr Tyr Tyr Lys Met Pro Lys	
145 150 155	
TAC GAT GGA GGC GTA CCG GAG AAA AAA TTC GCC TAC TCG CAT TAT GAT	529
Tyr Asp Gly Gly Val Pro Glu Lys Lys Phe Ala Tyr Ser His Tyr Asp	
160 165 170	
GAA GTT TCT CAA ATG GTG ATC GCA ACG ACT TCC TAT TAC ACT GAC ATT	577
Glu Val Ser Gln Met Val Ile Ala Thr Thr Ser Tyr Tyr Thr Asp Ile	
175 180 185 190	
AAC ACA GAA AAT AAA GCG ATC AAA GAA GGC GTG AAT AAG GTT TTT GAT	625
Asn Thr Glu Asn Lys Ala Ile Lys Glu Gly Val Asn Lys Val Phe Asp	
195 200 205	
GAA AAC ACC ACG AAA TTA TTC CTT TGG ATA CTG ACA GCG ACG ATA GCG	673
Glu Asn Thr Thr Lys Leu Phe Leu Trp Ile Leu Thr Ala Thr Ile Ala	
210 215 220	
CTA GTG GTT TTG ACG CTC ATA TAC GCT AAA TTA AGG ATC GTG AAA CGC	721
Leu Val Val Leu Thr Leu Ile Tyr Ala Lys Leu Arg Ile Val Lys Arg	
225 230 235	
ATT GAT GAA CTG GTC CTT AAA ATC AAC GCT TTT AGC CGT GGG GAT AAG	769
Ile Asp Glu Leu Val Leu Lys Ile Asn Ala Phe Ser Arg Gly Asp Lys	
240 245 250	
GAT TTG AGA GCC AAA ATT GAT GTG GGT GAT CGC AAC GAT GAA ATC TCG	817
Asp Leu Arg Ala Lys Ile Asp Val Gly Asp Arg Asn Asp Glu Ile Ser	
255 260 265 270	
CAA GTG GGC CGT GGG ATC AAT TTG TTT GTG GAA AAC GCC CGC TTG ATT	865
Gln Val Gly Arg Gly Ile Asn Leu Phe Val Glu Asn Ala Arg Leu Ile	
275 280 285	
ATG GAA GAG ATT AAA GGG ATT TCC ACC CTC AAT AAA ACT TCA ATG GAT	913
Met Glu Glu Ile Lys Gly Ile Ser Thr Leu Asn Lys Thr Ser Met Asp	
290 295 300	
AAA TTA GTC CAA ATC ACG CAA GAA ACC CAA AAG AGC ATG AAA GAT TCC	961
Lys Leu Val Gln Ile Thr Gln Glu Thr Gln Lys Ser Met Lys Asp Ser	
305 310 315	
TCA ACC ACC CTA AAT TCC GTG AAA AAT AAA GCC ACT GAT ATA GCG AGC	1009
Ser Thr Thr Leu Asn Ser Val Lys Asn Lys Ala Thr Asp Ile Ala Ser	
320 325 330	
ATG ATG AAT GCT TCC ATA GAG CAA TCT CAA GGG TTA AGG AAG CGT TTG	1057
Met Met Asn Ala Ser Ile Glu Gln Ser Gln Gly Leu Arg Lys Arg Leu	
335 340 345 350	
ATT GAA ACG CAA GGG CTG GTC AAA GAG AGC AAG GAT GCG ATC GGG GAT	1105
Ile Glu Thr Gln Gly Leu Val Lys Glu Ser Lys Asp Ala Ile Gly Asp	
355 360 365	

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1758 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 8...1702
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

GAGATAA ATG ATG TTT TCT TCA ATG TTT GCT TCG TTG GGG ACT CGT ATC	49
Met Met Phe Ser Ser Met Phe Ala Ser Leu Gly Thr Arg Ile	
1 5 10	
ATG CTG GTC GTG TTA GCC GCT CTT TTA GGT TTA GGG GGG CTT TTT ATT	97
Met Leu Val Val Leu Ala Ala Leu Leu Gly Leu Gly Gly Leu Phe Ile	
15 20 25 30	
GGT TTT GTA AAG GTT ATG CAA AAA GAT GTG TTA GCG CAA CTC ATG GAG	145
Gly Phe Val Lys Val Met Gln Lys Asp Val Leu Ala Gln Leu Met Glu	
35 40 45	
CAT TTA GAA ACC GGG CAA TAC AAA AAG CGT GAA AAA ACG CTC GCT TAC	193
His Leu Glu Thr Gly Gln Tyr Lys Lys Arg Glu Lys Thr Leu Ala Tyr	
50 55 60	
ATG ACA AAA ATT ATT GAA CAG GGC ATT CAT GAG TAT TAC AAA AAT TTT	241
Met Thr Lys Ile Ile Glu Gln Gly Ile His Glu Tyr Tyr Lys Asn Phe	
65 70 75	
GAC AAT GCT ACT GCA AGA AAA ATG GCG TTA GAT TAT TTC AAA CGC ATC	289
Asp Asn Ala Thr Ala Arg Lys Met Ala Leu Asp Tyr Phe Lys Arg Ile	
80 85 90	
AAC GAC GAT AAG GGC ATG ATT TAT ATG GTG GTG GTG GAT AAA AAC GGG	337
Asn Asp Asp Lys Gly Met Ile Tyr Met Val Val Val Asp Lys Asn Gly	
95 100 105 110	
GTG GTA TTG TTT GAT CCG GTC AAT CCT AAA ACC GTA GNC CAA TCA GGG	385
Val Val Leu Phe Asp Pro Val Asn Pro Lys Thr Val Xaa Gln Ser Gly	
115 120 125	
CTT GAC GCT CAG AGC GTT GAT GGG GTG TAT TAT GTT AGG GGG TAT TTG	433
Leu Asp Ala Gln Ser Val Asp Gly Val Tyr Tyr Val Arg Gly Tyr Leu	
130 135 140	

195	200	205
Asp Pro Phe Ser His Lys Glu	Asn Phe Leu Ala Val	Glu Thr Phe Lys
210	215	220
Met Leu Gly Lys Thr Glu Ser	Lys Asp Asn Leu Asn	Trp Met Ile Ala
225	230	235
Leu Ile Ile Glu Lys Asp Lys	Val Tyr Glu Gln Val	Gly Ser Val Arg
245	250	255
Phe Val Val Ile Ile Ala Ser	Ala Ile Met Val Leu Ala	Leu Ile Ile
260	265	270
Ala Ile Thr Leu Leu Met Arg	Ala Ile Val Ser Ser	Arg Leu Glu Ala
275	280	285
Val Ser Ser Thr Leu Ser His	Phe Phe Lys Leu Leu	Asn Asn Gln Ala
290	295	300
Asn Ser Ser Gly Ile Lys Leu	Ile Glu Ala Lys Ser	Asn Asp Glu Leu
305	310	315
Gly Arg Met Gln Thr Ala Ile	Asn Lys Asn Ile Leu	Gln Thr Gln Lys
325	330	335
Ile Met Gln Glu Asp Arg Gln	Ala Val Gln Asp Thr	Ile Lys Val Val
340	345	350
Ser Asp Val Lys Ala Gly Asn	Phe Ala Val Arg Ile	Thr Ala Glu Pro
355	360	365
Ala Ser Pro Asp Leu Lys Glu	Leu Arg Asp Ala Leu	Asn Gly Ile Met
370	375	380
Asp Tyr Leu Gln Glu Ser Val	Gly Thr His Met Pro	Ser Ile Phe Lys
385	390	395
Ile Phe Glu Ser Tyr Ser Gly	Leu Asp Phe Arg Gly	Arg Ile Gln Asn
405	410	415
Ala Ser Gly Arg Val Glu Leu	Val Thr Asn Ala Leu	Gly Gln Glu Ile
420	425	430
Gln Lys Met Leu Glu Thr Ser	Ser Asn Phe Ala Lys	Asp Leu Ala Asn
435	440	445
Asp Ser Ala Asn Leu Lys Glu	Cys Val Gln Asn Leu	Glu Lys Ala Ser
450	455	460
Asn Ser Gln His Lys Ser Leu	Met Glu Thr Ser Lys	Thr Ile Glu Asn
465	470	475
Ile Thr Thr Ser Ile Gln Gly	Val Ser Ser Gln Ser	Glu Ala Met Ile
485	490	495
Glu Gln Gly Gln Asp Ile Lys	Ser Ile Val Glu Ile	Ile Arg Asp Ile
500	505	510
Ala Asp Gln Thr Asn Leu Leu	Ala Leu Asn Ala Ala	Ile Glu Ala Ala
515	520	525
Arg Ala Gly Glu His Gly Arg	Gly Phe Ala Val Val	Ala Asp Glu Val
530	535	540
Arg Lys Leu Ala Glu Arg Thr	Gln Lys Ser Leu Ser	Glu Ile Glu Ala
545	550	555
Asn Ile Asn Ile Leu Val Gln	Ser Ile Ser Asp Thr	Ser Glu Ser Ile
565	570	575
Lys Asn Gln Val Lys Glu Val	Glu Glu Ile Asn Ala	Ser Ile Glu Ala
580	585	590
Leu Arg Ser Val Thr Glu Gly	Asn Leu Lys Ile Ala	Ser Asp Ser Leu
595	600	605
Glu Ile Ser Gln Glu Ile Asp	Lys Val Ser Asn Asp	Ile Leu Glu Asp
610	615	620
Val Asn Lys Lys Gln Phe		
625	630	

AAC CAG GTT AAA GAA GTG GAA GAA ATC AAC GCT TCT ATT GAA GCC TTA 1834
 Asn Gln Val Lys Glu Val Glu Glu Ile Asn Ala Ser Ile Glu Ala Leu
 580 585 590

AGA TCG GTT ACT GAG GGC AAT CTA AAA ATC GCT AGC GAT TCT TTA GAA 1882
 Arg Ser Val Thr Glu Gly Asn Leu Lys Ile Ala Ser Asp Ser Leu Glu
 595 600 605

ATC AGT CAA GAA ATT GAC AAA GTT TCT AAC GAT ATT TTA GAA GAT GTG 1930
 Ile Ser Gln Glu Ile Asp Lys Val Ser Asn Asp Ile Leu Glu Asp Val
 610 615 620 625

AAT AAA AAG CAG TTT TAATGCTCAT TCATATTTGC TGCTCAGTGG ATAACCTCTA T 1986
 Asn Lys Lys Gln Phe
 630

1986

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

Met Gln Asp Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu
 1 5 10 15
 Glu Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys
 20 25 30
 Asp Thr Lys Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu
 35 40 45
 Ala Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu
 50 55 60
 Asp Leu Arg Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val
 65 70 75 80
 Glu Asn Pro Ser Leu Glu Asn Ser Pro Leu Ala Gln Lys Ala Met Lys
 85 90 95
 Asn Lys Glu Ile Ser Lys Ser Leu Gly Tyr Tyr Arg Lys Met Pro Asn
 100 105 110
 Gly Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu
 115 120 125
 Asn Ala Gln Glu Val Val Gly Ala Leu Met Ile Phe Ile Ser Ile Asp
 130 135 140
 Ser Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile
 145 150 155 160
 Gly Thr Lys Gly Lys Val Leu Leu Ser Ala Asn Lys Ser Leu Gln Asp
 165 170 175
 Lys Pro Ile Ala Glu Ile Tyr Lys Ser Val Pro Lys Ala Thr Asn Glu
 180 185 190
 Val Met Ala Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu Glu Tyr Leu

GAT	GTG	AAA	GCA	GGG	AAT	TTT	GCG	GTG	CGC	ATC	ACG	GCT	GAG	CCC	GCA	1162
Asp	Val	Lys	Ala	Gly	Asn	Phe	Ala	Val	Arg	Ile	Thr	Ala	Glu	Pro	Ala	
	355					360					365					
AGC	CCT	GAT	TTG	AAA	GAA	TTG	AGG	GAC	GCG	CTA	AAT	GGG	ATC	ATG	GAT	1210
Ser	Pro	Asp	Leu	Lys	Glu	Leu	Arg	Asp	Ala	Leu	Asn	Gly	Ile	Met	Asp	
370					375					380					385	
TAT	TTG	CAA	GAA	AGC	GTA	GGG	ACT	CAC	ATG	CCA	AGC	ATT	TTC	AAA	ATC	1258
Tyr	Leu	Gln	Glu	Ser	Val	Gly	Thr	His	Met	Pro	Ser	Ile	Phe	Lys	Ile	
				390					395					400		
TTT	GAA	AGC	TAT	TCT	GGT	TTG	GAT	TTT	AGA	GGC	CGG	ATC	CAA	AAC	GCT	1306
Phe	Glu	Ser	Tyr	Ser	Gly	Leu	Asp	Phe	Arg	Gly	Arg	Ile	Gln	Asn	Ala	
			405					410					415			
TCG	GGT	AGG	GTG	GAA	CTG	GTT	ACT	AAC	GCT	TTA	GGG	CAA	GAA	ATC	CAA	1354
Ser	Gly	Arg	Val	Glu	Leu	Val	Thr	Asn	Ala	Leu	Gly	Gln	Glu	Ile	Gln	
		420						425				430				
AAA	ATG	CTA	GAA	ACT	TCG	TCT	AAT	TTT	GCC	AAA	GAT	TTA	GCG	AAC	GAT	1402
Lys	Met	Leu	Glu	Thr	Ser	Ser	Asn	Phe	Ala	Lys	Asp	Leu	Ala	Asn	Asp	
	435						440				445					
AGC	GCG	AAT	TTA	AAA	GAG	TGC	GTG	CAA	AAT	TTA	GAA	AAA	GCT	TCA	AAC	1450
Ser	Ala	Asn	Leu	Lys	Glu	Cys	Val	Gln	Asn	Leu	Glu	Lys	Ala	Ser	Asn	
450					455					460					465	
TCC	CAA	CAC	AAA	AGC	TTG	ATG	GAA	ACT	TCC	AAA	ACG	ATA	GAA	AAT	ATC	1498
Ser	Gln	His	Lys	Ser	Leu	Met	Glu	Thr	Ser	Lys	Thr	Ile	Glu	Asn	Ile	
				470					475					480		
ACC	ACT	TCC	ATT	CAA	GGC	GTG	AGC	TCT	CAA	AGT	GAA	GCC	ATG	ATT	GAA	1546
Thr	Thr	Ser	Ile	Gln	Gly	Val	Ser	Ser	Gln	Ser	Glu	Ala	Met	Ile	Glu	
			485					490					495			
CAA	GGG	CAA	GAC	ATT	AAA	AGC	ATT	GTA	GAA	ATC	ATT	AGA	GAT	ATT	GCT	1594
Gln	Gly	Gln	Asp	Ile	Lys	Ser	Ile	Val	Glu	Ile	Ile	Arg	Asp	Ile	Ala	
		500						505				510				
GAT	CAA	ACC	AAT	CTT	TTA	GCC	TTA	AAC	GCC	GCT	ATT	GAA	GCC	GCA	AGG	1642
Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Ala	Arg	
	515					520					525					
GCC	GGC	GAG	CAT	GGC	AGA	GGC	TTT	GCG	GTG	GTG	GCT	GAT	GAG	GTA	AGA	1690
Ala	Gly	Glu	His	Gly	Arg	Gly	Phe	Ala	Val	Val	Ala	Asp	Glu	Val	Arg	
530					535					540					545	
AAG	CTC	GCT	GAA	AGG	ACG	CAA	AAA	TCG	CTC	AGC	GAG	ATT	GAA	GCC	AAT	1738
Lys	Leu	Ala	Glu	Arg	Thr	Gln	Lys	Ser	Leu	Ser	Glu	Ile	Glu	Ala	Asn	
				550					555					560		
ATC	AAT	ATT	TTA	GTG	CAA	AGC	ATT	TCA	GAC	ACG	AGC	GAA	AGC	ATT	AAA	1786
Ile	Asn	Ile	Leu	Val	Gln	Ser	Ile	Ser	Asp	Thr	Ser	Glu	Ser	Ile	Lys	
			565					570					575			

GCT CAA GAG GTT GTA GGG GCT TTG ATG ATT TTT ATT TCC ATT GAC AGC	490
Ala Gln Glu Val Val Gly Ala Leu Met Ile Phe Ile Ser Ile Asp Ser	
130 135 140 145	
TTC AGC AAT GAA ATC ACT AAA AAC AGG AGC GAT TTA TTT TTA ATT GGC	538
Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile Gly	
150 155 160	
ACT AAA GGT AAA GTG CTT TTG AGC GCG AAT AAG AGT TTG CAA GAC AAA	586
Thr Lys Gly Lys Val Leu Leu Ser Ala Asn Lys Ser Leu Gln Asp Lys	
165 170 175	
CCT ATC GCA GAA ATT TAT AAG AGC GTG CCT AAA GCC ACC AAC GAA GTG	634
Pro Ile Ala Glu Ile Tyr Lys Ser Val Pro Lys Ala Thr Asn Glu Val	
180 185 190	
ATG GCT ATT TTA GAA AAC GGC TCT AAA GCG ACT TTA GAA TAC TTA GAT	682
Met Ala Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu Glu Tyr Leu Asp	
195 200 205	
CCC TTT AGC CAT AAG GAA AAT TTT TTA GCC GTT GAA ACC TTT AAA ATG	730
Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe Lys Met	
210 215 220 225	
CTA GGC AAA ACA GAA AGT AAA GAC AAT CTT AAT TGG ATG ATC GCT TTA	778
Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile Ala Leu	
230 235 240	
ATC ATT GAA AAA GAC AAG GTC TAT GAG CAA GTA GGC TCG GTG CGT TTT	826
Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val Arg Phe	
245 250 255	
GTG GTG ATC ATA GCG AGC GCA ATC ATG GTG TTA GCC TTG ATT ATA GCG	874
Val Val Ile Ile Ala Ser Ala Ile Met Val Leu Ala Leu Ile Ile Ala	
260 265 270	
ATC ACT CTC TTA ATG CGA GCG ATC GTG AGC AGT CGT TTG GAA GCC GTT	922
Ile Thr Leu Leu Met Arg Ala Ile Val Ser Ser Arg Leu Glu Ala Val	
275 280 285	
TCT AGC ACC TTG TCT CAT TTC TTT AAA TTA TTG AAC AAT CAA GCC AAT	970
Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln Ala Asn	
290 295 300 305	
TCT AGC GGT ATT AAA TTG ATT GAA GCG AAA TCC AAT GAC GAG TTA GGC	1018
Ser Ser Gly Ile Lys Leu Ile Glu Ala Lys Ser Asn Asp Glu Leu Gly	
310 315 320	
CGC ATG CAA ACA GCG ATC AAT AAA AAT ATC TTG CAA ACC CAA AAA ATC	1066
Arg Met Gln Thr Ala Ile Asn Lys Asn Ile Leu Gln Thr Gln Lys Ile	
325 330 335	
ATG CAA GAA GAC AGG CAA GCC GTC CAA GAC ACC ATT AAA GTG GTT TCA	1114
Met Gln Glu Asp Arg Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser	
340 345 350	

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...1945
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

```

GGTGTCTTA AACAGCAGGG TGAAAGAGAT TTAAAGAA AGCGCTCTGC ATTCT ATG      58
                                     Met
                                     1

CAA GAT AGT TTG CAT TTT AAG GTT AAT GAA GTG CAA GGG GTT TTA GAA      106
Gln Asp Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu Glu
      5                      10                      15

AAC ACT TAT ACG AGC ATG GGC ATT GTT AAA GAA ATG CTC CCT AAA GAC      154
Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp
      20                      25                      30

ACC AAA AGA GAA ATC AAA ATC GGC TTG TTA AAA AAC TTC ATT TTA GCC      202
Thr Lys Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu Ala
      35                      40                      45

AAT TCG CAT GTC GCT GGG GTG AGC ATG TTT TTT AAA GGC AGA GAA GAT      250
Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu Asp
      50                      55                      60                      65

TTA AGA TTA ACG CTT TTA AGG GAT AAC AAT ACG ATT AAG CTA GTG GAA      298
Leu Arg Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val Glu
      70                      75                      80

AAT CCG TCA TTA GAG AAT AGC CCT TTA GCG CAA AAA GCG ATG AAA AAT      346
Asn Pro Ser Leu Glu Asn Ser Pro Leu Ala Gln Lys Ala Met Lys Asn
      85                      90                      95

AAA GAA ATT TCT AAA AGT TTG GGT TAT TAT AGG AAA ATG CCT AAT GGG      394
Lys Glu Ile Ser Lys Ser Leu Gly Tyr Tyr Arg Lys Met Pro Asn Gly
      100                      105                      110

GCG GAA GTT TAT GGG GTG GAT ATT CTT TTA CCT TTA TTG AAT GAG AAC      442
Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu Asn
      115                      120                      125

```

```

Lys Phe Gly Val Pro Cys Cys Val Leu Arg Ser Ile Ser Asp Asn Ala
      190                      195                      200

GAT GAG GAA GCT AAC ATG AGC TTT GAT GCG TTT TTA GAA AAA AGC GCT      675
Asp Glu Glu Ala Asn Met Ser Phe Asp Ala Phe Leu Glu Lys Ser Ala
      205                      210                      215

CAA ACT TCA GCG AAA TTC TTA AAA AGC ATG GTG GAT GAG CTT TAGGGTTTG      726
Gln Thr Ser Ala Lys Phe Leu Lys Ser Met Val Asp Glu Leu
      220                      225                      230

TTTTTATAGA GGGGTGGAA                                          745

```

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

```

Met Val Gln Lys Ile Gly Ile Leu Gly Ala Met Arg Glu Glu Ile Thr
 1              5              10              15
Pro Ile Leu Glu Leu Phe Gly Val Asp Phe Glu Glu Ile Pro Leu Gly
      20              25              30
Gly Asn Val Phe His Lys Gly Val Tyr His Asn Lys Glu Ile Ile Val
      35              40              45
Ala Tyr Ser Lys Ile Gly Lys Val His Ser Thr Leu Thr Thr Thr Ser
      50              55              60
Met Ile Leu Ala Phe Gly Val Gln Lys Val Leu Phe Ser Gly Val Ala
65              70              75              80
Gly Ser Leu Val Lys Asp Leu Lys Ile Asn Asp Leu Leu Val Ala Ile
      85              90              95
Gln Leu Val Gln His Asp Val Asp Leu Ser Ala Phe Asp His Pro Leu
      100             105             110
Gly Phe Ile Pro Glu Ser Ala Ile Phe Ile Glu Thr Ser Glu Ser Leu
      115             120             125
Asn Ala Leu Ala Lys Glu Val Ala Asn Glu Gln His Ile Val Leu Lys
      130             135             140
Glu Gly Val Ile Ala Ser Gly Asp Gln Phe Val His Ser Lys Glu Arg
145             150             155             160
Lys Glu Phe Leu Val Ser Glu Phe Lys Ala Ser Ala Val Glu Met Glu
      165             170             175
Gly Ala Ser Val Ala Phe Val Cys Gln Lys Phe Gly Val Pro Cys Cys
      180             185             190
Val Leu Arg Ser Ile Ser Asp Asn Ala Asp Glu Glu Ala Asn Met Ser
      195             200             205
Phe Asp Ala Phe Leu Glu Lys Ser Ala Gln Thr Ser Ala Lys Phe Leu
      210             215             220
Lys Ser Met Val Asp Glu Leu
225             230

```

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

AAGAATACGT GTGATTGGGA GAAA ATG GTG CAA AAA ATT GGC ATT TTA GGG	51
Met Val Gln Lys Ile Gly Ile Leu Gly	
1 5	
GCG ATG AGA GAA GAA ATA ACC CCT ATA CTA GAA TTG TTT GGC GTG GAT	99
Ala Met Arg Glu Glu Ile Thr Pro Ile Leu Glu Leu Phe Gly Val Asp	
10 15 20 25	
TTT GAA GAG ATC CCT TTA GGG GGG AAT GTC TTC CAT AAA GGC GTT TAT	147
Phe Glu Glu Ile Pro Leu Gly Gly Asn Val Phe His Lys Gly Val Tyr	
30 35 40	
CAC AAC AAG GAA ATC ATT GTC GCT TAT AGC AAG ATT GGC AAG GTG CAT	195
His Asn Lys Glu Ile Ile Val Ala Tyr Ser Lys Ile Gly Lys Val His	
45 50 55	
TCC ACT TTA ACC ACA ACG AGC ATG ATT TTA GCG TTT GGC GTT CAA AAG	243
Ser Thr Leu Thr Thr Thr Ser Met Ile Leu Ala Phe Gly Val Gln Lys	
60 65 70	
GTG CTT TTT AGC GGG GTG GCT GGA AGC TTA GTT AAA GAT TTA AAA ATC	291
Val Leu Phe Ser Gly Val Ala Gly Ser Leu Val Lys Asp Leu Lys Ile	
75 80 85	
AAT GAT TTA CTA GTG GCT ATT CAA TTA GTC CAG CAT GAT GTG GAT TTG	339
Asn Asp Leu Leu Val Ala Ile Gln Leu Val Gln His Asp Val Asp Leu	
90 95 100 105	
AGC GCG TTT GAT CAC CCT TTA GGG TTC ATC CCA GAA AGC GCG ATT TTT	387
Ser Ala Phe Asp His Pro Leu Gly Phe Ile Pro Glu Ser Ala Ile Phe	
110 115 120	
ATT GAA ACG AGC GAA AGT TTG AAC GCT TTG GCT AAA GAA GTC GCT AAT	435
Ile Glu Thr Ser Glu Ser Leu Asn Ala Leu Ala Lys Glu Val Ala Asn	
125 130 135	
GAA CAG CAT ATC GTG CTC AAA GAA GGC GTC ATC GCA TCA GGC GAT CAG	483
Glu Gln His Ile Val Leu Lys Glu Gly Val Ile Ala Ser Gly Asp Gln	
140 145 150	
TTT GTG CAT AGC AAA GAA AGG AAA GAG TTT TTA GTT AGC GAG TTT AAA	531
Phe Val His Ser Lys Glu Arg Lys Glu Phe Leu Val Ser Glu Phe Lys	
155 160 165	
GCG AGC GCG GTG GAA ATG GAG GGG GCG AGC GTG GCG TTT GTG TGC CAA	579
Ala Ser Ala Val Glu Met Glu Gly Ala Ser Val Ala Phe Val Cys Gln	
170 175 180 185	
AAA TTT GGC GTG CCA TGC TGT GTG TTA AGG AGC ATT AGC GAT AAC GCT	627

		355					360					365				
Ile	Ala	Asn	His	Lys	Lys	Ile	Leu	Ala	Asn	Ile	Thr	Asn	Met	Thr	Lys	
	370					375					380					
Glu	Asp	Ile	Ile	Ala	Gln	Val	Pro	Glu	Ala	Thr	Met	Val	Ser	Val	Tyr	
385					390					395					400	
Met	Asp	Leu	Lys	Lys	Leu	Phe	Leu	Thr	Lys	Glu	Ala	Ser	Glu	Glu	Gly	
				405					410					415		
Phe	Asp	Leu	Ala	Pro	Asn	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Gln	Ile	Lys	
			420					425					430			
Arg	Gly	Lys	Leu	Ile	Ser	Asp	Arg	Ala	Lys	Asn	Lys	Met	Ala	Lys	Ser	
		435					440					445				
Asn	Leu	Arg	Leu	Val	Val	Ser	Ile	Ala	Lys	Arg	Phe	Thr	Ser	Arg	Gly	
	450					455					460					
Leu	Pro	Phe	Leu	Asp	Leu	Ile	Gln	Glu	Gly	Asn	Ile	Gly	Leu	Met	Lys	
465					470					475					480	
Ala	Val	Asp	Lys	Phe	Glu	His	Glu	Lys	Gly	Phe	Lys	Phe	Ser	Thr	Tyr	
				485					490					495		
Ala	Thr	Trp	Trp	Ile	Lys	Gln	Ala	Ile	Ser	Arg	Ala	Ile	Ala	Asp	Gln	
			500					505					510			
Ala	Arg	Thr	Ile	Arg	Ile	Pro	Ile	His	Met	Ile	Asp	Thr	Ile	Asn	Arg	
		515					520					525				
Ile	Asn	Lys	Val	Met	Arg	Lys	His	Ile	Gln	Glu	Asn	Gly	Lys	Glu	Pro	
	530					535					540					
Asp	Leu	Glu	Val	Val	Ala	Glu	Glu	Val	Gly	Leu	Ser	Leu	Asp	Lys	Val	
545					550					555					560	
Lys	Asn	Val	Ile	Lys	Val	Thr	Lys	Glu	Pro	Ile	Ser	Leu	Glu	Thr	Pro	
				565					570					575		
Val	Gly	Asn	Asp	Asp	Asp	Gly	Lys	Phe	Gly	Asp	Phe	Val	Glu	Asp	Lys	
			580					585					590			
Asn	Ile	Val	Ser	Ser	Ile	Asp	His	Ile	Met	Arg	Glu	Asp	Leu	Lys	Ala	
		595					600					605				
Gln	Ile	Glu	Ser	Val	Leu	Asp	Gln	Leu	Asn	Glu	Arg	Glu	Lys	Ala	Val	
	610					615					620					
Ile	Arg	Met	Arg	Phe	Gly	Leu	Leu	Asp	Asp	Glu	Ser	Asp	Arg	Thr	Leu	
625					630					635					640	
Glu	Glu	Ile	Gly	Lys	Glu	Leu	Asn	Val	Thr	Arg	Glu	Arg	Val	Arg	Gln	
				645					650					655		
Ile	Glu	Ser	Ser	Ala	Ile	Lys	Lys	Leu	Arg	Ser	Pro	Gln	Tyr	Gly	Arg	
			660					665					670			
Ile	Leu	Arg	Asn	Tyr	Leu	Arg	Ile									
		675					680									

(2) INFORMATION FOR SEO ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 25...717

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

```

Met Gly Ser Tyr Phe Met Glu Cys Pro Met Lys Lys Lys Ala Asn Glu
 1           5           10           15
Glu Lys Ala Gln Lys Arg Ala Lys Thr Glu Ala Lys Ala Glu Ala Thr
      20           25           30
Gln Glu Asn Lys Thr Lys Glu Asn Asn Lys Ala Lys Glu Ser Lys Ile
      35           40           45
Lys Glu Ser Lys Ile Lys Glu Ala Lys Ala Lys Glu Pro Ile Pro Val
      50           55           60
Lys Lys Leu Ser Phe Asn Glu Ala Leu Glu Glu Leu Phe Ala Asn Ser
      65           70           75           80
Leu Ser Asp Cys Val Ser Tyr Glu Ser Ile Ile Gln Ile Ser Ala Lys
      85           90           95
Val Pro Thr Leu Ala Gln Ile Lys Lys Ile Lys Glu Leu Cys Gln Lys
      100          105          110
Tyr Gln Lys Lys Leu Val Ser Ser Ser Glu Tyr Ala Lys Lys Leu Asn
      115          120          125
Ala Ile Asp Lys Ile Lys Lys Thr Glu Glu Lys Gln Lys Val Leu Asp
      130          135          140
Glu Glu Leu Glu Asp Gly Tyr Asp Phe Leu Lys Glu Lys Asp Phe Leu
      145          150          155          160
Glu Trp Ser Arg Ser Asp Ser Pro Val Arg Met Tyr Leu Arg Glu Met
      165          170          175
Gly Asp Ile Lys Leu Leu Ser Lys Asp Glu Glu Ile Glu Leu Ser Lys
      180          185          190
Gln Ile Arg Leu Gly Glu Asp Ile Ile Leu Asp Ala Ile Cys Ser Val
      195          200          205
Pro Tyr Leu Ile Asp Phe Ile Tyr Ala Tyr Lys Asp Ala Leu Ile Asn
      210          215          220
Arg Glu Arg Arg Val Lys Glu Leu Phe Arg Ser Phe Asp Asp Asp Asp
      225          230          235          240
Glu Asn Ser Val Ser Asp Ser Lys Lys Asp Glu Asp Asn Glu Glu Asp
      245          250          255
Glu Glu Asn Glu Glu Arg Lys Lys Val Val Ser Glu Lys Asp Lys Lys
      260          265          270
Arg Val Glu Lys Val Gln Glu Ser Phe Lys Ala Leu Asp Lys Ala Lys
      275          280          285
Lys Glu Trp Leu Lys Ala Leu Glu Ala Pro Ile Asp Glu Arg Glu Asp
      290          295          300
Glu Leu Val Arg Ser Leu Thr Leu Ala Tyr Lys Arg Gln Thr Leu Lys
      305          310          315          320
Asp Arg Leu Tyr Asp Leu Glu Pro Thr Ser Lys Leu Ile Asn Glu Leu
      325          330          335
Val Lys Thr Met Glu Thr Thr Leu Lys Ser Gly Asp Gly Phe Glu Lys
      340          345          350
Glu Leu Lys Arg Leu Glu Tyr Lys Leu Pro Leu Phe Asn Asp Thr Leu

```

ATT GGC TTG ATG AAA GCG GTG GAT AAG TTT GAG CAT GAA AAG GGC TTC	1491
Ile Gly Leu Met Lys Ala Val Asp Lys Phe Glu His Glu Lys Gly Phe	
480 485 490	
AAG TTT TCT ACC TAT GCG ACC TGG TGG ATC AAA CAA GCT ATC AGC AGA	1539
Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Lys Gln Ala Ile Ser Arg	
495 500 505	
GCC ATA GCC GAT CAG GCC CGC ACT ATC CGC ATC CCC ATT CAC ATG ATT	1587
Ala Ile Ala Asp Gln Ala Arg Thr Ile Arg Ile Pro Ile His Met Ile	
510 515 520	
GAT ACG ATT AAT CGC ATC AAT AAA GTC ATG CGC AAA CAC ATT CAA GAA	1635
Asp Thr Ile Asn Arg Ile Asn Lys Val Met Arg Lys His Ile Gln Glu	
525 530 535	
AAC GGC AAA GAG CCT GAT TTA GAA GTG GTG GCT GAA GAA GTG GGG CTT	1683
Asn Gly Lys Glu Pro Asp Leu Glu Val Val Ala Glu Glu Val Gly Leu	
540 545 550 555	
TCG TTA GAT AAA GTG AAG AAT GTG ATT AAG GTG ACT AAA GAG CCT ATC	1731
Ser Leu Asp Lys Val Lys Asn Val Ile Lys Val Thr Lys Glu Pro Ile	
560 565 570	
AGT TTG GAA ACC CCA GTC GGC AAT GAT GAT GAT GGC AAG TTT GGG GAT	1779
Ser Leu Glu Thr Pro Val Gly Asn Asp Asp Asp Gly Lys Phe Gly Asp	
575 580 585	
TTC GTG GAA GAT AAG AAT ATC GTC AGC TCC ATT GAT CAC ATC ATG CGA	1827
Phe Val Glu Asp Lys Asn Ile Val Ser Ser Ile Asp His Ile Met Arg	
590 595 600	
GAA GAT TTG AAA GCA CAA ATT GAA AGC GTT TTG GAT CAG TTG AAT GAG	1875
Glu Asp Leu Lys Ala Gln Ile Glu Ser Val Leu Asp Gln Leu Asn Glu	
605 610 615	
CGA GAA AAA GCG GTG ATC CGC ATG CGT TTT GGG CTT TTA GAC GAT GAA	1923
Arg Glu Lys Ala Val Ile Arg Met Arg Phe Gly Leu Leu Asp Asp Glu	
620 625 630 635	
AGC GAT CGA ACT TTA GAA GAA ATT GGC AAG GAA TTG AAT GTT ACT AGA	1971
Ser Asp Arg Thr Leu Glu Glu Ile Gly Lys Glu Leu Asn Val Thr Arg	
640 645 650	
GAA AGG GTG CGC CAG ATT GAA AGC TCT GCG ATT AAA AAA TTG AGA AGC	2019
Glu Arg Val Arg Gln Ile Glu Ser Ser Ala Ile Lys Lys Leu Arg Ser	
655 660 665	
CCG CAG TAC GGG CGC ATT TTA AGA AAC TAT TTG CGC ATT TGATGTTAAG GT	2070
Pro Gln Tyr Gly Arg Ile Leu Arg Asn Tyr Leu Arg Ile	
670 675 680	
TTCTCTAAAG CATGCGTTAT TTTCTTGTAG TTTTCTT	2107

(2) INFORMATION FOR SEQ ID NO:1190:

GAC AAC GAA GAA GAT GAA GAA AAC GAA GAA AGG AAA AAA GTC GTT TCT	819
Asp Asn Glu Glu Asp Glu Glu Asn Glu Glu Arg Lys Lys Val Val Ser	
255 260 265	
GAA AAA GAC AAG AAG CGT GTA GAA AAG GTT CAA GAA AGC TTT AAA GCC	867
Glu Lys Asp Lys Lys Arg Val Glu Lys Val Gln Glu Ser Phe Lys Ala	
270 275 280	
CTA GAC AAG GCT AAA AAA GAA TGG CTT AAA GCC CTT GAA GCC CCC ATA	915
Leu Asp Lys Ala Lys Lys Glu Trp Leu Lys Ala Leu Glu Ala Pro Ile	
285 290 295	
GAT GAA AGA GAA GAC GAA TTG GTG CGT TCA TTG ACC CTA GCT TAC AAA	963
Asp Glu Arg Glu Asp Glu Leu Val Arg Ser Leu Thr Leu Ala Tyr Lys	
300 305 310 315	
CGC CAA ACA CTC AAA GAC AGA CTC TAT GAT TTA GAA CCT ACC AGC AAA	1011
Arg Gln Thr Leu Lys Asp Arg Leu Tyr Asp Leu Glu Pro Thr Ser Lys	
320 325 330	
CTG ATT AAT GAA TTA GTC AAA ACG ATG GAA ACC ACT TTA AAA AGC GGC	1059
Leu Ile Asn Glu Leu Val Lys Thr Met Glu Thr Thr Leu Lys Ser Gly	
335 340 345	
GAT GGG TTT GAA AAA GAG TTG AAA CGC TTG GAA TAC AAA CTG CCC TTA	1107
Asp Gly Phe Glu Lys Glu Leu Lys Arg Leu Glu Tyr Lys Leu Pro Leu	
350 355 360	
TTC AAT GAC ACT CTC ATC GCA AAC CAT AAA AAA ATC CTT GCC AAT ATC	1155
Phe Asn Asp Thr Leu Ile Ala Asn His Lys Lys Ile Leu Ala Asn Ile	
365 370 375	
ACT AAC ATG ACT AAA GAA GAT ATT ATC GCT CAA GTG CCA GAA GCG ACT	1203
Thr Asn Met Thr Lys Glu Asp Ile Ile Ala Gln Val Pro Glu Ala Thr	
380 385 390 395	
ATG GTG AGC GTG TAT ATG GAT CTT AAA AAG CTT TTT TTG ACT AAA GAA	1251
Met Val Ser Val Tyr Met Asp Leu Lys Lys Leu Phe Leu Thr Lys Glu	
400 405 410	
GCG AGC GAA GAA GGC TTT GAT CTA GCC CCC AAC AAG CTA AAA GAA ATT	1299
Ala Ser Glu Glu Gly Phe Asp Leu Ala Pro Asn Lys Leu Lys Glu Ile	
415 420 425	
TTA GAG CAA ATC AAA AGA GGG AAG TTG ATT TCC GAT CGC GCT AAA AAC	1347
Leu Glu Gln Ile Lys Arg Gly Lys Leu Ile Ser Asp Arg Ala Lys Asn	
430 435 440	
AAA ATG GCT AAA TCC AAT TTA AGG TTG GTG GTG AGC ATC GCT AAA CGA	1395
Lys Met Ala Lys Ser Asn Leu Arg Leu Val Val Ser Ile Ala Lys Arg	
445 450 455	
TTC ACG AGC AGA GGC TTA CCA TTC TTG GAT TTG ATT CAA GAG GGC AAT	1443
Phe Thr Ser Arg Gly Leu Pro Phe Leu Asp Leu Ile Gln Glu Gly Asn	
460 465 470 475	

AAA GCA GAA GCC ACA CAA GAA AAT AAA ACT AAA GAA AAC AAT AAA GCC	147
Lys Ala Glu Ala Thr Gln Glu Asn Lys Thr Lys Glu Asn Asn Lys Ala	
30 35 40	
AAA GAA AGC AAA ATT AAA GAA AGC AAA ATC AAA GAA GCT AAA GCG AAA	195
Lys Glu Ser Lys Ile Lys Glu Ser Lys Ile Lys Glu Ala Lys Ala Lys	
45 50 55	
GAA CCT ATT CCT GTT AAA AAG CTT AGT TTT AAT GAA GCG TTA GAA GAA	243
Glu Pro Ile Pro Val Lys Lys Leu Ser Phe Asn Glu Ala Leu Glu Glu	
60 65 70 75	
TTG TTC GCT AAT TCC TTA AGC GAT TGC GTT TCT TAT GAG TCC ATC ATT	291
Leu Phe Ala Asn Ser Leu Ser Asp Cys Val Ser Tyr Glu Ser Ile Ile	
80 85 90	
CAA ATC AGC GCG AAA GTC CCC ACT CTA GCC CAA ATC AAA AAA ATC AAA	339
Gln Ile Ser Ala Lys Val Pro Thr Leu Ala Gln Ile Lys Lys Ile Lys	
95 100 105	
GAA TTG TGC CAA AAA TAC CAA AAG AAA TTA GTC AGC TCT TCA GAA TAC	387
Glu Leu Cys Gln Lys Tyr Gln Lys Lys Leu Val Ser Ser Ser Glu Tyr	
110 115 120	
GCT AAA AAA CTC AAT GCG ATT GAC AAG ATT AAA AAA ACC GAA GAA AAG	435
Ala Lys Lys Leu Asn Ala Ile Asp Lys Ile Lys Lys Thr Glu Glu Lys	
125 130 135	
CAA AAA GTT TTA GAT GAA GAA TTA GAA GAT GGC TAT GAC TTT TTG AAA	483
Gln Lys Val Leu Asp Glu Glu Leu Glu Asp Gly Tyr Asp Phe Leu Lys	
140 145 150 155	
GAA AAG GAT TTT TTA GAG TGG AGC AGA AGC GAT AGC CCA GTG CGC ATG	531
Glu Lys Asp Phe Leu Glu Trp Ser Arg Ser Asp Ser Pro Val Arg Met	
160 165 170	
TAT TTG CGC GAA ATG GGG GAT ATA AAA CTT TTA AGC AAA GAT GAA GAG	579
Tyr Leu Arg Glu Met Gly Asp Ile Lys Leu Leu Ser Lys Asp Glu Glu	
175 180 185	
ATT GAA TTG AGC AAG CAA ATC CGC TTG GGT GAA GAC ATT ATT TTA GAC	627
Ile Glu Leu Ser Lys Gln Ile Arg Leu Gly Glu Asp Ile Ile Leu Asp	
190 195 200	
GCG ATC TGC TCG GTG CCG TAT TTG ATT GAT TTT ATC TAT GCG TAT AAA	675
Ala Ile Cys Ser Val Pro Tyr Leu Ile Asp Phe Ile Tyr Ala Tyr Lys	
205 210 215	
GAC GCT TTA ATC AAT CGT GAA AGA AGG GTT AAA GAG CTT TTC AGG AGC	723
Asp Ala Leu Ile Asn Arg Glu Arg Arg Val Lys Glu Leu Phe Arg Ser	
220 225 230 235	
TTT GAT GAT GAC GAT GAA AAT AGC GTG AGC GAT TCT AAA AAA GAT GAA	771
Phe Asp Asp Asp Asp Glu Asn Ser Val Ser Asp Ser Lys Lys Asp Glu	
240 245 250	

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

```

Met Thr Lys Thr Ala Lys Val Asn Asp Ile Val Arg Asp Trp Val Val
 1           5           10           15
Leu Asp Ala Lys Asp Lys Val Phe Gly Arg Leu Ile Thr Glu Ile Ala
      20           25           30
Val Leu Leu Arg Gly Lys His Arg Pro Phe Tyr Thr Pro Asn Val Asp
      35           40           45
Cys Gly Asp Phe Val Val Val Ile Asn Ala Asn Lys Val Lys Phe Ser
      50           55           60
Gly Met Lys Leu Glu Asp Lys Glu Tyr Phe Thr His Ser Gly Tyr Phe
      65           70           75           80
Gly Ser Thr Lys Ser Lys Thr Leu Gln Glu Met Leu Glu Lys Ala Pro
      85           90           95
Glu Lys Leu Tyr His Leu Ala Val Arg Gly Met Leu Pro Lys Thr Lys
      100          105          110
Leu Gly Lys Ala Met Ile Lys Lys Leu Lys Val Tyr Arg Asp Asp Lys
      115          120          125
His Pro His Thr Ala Gln Thr Ser Lys Lys Asp Ala Lys
      130          135          140

```

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...2058
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

```

TAGCTTTTGA TTGAAAGC ATG GGT TCT TAC TTT ATG GAG TGT CCA ATG AAA      51
      Met Gly Ser Tyr Phe Met Glu Cys Pro Met Lys
      1           5           10

AAG AAA GCT AAC GAA GAA AAA GCC CAA AAA AGA GCT AAA ACA GAA GCC      99
Lys Lys Ala Asn Glu Glu Lys Ala Gln Lys Arg Ala Lys Thr Glu Ala
      15           20           25

```

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 19...441
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

TTTTATCAAA GGATTCTT ATG ACA AAG ACC GCT AAA GTC AAT GAC ATC GTT	51
Met Thr Lys Thr Ala Lys Val Asn Asp Ile Val	
1 5 10	
CGT GAT TGG GTC GTT TTA GAC GCC AAA GAC AAG GTT TTT GGC CGC TTG	99
Arg Asp Trp Val Val Leu Asp Ala Lys Asp Lys Val Phe Gly Arg Leu	
15 20 25	
ATC ACT GAA ATC GCT GTG CTT TTA AGA GGG AAA CAC CGC CCT TTT TAC	147
Ile Thr Glu Ile Ala Val Leu Leu Arg Gly Lys His Arg Pro Phe Tyr	
30 35 40	
ACC CCT AAT GTG GAT TGT GGG GAT TTT GTG GTG GTT ATC AAC GCT AAT	195
Thr Pro Asn Val Asp Cys Gly Asp Phe Val Val Val Ile Asn Ala Asn	
45 50 55	
AAG GTT AAA TTT TCA GGC ATG AAA TTA GAG GAT AAA GAG TAT TTT ACC	243
Lys Val Lys Phe Ser Gly Met Lys Leu Glu Asp Lys Glu Tyr Phe Thr	
60 65 70 75	
CAT TCA GGC TAT TTT GGC AGC ACT AAG AGC AAG ACT CTC CAA GAA ATG	291
His Ser Gly Tyr Phe Gly Ser Thr Lys Ser Lys Thr Leu Gln Glu Met	
80 85 90	
CTA GAA AAA GCC CCT GAA AAG CTC TAC CAC TTA GCC GTT AGG GGC ATG	339
Leu Glu Lys Ala Pro Glu Lys Leu Tyr His Leu Ala Val Arg Gly Met	
95 100 105	
CTC CCT AAA ACG AAA TTA GGG AAA GCG ATG ATT AAA AAA CTC AAA GTT	387
Leu Pro Lys Thr Lys Leu Gly Lys Ala Met Ile Lys Lys Leu Lys Val	
110 115 120	
TAT CGT GAT GAT AAG CAC CCT CAC ACC GCA CAA ACT AGC AAA AAG GAC	435
Tyr Arg Asp Asp Lys His Pro His Thr Ala Gln Thr Ser Lys Lys Asp	
125 130 135	
GCT AAA TGAGAAAAAT CTATGCTACC GGTAAAAGAA AAACCGCTAT CG	483
Ala Lys	
140	

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

```

Ile Ala Phe Leu Thr Glu Asp Met Arg Cys Asp Ala Gly Ile Met Ile
      85                      90                      95
Ser Ala Ser His Asn Pro Phe Glu Asp Asn Gly Ile Lys Phe Phe Asn
      100                    105                    110
Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu Lys Ala Ile Glu Glu
      115                    120                    125
Ile Phe His Asp Glu Glu Leu Leu His Ser Ser Tyr Lys Val Gly Glu
      130                    135                    140
Ser Val Gly Ser Ala Lys Arg Ile Asp Asp Val Ile Gly Arg Tyr Ile
      145                    150                    155                    160
Ala His Leu Lys His Ser Phe Pro Lys His Leu Asn Leu Gln Ser Leu
      165                    170                    175
Arg Ile Val Leu Asp Thr Ala Asn Gly Ala Ala Tyr Lys Val Ala Pro
      180                    185                    190
Val Val Phe Ser Glu Leu Gly Ala Asp Val Leu Val Ile Asn Asp Glu
      195                    200                    205
Pro Asn Gly Cys Asn Ile Asn Asp Gln Cys Gly Ala Leu His Pro Asn
      210                    215                    220
Gln Leu Ser Gln Glu Val Lys Lys Tyr Arg Ala Asp Leu Gly Phe Ala
      225                    230                    235                    240
Phe Asp Gly Asp Ala Asp Arg Leu Val Val Val Asp Asn Leu Gly Asn
      245                    250                    255
Ile Val His Gly Asp Lys Leu Leu Gly Val Leu Gly Val Tyr Gln Lys
      260                    265                    270
Ser Lys Asn Ala Leu Ser Ser Gln Ala Val Val Ala Thr Asn Met Ser
      275                    280                    285
Asn Leu Ala Leu Lys Glu Tyr Leu Lys Ser Gln Asp Leu Glu Leu Lys
      290                    295                    300
His Cys Ala Ile Gly Asp Lys Phe Val Ser Glu Cys Met Gln Leu Asn
      305                    310                    315                    320
Lys Ala Asn Phe Gly Gly Glu Gln Ser Gly His Ile Ile Phe Ser Asp
      325                    330                    335
Tyr Ala Lys Thr Gly Asp Gly Leu Val Cys Ala Leu Gln Val Ser Ala
      340                    345                    350
Leu Val Leu Glu Ser Lys Gln Val Ser Ser Val Ala Leu Asn Pro Phe
      355                    360                    365
Glu Leu Tyr Pro Gln Ser Leu Val Asn Leu Asn Val Gln Lys Lys Pro
      370                    375                    380
Pro Leu Glu Ser Leu Lys Gly Tyr Ser Ala Leu Leu Lys Glu Leu Asp
      385                    390                    395                    400
Lys Leu Glu Ile Arg His Leu Ile Arg Tyr Ser Gly Thr Glu Asn Lys
      405                    410                    415
Leu Arg Ile Leu Leu Glu Ala Lys Asp Glu Lys Leu Leu Glu Ser Lys
      420                    425                    430
Met Gln Glu Leu Lys Glu Phe Phe Glu Gly His Leu Cys
      435                    440                    445

```

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

CAT ATC ATT TTT AGC GAT TAC GCT AAA ACA GGC GAT GGT TTG GTG TGC	1059
His Ile Ile Phe Ser Asp Tyr Ala Lys Thr Gly Asp Gly Leu Val Cys	
335 340 345	
GCT TTG CAA GTG AGC GCG TTA GTG TTA GAA AGC AAG CAG GTA AGC TCT	1107
Ala Leu Gln Val Ser Ala Leu Val Leu Glu Ser Lys Gln Val Ser Ser	
350 355 360	
GTT GCG TTA AAC CCC TTT GAA TTA TAC CCC CAA AGC CTA GTG AAT TTG	1155
Val Ala Leu Asn Pro Phe Glu Leu Tyr Pro Gln Ser Leu Val Asn Leu	
365 370 375	
AAT GTC CAA AAA AAG CCC CCT TTA GAA AGC CTG AAA GGT TAT AGC GCT	1203
Asn Val Gln Lys Lys Pro Pro Leu Glu Ser Leu Lys Gly Tyr Ser Ala	
380 385 390	
CTT TTA AAA GAA TTA GAC AAG CTA GAA ATC CGC CAT TTG ATC CGT TAT	1251
Leu Leu Lys Glu Leu Asp Lys Leu Glu Ile Arg His Leu Ile Arg Tyr	
395 400 405 410	
AGC GGC ACT GAA AAC AAA TTG CGA ATC CTT TTA GAA GCT AAA GAT GAA	1299
Ser Gly Thr Glu Asn Lys Leu Arg Ile Leu Leu Glu Ala Lys Asp Glu	
415 420 425	
AAG CTT TTA GAA TCC AAA ATG CAA GAA TTA AAA GAG TTT TTT GAA GGG	1347
Lys Leu Leu Glu Ser Lys Met Gln Glu Leu Lys Glu Phe Phe Glu Gly	
430 435 440	
CAT TTG TGC TAAAAACCAC TAAAAAAGC CTGTTGGTTT TTATGG	1392
His Leu Cys	
445	

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

Met Lys Ile Phe Gly Thr Asp Gly Val Arg Gly Lys Ala Gly Val Lys	
1 5 10 15	
Leu Thr Pro Met Phe Val Met Arg Leu Gly Ile Ala Ala Gly Leu Tyr	
20 25 30	
Phe Lys Lys His Ser Gln Thr Asn Lys Ile Leu Ile Gly Lys Asp Thr	
35 40 45	
Arg Lys Ser Gly Tyr Met Val Glu Asn Ala Leu Val Ser Ala Leu Thr	
50 55 60	
Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly Pro Met Pro Thr Pro Ala	
65 70 75 80	

GGC ATT AAG TTT TTC AAT TCT TAT GGC TAT AAG CTT AAA GAA GAA GAA	387
Gly Ile Lys Phe Phe Asn Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu	
110 115 120	
GAA AAA GCG ATT GAA GAA ATC TTT CAT GAT GAA GAA TTA CTG CAT TCT	435
Glu Lys Ala Ile Glu Glu Ile Phe His Asp Glu Glu Leu Leu His Ser	
125 130 135	
AGC TAT AAA GTG GGT GAG AGC GTC GGT AGC GCT AAA AGG ATA GAC GAT	483
Ser Tyr Lys Val Gly Glu Ser Val Gly Ser Ala Lys Arg Ile Asp Asp	
140 145 150	
GTC ATA GGG CGC TAT ATT GCA CAT TTA AAA CAC TCT TTC CCC AAA CAT	531
Val Ile Gly Arg Tyr Ile Ala His Leu Lys His Ser Phe Pro Lys His	
155 160 165 170	
TTG AAT TTA CAG AGT TTA AGG ATC GTG CTA GAT ACG GCT AAT GGC GCG	579
Leu Asn Leu Gln Ser Leu Arg Ile Val Leu Asp Thr Ala Asn Gly Ala	
175 180 185	
GCT TAT AAG GTG GCT CCG GTC GTT TTT AGC GAG CTT GGG GCT GAT GTG	627
Ala Tyr Lys Val Ala Pro Val Val Phe Ser Glu Leu Gly Ala Asp Val	
190 195 200	
TTA GTG ATT AAT GAT GAG CCT AAC GGG TGT AAC ATT AAT GAT CAA TGC	675
Leu Val Ile Asn Asp Glu Pro Asn Gly Cys Asn Ile Asn Asp Gln Cys	
205 210 215	
GGG GCT TTA CAC CCC AAC CAA TTA AGC CAG GAA GTG AAA AAA TAC CGC	723
Gly Ala Leu His Pro Asn Gln Leu Ser Gln Glu Val Lys Lys Tyr Arg	
220 225 230	
GCA GAT TTA GGC TTT GCT TTT GAT GGC GAT GCT GAC AGG CTA GTG GTG	771
Ala Asp Leu Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Leu Val Val	
235 240 245 250	
GTG GAT AAT TTA GGG AAT ATC GTG CAT GGG GAT AAG CTT TTA GGG GTG	819
Val Asp Asn Leu Gly Asn Ile Val His Gly Asp Lys Leu Leu Gly Val	
255 260 265	
TTA GGG GTT TAT CAA AAA TCT AAA AAC GCC CTT TCT TCT CAA GCG GTT	867
Leu Gly Val Tyr Gln Lys Ser Lys Asn Ala Leu Ser Ser Gln Ala Val	
270 275 280	
GTC GCC ACA AAC ATG AGC AAT TTA GCC CTT AAA GAA TAT TTA AAA TCC	915
Val Ala Thr Asn Met Ser Asn Leu Ala Leu Lys Glu Tyr Leu Lys Ser	
285 290 295	
CAA GAT TTG GAA TTG AAG CAT TGC GCG ATT GGG GAT AAG TTT GTG AGC	963
Gln Asp Leu Glu Leu Lys His Cys Ala Ile Gly Asp Lys Phe Val Ser	
300 305 310	
GAA TGC ATG CAA TTG AAT AAA GCC AAT TTT GGA GGC GAG CAA AGC GGG	1011
Glu Cys Met Gln Leu Asn Lys Ala Asn Phe Gly Gly Glu Gln Ser Gly	
315 320 325 330	

```

                100                105                110
Ala Ile Phe Asn Phe Ala Asp Val Met Ile Asp Val Gly Val Gly Val
                115                120                125
Leu Leu Leu Lys Gln Phe Phe Phe Lys Gln Lys Gln Asn Lys Ile Lys
                130                135                140
Ala
145

```

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1356
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

```

TTTAAAAGGT ATTTTATAAC G ATG AAA ATT TTT GGG ACT GAT GGC GTG AGG      51
                        Met Lys Ile Phe Gly Thr Asp Gly Val Arg
                          1                5                10

GGT AAA GCA GGG GTG AAA CTC ACC CCC ATG TTT GTG ATG CGT TTA GGC      99
Gly Lys Ala Gly Val Lys Leu Thr Pro Met Phe Val Met Arg Leu Gly
                        15                20                25

ATT GCT GCC GGA TTG TAT TTT AAA AAA CAT TCT CAA ACG AAT AAA ATT     147
Ile Ala Ala Gly Leu Tyr Phe Lys Lys His Ser Gln Thr Asn Lys Ile
                        30                35                40

CTA ATC GGT AAA GAC ACC AGA AAA AGC GGC TAT ATG GTA GAA AAC GCT     195
Leu Ile Gly Lys Asp Thr Arg Lys Ser Gly Tyr Met Val Glu Asn Ala
                        45                50                55

TTA GTG AGC GCT CTA ACT TCC ATA GGC TAT AAT GTG ATT CAA ATA GGG     243
Leu Val Ser Ala Leu Thr Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly
                        60                65                70

CCT ATG CCC ACC CCT GCG ATT GCG TTT TTA ACT GAA GAC ATG CGC TGT     291
Pro Met Pro Thr Pro Ala Ile Ala Phe Leu Thr Glu Asp Met Arg Cys
                        75                80                85                90

GAT GCG GGT ATT ATG ATA AGC GCG AGC CAC AAC CCT TTT GAA GAT AAT     339
Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Phe Glu Asp Asn
                        95                100                105

```

```

AAT AAA GGC GTG GCG TTT TCC TTG CTC AGT TTT TTA GAG GGG GGT TTG      200
Asn Lys Gly Val Ala Phe Ser Leu Leu Ser Phe Leu Glu Gly Gly Leu
                40                      45                      50

AAA TAC TTG CAA ATC CTT TTG ATT TTA GGG CTT TTT ATC TTT TTA ATG      248
Lys Tyr Leu Gln Ile Leu Leu Ile Leu Gly Leu Phe Ile Phe Leu Met
                55                      60                      65

CGC CAA AGG GAG CTT TTT AAA AAC CAT GCG ATA GAG TTT GGC ATG GTG      296
Arg Gln Arg Glu Leu Phe Lys Asn His Ala Ile Glu Phe Gly Met Val
                70                      75                      80

TTT GGC GCC GGG GTT TCT AAT GTT TTA GAC CGG TTT GTG CAT GGG GGC      344
Phe Gly Ala Gly Val Ser Asn Val Leu Asp Arg Phe Val His Gly Gly
                85                      90                      95

GTG GTG GAT TAT GTG TAT TAT CAT TAT GGC TTT GAT TTT GCC ATT TTT      392
Val Val Asp Tyr Val Tyr Tyr His Tyr Gly Phe Asp Phe Ala Ile Phe
100                      105                      110                      115

AAT TTC GCT GAT GTC ATG ATA GAT GTG GGC GTG GGC GTT TTA TTG TTG      440
Asn Phe Ala Asp Val Met Ile Asp Val Gly Val Gly Val Leu Leu Leu
                120                      125                      130

AAA CAA TTC TTT TTT AAG CAA AAA CAA AAC AAA ATT AAG GCA TAATCACTC      491
Lys Gln Phe Phe Phe Lys Gln Lys Gln Asn Lys Ile Lys Ala
                135                      140                      145

TTTTTTAAAT GAAAGGTCGC GTAGCTCAGT TGGTA      526

```

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

```

Met Gly Val Phe Phe Leu Ile Phe Gly Val Asp Gln Ala Ile Lys Tyr
 1           5           10           15
Ala Ile Leu Glu Gly Phe Arg Tyr Glu Ser Leu Met Ile Asp Ile Val
 20           25           30
Leu Val Phe Asn Lys Gly Val Ala Phe Ser Leu Leu Ser Phe Leu Glu
 35           40           45
Gly Gly Leu Lys Tyr Leu Gln Ile Leu Leu Ile Leu Gly Leu Phe Ile
 50           55           60
Phe Leu Met Arg Gln Arg Glu Leu Phe Lys Asn His Ala Ile Glu Phe
 65           70           75           80
Gly Met Val Phe Gly Ala Gly Val Ser Asn Val Leu Asp Arg Phe Val
 85           90           95
His Gly Gly Val Val Asp Tyr Val Tyr Tyr His Tyr Gly Phe Asp Phe

```

BNSDOCID: <WO 9843478A1 I >

Gly	Gly	Leu	Ser	Ile	Ile	Cys	Asn	Ile	Val	Val	Ile	Thr	Tyr	Ser	Ala		
			40					45					50				
CTC	CAC	CCT	ACA	GCC	CCT	GTA	GAA	GGT	GCT	GAA	GAT	ATT	GCT	CAA	GTA	246	
Leu	His	Pro	Thr	Ala	Pro	Val	Glu	Gly	Ala	Glu	Asp	Ile	Ala	Gln	Val		
		55					60				65						
TCG	CAC	CAT	TTG	ACT	AGT	TTC	TAT	GGA	CCA	GCG	ACT	GGG	TTA	TTG	TTT	294	
Ser	His	His	Leu	Thr	Ser	Phe	Tyr	Gly	Pro	Ala	Thr	Gly	Leu	Leu	Phe		
	70					75					80						
GGT	TTC	ACC	TAC	TTG	TAT	GCG	GCT	ATC	AAC	CAC	ACT	TTT	GGT	TTG	GAT	342	
Gly	Phe	Thr	Tyr	Leu	Tyr	Ala	Ala	Ile	Asn	His	Thr	Phe	Gly	Leu	Asp		
85					90					95					100		
TGG	AGG	CCC	TAC	TCT	TGG	TAT	AGC	TTA	TTC	GTA	GCG	ATC	AAC	ACG	ATT	390	
Trp	Arg	Pro	Tyr	Ser	Trp	Tyr	Ser	Leu	Phe	Val	Ala	Ile	Asn	Thr	Ile		
			105						110					115			
CCT	GCT	GCG	ATT	TTA	TCC	CAC	TAT	AGC	GAT	ATG	CTT	GAT	GAC	CAC	AAA	438	
Pro	Ala	Ala	Ile	Leu	Ser	His	Tyr	Ser	Asp	Met	Leu	Asp	Asp	His	Lys		
			120					125					130				
GTG	TTA	GGC	ATC	ACT	GAA	GGC	GAT	TGG	TGG	GCG	ATC	ATT	TGG	TTG	GCT	486	
Val	Leu	Gly	Ile	Thr	Glu	Gly	Asp	Trp	Trp	Ala	Ile	Ile	Trp	Leu	Ala		
	135						140					145					
TGG	GGT	GTT	TTG	TGG	CTT	ACC	GCT	TTC	ATT	GAA	AAC	ATC	TTG	AAA	ATC	534	
Trp	Gly	Val	Leu	Trp	Leu	Thr	Ala	Phe	Ile	Glu	Asn	Ile	Leu	Lys	Ile		
	150					155					160						
CCT	TTA	GGG	AAA	TTC	ACT	CCA	TGG	CTT	GCT	ATC	ATT	GAG	GGT	ATT	TTA	582	
Pro	Leu	Gly	Lys	Phe	Thr	Pro	Trp	Leu	Ala	Ile	Ile	Glu	Gly	Ile	Leu		
165					170					175					180		
ACC	GCT	TGG	ATC	CCT	GCT	TGG	TTG	CTC	TTT	ATC	CAA	CAC	TGG	GTG	TGAGA	632	
Thr	Ala	Trp	Ile	Pro	Ala	Trp	Leu	Leu	Phe	Ile	Gln	His	Trp	Val			
			185					190					195				
TGATCATAGA	GCGTTTAGT															651	

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

Met	Leu	Gly	Leu	Val	Leu	Leu	Tyr	Val	Gly	Ile	Val	Leu	Ile	Ser	Asn
1				5					10					15	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

```

Met Phe Ser His Glu Val Tyr Leu Glu Gly Cys Thr Leu Glu Leu Arg
 1           5           10           15
Lys Ile Cys Asp Asp Phe Glu Lys Asn Ala Met Gln Asp Asp Leu Gly
          20           25           30
Gln Lys Leu Arg Ser Asp Val Leu Glu Asp Met Leu Lys Ile Ala His
          35           40           45
Asp Leu Glu Asn Leu Glu Asp Asp Thr Gln Tyr Gln Arg Arg Ile Ile
          50           55           60
Asp Glu Gln Ile Glu Glu Ala Lys Ser Leu Met Arg Gln Ile Asp Met
          65           70           75           80
Asn Phe His Pro Ser Ser Glu Ile Asp Arg Leu Met Arg Glu Ala Lys
          85           90           95
Glu His Glu Arg Glu Ala Ser Lys Arg Tyr Asp Glu Tyr Leu Lys Ser
          100          105          110
Lys Asp Lys Asn Asp
          115

```

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 43...627
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

```

GGTGCGTTTG TTGTAAAAAT TTTTGTTTGG AAGGAAAAGG CA ATG CTA GGA CTT      54
                               Met Leu Gly Leu
                               1

GTA TTG TTA TAT GTT GGG ATT GTT TTA ATC AGC AAT GGG ATT TGC GGG      102
Val Leu Leu Tyr Val Gly Ile Val Leu Ile Ser Asn Gly Ile Cys Gly
 5           10           15           20

TTA ACC AAA GTC GAT CCT AAA AGC ACT GCG GTG ATG AAC TTT TTT GTG      150
Leu Thr Lys Val Asp Pro Lys Ser Thr Ala Val Met Asn Phe Phe Val
          25           30           35

GGC GGA CTT TCC ATT ATT TGT AAT ATA GTT GTC ATC ACT TAT TCT GCA      198

```

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...375
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

AAAACTGGA ATCAAGGGGT TAAA ATG TTT TCT CAT GAA GTT TAT TTG GAG	51
Met Phe Ser His Glu Val Tyr Leu Glu	
1 5	
GGT TGC ACC CTT GAA TTA AGA AAG ATT TGC GAT GAT TTT GAA AAA AAT	99
Gly Cys Thr Leu Glu Leu Arg Lys Ile Cys Asp Asp Phe Glu Lys Asn	
10 15 20 25	
GCC ATG CAA GAT GAT TTA GGG CAG AAA CTC AGG AGT GAT GTG CTA GAG	147
Ala Met Gln Asp Asp Leu Gly Gln Lys Leu Arg Ser Asp Val Leu Glu	
30 35 40	
GAC ATG CTA AAA ATC GCG CAT GAT TTA GAA AAT TTA GAA GAT GAC ACC	195
Asp Met Leu Lys Ile Ala His Asp Leu Glu Asn Leu Glu Asp Asp Thr	
45 50 55	
CAA TAC CAA AGA AGA ATA ATT GAC GAG CAA ATT GAA GAA GCC AAA TCT	243
Gln Tyr Gln Arg Arg Ile Ile Asp Glu Gln Ile Glu Glu Ala Lys Ser	
60 65 70	
TTG ATG AGG CAA ATT GAT ATG AAT TTC CAT CCA TCA AGC GAG ATC GAT	291
Leu Met Arg Gln Ile Asp Met Asn Phe His Pro Ser Ser Glu Ile Asp	
75 80 85	
AGG CTT ATG CGT GAA GCC AAA GAG CAT GAA AGA GAA GCT AGT AAA AGA	339
Arg Leu Met Arg Glu Ala Lys Glu His Glu Arg Glu Ala Ser Lys Arg	
90 95 100 105	
TAT GAT GAG TAT CTT AAA TCT AAG GAT AAA AAT GAT TGATGTGAAT GGTTTA	391
Tyr Asp Glu Tyr Leu Lys Ser Lys Asp Lys Asn Asp	
110 115	
TTAAAAGAAC TGGATGATGC CTTAGATAA	420

(2) INFORMATION FOR SEQ ID NO:1180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

```

Ile Pro Thr Thr Leu Lys Tyr Met Ile Ser Leu Gly Lys Ile Arg Glu
30          35          40          45

TTA GAT GTT TTA GCA AAT CTT GCT AAA CTT TGC CCT ACT TGT CAT AGG      255
Leu Asp Val Leu Ala Asn Leu Ala Lys Leu Cys Pro Thr Cys His Arg
          50          55          60

GCT TTA AAA AAA GGA TCT AGC GAA GAG GAG TTT CAA AAA CGC TTG ATT      303
Ala Leu Lys Lys Gly Ser Ser Glu Glu Glu Phe Gln Lys Arg Leu Ile
          65          70          75

AGA AAC ATT CTC AAT CGC AAT AAA GAC AAT TTA GAG TTT GCG CAA TTG      351
Arg Asn Ile Leu Asn Arg Asn Lys Asp Asn Leu Glu Phe Ala Gln Leu
          80          85          90

CGT TTT GAA ACC GAT GAT TTT TCA ACG CTT ATT GAT CGT ATT TGT GAA      399
Arg Phe Glu Thr Asp Asp Phe Ser Thr Leu Ile Asp Arg Ile Cys Glu
          95          100          105

AGC TTG AAA TGAATTATAA AATTTTAGAT TTATTTTGTG GGGCTGGGGG T      449
Ser Leu Lys
110

```

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

```

Met Phe Ala Val His Ala Ala Met Ile Thr Thr Leu Lys Lys Glu Val
1          5          10          15
Phe Phe Leu Tyr Leu Tyr Ile Lys Ser Leu Lys Ile Pro Ile Pro Thr
          20          25          30
Thr Leu Lys Tyr Met Ile Ser Leu Gly Lys Ile Arg Glu Leu Asp Val
          35          40          45
Leu Ala Asn Leu Ala Lys Leu Cys Pro Thr Cys His Arg Ala Leu Lys
          50          55          60
Lys Gly Ser Ser Glu Glu Phe Gln Lys Arg Leu Ile Arg Asn Ile
65          70          75          80
Leu Asn Arg Asn Lys Asp Asn Leu Glu Phe Ala Gln Leu Arg Phe Glu
          85          90          95
Thr Asp Asp Phe Ser Thr Leu Ile Asp Arg Ile Cys Glu Ser Leu Lys
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs

130		135		140
Glu Ser Asp Gly Ala Gly Ser Val Leu Thr Asn Thr Gln Cys Leu Leu				
145		150		155
Glu Lys Asn Arg Asn Pro His Leu Asn Gln Asn Gly Ile Glu Asn Met				
	165		170	175
Leu Lys Lys Glu Leu Gly Ala Lys Gln Val Leu Trp Tyr Ser Tyr Gly				
	180		185	190
Tyr Leu Lys Gly Asp Asp Thr Asp Ser His Thr Asp Thr Leu Ala Arg				
	195		200	205
Phe Leu Asp Lys Asp Thr Ile Val Tyr Ser Thr Cys Glu Asp Glu Asn				
	210		215	220
Asp Glu His Tyr Thr Ala Leu Lys Lys Met Gln Glu Glu Leu Lys Thr				
225		230		235
Phe Lys Lys Leu Asp Gly Thr Pro Tyr Lys Leu Ile Pro Leu Glu Ile				
	245		250	255
Pro Lys Ala Ile Phe Asp Glu Asn Gln Gln Arg Leu Pro Ala Thr Tyr				
	260		265	270
Val Asn Phe Leu Leu Cys Asn Asn Ala Leu Ile Val Pro Thr Tyr Asn				
	275		280	285
Asp Pro Lys Asp Ala Leu Ile Leu Glu Thr Leu Lys Gln His Thr Pro				
	290		295	300
Leu Glu Val Ile Gly Val Asp Cys Asn Thr Leu Ile Lys Gln His Gly				
305		310		315
Ser Leu His Cys Val Thr Met Gln Leu Tyr				320
	325		330	

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...408
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

GCTTTATTCA AAAGAGCGAG GAGTTTAGAC GAGATAGCAA AATCATCAAT CTTTATCGCC	60
TTTCAACGCC TA ATG TTT GCA GTG CAT GCT GCG ATG ATT ACG ACA TTA AAG	111
Met Phe Ala Val His Ala Ala Met Ile Thr Thr Leu Lys	
1 5 10	
AAA GAA GTT TTC TTT CTT TAC CTT TAT ATC AAA TCA CTC AAA ATC CCG	159
Lys Glu Val Phe Phe Leu Tyr Leu Tyr Ile Lys Ser Leu Lys Ile Pro	
15 20 25	
ATT CCT ACT ACA CTG AAA TAC ATG ATT TCT TTA GGC AAA ATC AGA GAA	207

```

GAA TTA AAA ACC TTT AAA AAA CTA GAC GGC ACG CCC TAT AAA CTC ATC      771
Glu Leu Lys Thr Phe Lys Lys Leu Asp Gly Thr Pro Tyr Lys Leu Ile
                240                      245                      250

CCC CTA GAA ATC CCT AAA GCC ATT TTT GAT GAA AAC CAA CAA CGC TTG      819
Pro Leu Glu Ile Pro Lys Ala Ile Phe Asp Glu Asn Gln Gln Arg Leu
                255                      260                      265

CCG GCA ACT TAT GTG AAT TTT TTA TTG TGC AAT AAC GCT TTA ATC GTG      867
Pro Ala Thr Tyr Val Asn Phe Leu Leu Cys Asn Asn Ala Leu Ile Val
                270                      275                      280

CCC ACT TAC AAC GAC CCT AAA GAC GCG CTC ATT TTA GAA ACC TTG AAA      915
Pro Thr Tyr Asn Asp Pro Lys Asp Ala Leu Ile Leu Glu Thr Leu Lys
285                      290                      295                      300

CAA CAC ACG CCC TTA GAA GTG ATA GGG GTT GAT TGC AAC ACC TTA ATC      963
Gln His Thr Pro Leu Glu Val Ile Gly Val Asp Cys Asn Thr Leu Ile
                305                      310                      315

AAA CAG CAT GGA AGT TTG CAT TGT GTA ACG ATG CAA CTT TAT TGAACAAAA 1014
Lys Gln His Gly Ser Leu His Cys Val Thr Met Gln Leu Tyr
                320                      325                      330

TCACGCTTTT TGGCGTGGT                                          1033

```

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

```

Met Lys Arg Met Leu Ala Glu Phe Glu Lys Ile Gln Ala Ile Leu Met
 1           5           10           15
Ala Phe Pro His Glu Phe Ser Asp Trp Ala Tyr Cys Ile Lys Glu Ala
 20           25           30
Arg Glu Ser Phe Leu Asn Ile Ile Gln Thr Ile Ala Lys His Ala Lys
 35           40           45
Val Leu Val Cys Val His Thr Asn Asp Ile Ile Gly Tyr Glu Thr Leu
 50           55           60
Lys Asn Leu Pro Gly Val Glu Ile Ala Arg Ile Asp Thr Asn Asp Thr
 65           70           75           80
Trp Ala Arg Asp Phe Gly Ala Ile Ser Val Glu Asn His Gly Val Leu
 85           90           95
Glu Cys Leu Asp Phe Gly Phe Asn Gly Trp Gly Leu Lys Tyr Pro Ser
100           105           110
Asn Leu Asp Asn Gln Val Asn Phe Lys Leu Lys Ser Leu Gly Phe Leu
115           120           125
Lys His Pro Leu Lys Thr Met Pro Tyr Ile Leu Glu Gly Gly Ser Ile

```

GCG ATT CTA ATG GCT TTC CCC CAT GAG TTT AGC GAC TGG GCG TAT TGT	99
Ala Ile Leu Met Ala Phe Pro His Glu Phe Ser Asp Trp Ala Tyr Cys	
15 20 25	
ATC AAA GAG GCT AGG GAA AGT TTT TTA AAC ATC ATT CAA ACC ATA GCC	147
Ile Lys Glu Ala Arg Glu Ser Phe Leu Asn Ile Ile Gln Thr Ile Ala	
30 35 40	
AAA CAC GCT AAA GTG CTA GTG TGC GTC CAC ACT AAC GAT ATT ATC GGT	195
Lys His Ala Lys Val Leu Val Cys Val His Thr Asn Asp Ile Ile Gly	
45 50 55 60	
TAT GAA ACG CTT AAA AAC TTA CCC GGT GTA GAG ATC GCA AGG ATT GAC	243
Tyr Glu Thr Leu Lys Asn Leu Pro Gly Val Glu Ile Ala Arg Ile Asp	
65 70 75	
ACT AAC GAC ACA TGG GCT AGG GAT TTT GGA GCG ATC AGC GTT GAA AAT	291
Thr Asn Asp Thr Trp Ala Arg Asp Phe Gly Ala Ile Ser Val Glu Asn	
80 85 90	
CAT GGC GTT TTA GAG TGC TTG GAT TTT GGC TTT AAT GGC TGG GGG TTA	339
His Gly Val Leu Glu Cys Leu Asp Phe Gly Phe Asn Gly Trp Gly Leu	
95 100 105	
AAA TAC CCG TCC AAT TTA GAC AAT CAA GTG AAT TTC AAA CTC AAA AGT	387
Lys Tyr Pro Ser Asn Leu Asp Asn Gln Val Asn Phe Lys Leu Lys Ser	
110 115 120	
TTA GGG TTT TTA AAA CAC CCT TTA AAA ACG ATG CCC TAT ATT TTA GAG	435
Leu Gly Phe Leu Lys His Pro Leu Lys Thr Met Pro Tyr Ile Leu Glu	
125 130 135 140	
GGC GGG AGT ATA GAA AGC GAT GGG GCT GGG AGC GTT TTA ACC AAC ACC	483
Gly Gly Ser Ile Glu Ser Asp Gly Ala Gly Ser Val Leu Thr Asn Thr	
145 150 155	
CAA TGC CTG TTA GAA AAA AAT CGT AAC CCC CAT TTG AAT CAA AAT GGA	531
Gln Cys Leu Leu Glu Lys Asn Arg Asn Pro His Leu Asn Gln Asn Gly	
160 165 170	
ATA GAA AAC ATG CTT AAA AAG GAA TTA GGG GCT AAA CAA GTG CTG TGG	579
Ile Glu Asn Met Leu Lys Lys Glu Leu Gly Ala Lys Gln Val Leu Trp	
175 180 185	
TAT TCT TAT GGC TAT CTC AAA GGC GAT GAT ACC GAT AGC CAT ACC GAC	627
Tyr Ser Tyr Gly Tyr Leu Lys Gly Asp Asp Thr Asp Ser His Thr Asp	
190 195 200	
ACG CTC GCT CGT TTT TTA GAT AAA GAC ACC ATT GTT TAT AGC ACA TGC	675
Thr Leu Ala Arg Phe Leu Asp Lys Asp Thr Ile Val Tyr Ser Thr Cys	
205 210 215 220	
GAA GAT GAA AAC GAT GAG CAC TAC ACA GCC TTA AAA AAA ATG CAA GAA	723
Glu Asp Glu Asn Asp Glu His Tyr Thr Ala Leu Lys Lys Met Gln Glu	
225 230 235	

85								90				95				
Gly	Leu	Glu	Ile	Ser	Leu	Leu	Lys	Gln	Ile	Leu	Gln	Ser	Ile	Gln	Lys	
100								105				110				
Glu	Leu	Phe	Lys	Ala	Asn	Leu	Lys	Leu	Leu	Ser	Leu	Asp	Thr	Lys	Val	
115				120				125								
Val	Pro	Lys	Gly	Ser	Val	Asp	Lys	Leu	Phe	Ile	Asn	Thr	Thr	Cys	Ile	
130				135				140								
Gly	Lys	Ile	Ile	Lys	Pro	Gly	Ile	Ser	Ser	Tyr	His	Leu	Gln	Gln	Gly	
145					150				155				160			
Gln	Ala	Ile	Ile	Leu	Ser	Asp	Thr	Ile	Ala	Asn	His	Gly	Ala	Ser	Leu	
165				170				175								
Phe	Ala	Met	Arg	Asn	Glu	Ile	Lys	Leu	Lys	Thr	Asn	Leu	Glu	Ser	Asp	
180				185				190								
Cys	Gln	Leu	Leu	Tyr	Pro	Leu	Leu	Lys	Pro	Leu	Phe	Leu	Ser	Asp	Leu	
195				200				205								
Lys	Ile	Asp	Ala	Leu	Arg	Asp	Ala	Thr	Arg	Gly	Gly	Leu	Ala	Ser	Val	
210				215				220								
Leu	Asn	Glu	Trp	Ala	Asn	Ser	Ser	Arg	Val	Lys	Ile	Val	Ile	Glu	Glu	
225					230				235				240			
Glu	Lys	Ile	Pro	Leu	Lys	Glu	Glu	Thr	Lys	Gly	Ile	Cys	Glu	Ile	Leu	
245				250				255								
Gly	Leu	Glu	Pro	Tyr	Ala	Leu	Ala	Asn	Glu	Gly	Val	Phe	Val	Leu	Ala	
260				265				270								
Leu	Asn	Gln	Lys	Asp	Ala	Pro	Lys	Ala	Leu	Glu	Ile	Leu	Lys	Ser	Asn	
275				280				285								
Glu	Lys	Ala	Lys	Asn	Ala	Cys	Val	Ile	Gly	Lys	Val	Phe	Glu	Asn	Pro	
290				295				300								
Tyr	Pro	Ser	Val	Val	Leu	Lys	Asn	Ala	Trp	Gly	Phe	Glu	Arg	Ile	Leu	
305					310				315				320			
Glu	Val	Pro	Glu	Gly	Glu	Leu	Leu	Pro	Arg	Ile	Cys					
325				330												

(2) INFORMATION FOR SEO ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 16...1005
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

AAAAGGATAT TTTGA ATG AAA AGA ATG TTA GCG GAG TTT GAA AAA ATC CAA 51
Met Lys Arg Met Leu Ala Glu Phe Glu Lys Ile Gln
1 5 10

210	215	220	
AGC GTG CTG AAC GAA TGG GCG AAC AGC TCT AGA GTG AAA ATC GTT ATA			783
Ser Val Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys Ile Val Ile			
225	230	235	
GAA GAA GAA AAA ATC CCC TTA AAA GAA GAA ACG AAA GGG ATT TGT GAG			831
Glu Glu Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly Ile Cys Glu			
240	245	250	
ATT TTA GGG TTA GAA CCC TAC GCG CTA GCC AAT GAG GGG GTG TTT GTT			879
Ile Leu Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly Val Phe Val			
255	260	265	270
TTA GCG CTC AAT CAA AAA GAC GCC CCT AAA GCC TTA GAA ATT TTA AAA			927
Leu Ala Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu Ile Leu Lys			
275	280	285	
AGT AAC GAA AAA GCT AAA AAC GCT TGC GTG ATT GGC AAA GTG TTT GAA			975
Ser Asn Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys Val Phe Glu			
290	295	300	
AAC CCT TAT CCT AGC GTG GTT TTA AAG AAC GCA TGG GGT TTT GAA AGG			1023
Asn Pro Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly Phe Glu Arg			
305	310	315	
ATT TTA GAG GTG CCA GAG GGC GAA TTA TTG CCT AGG ATT TGT TAACACGCC			1074
Ile Leu Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile Cys			
320	325	330	
GTCATTTTTT AATCGTTTTTA AGCCTGCCCT AAAAAATGGTT TA			1116

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

Met	Asp	Ser	Val	Thr	Leu	Ala	Cys	Gly	Asn	Gly	Gly	Lys	Glu	Thr	Asn
1				5				10				15			
Ala	Leu	Ile	Glu	Arg	Val	Phe	Met	Pro	Tyr	Leu	Lys	Glu	Trp	Ile	Val
		20						25				30			
Ala	Phe	Asp	Glu	Asp	Ala	Pro	Lys	Phe	Glu	Ala	Ser	Gly	Glu	Tyr	Cys
	35					40					45				
Val	Ser	Thr	Asp	Ser	Phe	Val	Ile	Thr	Pro	Leu	Ile	Phe	Asn	Gly	Gly
	50				55					60					
Asp	Ile	Gly	Lys	Leu	Cys	Val	Cys	Gly	Ser	Ala	Asn	Asp	Val	Ser	Val
65				70				75				80			
Gln	Gly	Gly	Glu	Pro	Leu	Tyr	Leu	Asn	Met	Gly	Phe	Ile	Leu	Glu	Glu

CAGCAGTATC CCTATCGGTC AAGCCTTAAT GGCATATTTC AACCTACAA TCATCAAAAA 60
 AGGATAAAA ATG GAT AGC GTA ACT CTA GCA TGC GGG AAC GGA GGG AAA GAA 111
 Met Asp Ser Val Thr Leu Ala Cys Gly Asn Gly Gly Lys Glu
 1 5 10

ACA AAC GCT TTG ATT GAG CGA GTC TTT ATG CCC TAT TTA AAA GAA TGG 159
 Thr Asn Ala Leu Ile Glu Arg Val Phe Met Pro Tyr Leu Lys Glu Trp
 15 20 25 30

ATT GTT GCA TTT GAT GAA GAC GCC CCT AAA TTT GAA GCT AGT GGG GAA 207
 Ile Val Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala Ser Gly Glu
 35 40 45

TAT TGC GTG AGC ACG GAT AGT TTT GTC ATC ACG CCC TTA ATT TTT AAT 255
 Tyr Cys Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu Ile Phe Asn
 50 55 60

GGG GGC GAT ATA GGC AAG CTT TGC GTT TGC GGG AGT GCG AAT GAT GTG 303
 Gly Gly Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala Asn Asp Val
 65 70 75

AGC GTG CAA GGG GGC GAA CCT TTG TAT TTG AAT ATG GGT TTT ATT TTA 351
 Ser Val Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly Phe Ile Leu
 80 85 90

GAA GAA GGC TTA GAA ATT TCT CTT TTA AAA CAA ATT TTA CAA TCC ATA 399
 Glu Glu Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu Gln Ser Ile
 95 100 105 110

CAA AAA GAA TTG TTT AAA GCC AAC CTG AAA CTC CTC TCC CTA GAC ACT 447
 Gln Lys Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser Leu Asp Thr
 115 120 125

AAA GTC GTG CCA AAG GGG AGC GTG GAT AAG CTT TTT ATC AAC ACA ACC 495
 Lys Val Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile Asn Thr Thr
 130 135 140

TGC ATT GGT AAA ATC ATC AAG CCA GGG ATT TCT TCG TAC CAT TTA CAA 543
 Cys Ile Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr His Leu Gln
 145 150 155

CAA GGG CAA GCC ATT ATC CTA AGC GAC ACT ATC GCC AAT CAT GGG GCA 591
 Gln Gly Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn His Gly Ala
 160 165 170

AGC TTA TTT GCG ATG CGT AAT GAA ATC AAG CTT AAA ACG AAT CTA GAA 639
 Ser Leu Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr Asn Leu Glu
 175 180 185 190

AGC GAT TGC CAA CTG CTC TAT CCC TTA TTA AAA CCC CTA TTT TTA AGC 687
 Ser Asp Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu Phe Leu Ser
 195 200 205

GAT CTC AAA ATT GAT GCT TTA AGA GAT GCG ACT AGG GGC GGG TTA GCG 735
 Asp Leu Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly Gly Leu Ala

100	105	110
Leu Arg Ile Leu Glu Ala Met Arg Ile Leu Gly Leu Glu Lys Lys Thr		
115	120	125
Arg Phe Tyr Gln Ala Ser Thr Ser Glu Leu Tyr Gly Glu Val Leu Glu		
130	135	140
Thr Pro Gln Asn Glu Asn Thr Pro Phe Asn Pro Arg Ser Pro Tyr Ala		
145	150	155
Val Ala Lys Met Tyr Ala Phe Tyr Ile Thr Lys Asn Tyr Arg Glu Ala		
165	170	175
Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn His Glu Ser Arg		
180	185	190
Val Arg Gly Glu Thr Phe Val Thr Arg Lys Ile Thr Arg Ala Ala Ser		
195	200	205
Ala Ile Ala Tyr Asn Leu Thr Asp Cys Leu Tyr Leu Gly Asn Leu Asp		
210	215	220
Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val Lys Met Met His		
225	230	235
Leu Met Leu Gln Ala Pro Ile Pro Gln Asp Tyr Val Ile Ala Thr Gly		
245	250	255
Lys Thr Thr Ser Val Arg Asp Phe Val Lys Met Ser Phe Glu Phe Ile		
260	265	270
Gly Ile Asn Leu Glu Phe Gln Asn Thr Gly Ile Lys Glu Ile Gly Leu		
275	280	285
Ile Lys Ser Val Asp Glu Lys Arg Ala Asn Ala Leu Lys Leu Asn Leu		
290	295	300
Ser His Leu Lys Lys Gly Gln Ile Val Val Arg Ile Asp Glu Arg Tyr		
305	310	315
Phe Arg Pro Thr Glu Val Asp Leu Leu Leu Gly Asp Pro Thr Lys Ala		
325	330	335
Glu Lys Glu Leu Asp Trp Val Arg Glu Tyr Asp Leu Lys Glu Leu Val		
340	345	350
Lys Asp Met Leu Glu Tyr Asp Leu Lys Glu Cys Gln Lys Asn Leu Tyr		
355	360	365
Leu Gln Asp Gly Gly Tyr Ile Leu Arg Asn Phe Tyr Glu		
370	375	380

(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...1065
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

GGG ATT AAA GAA ATC GGT TTG ATT AAA AGC GTT GAT GAA AAA AGA GCG 917
 Gly Ile Lys Glu Ile Gly Leu Ile Lys Ser Val Asp Glu Lys Arg Ala
 285 290 295

AAC GCT TTA AAA TTG AAC TTA AGC CAT TTA AAA AAA GGC CAA ATC GTG 965
 Asn Ala Leu Lys Leu Asn Leu Ser His Leu Lys Lys Gly Gln Ile Val
 300 305 310

GTG CGC ATA GAC GAG CGT TAT TTC AGG CCT ACC GAA GTG GAT TTG CTT 1013
 Val Arg Ile Asp Glu Arg Tyr Phe Arg Pro Thr Glu Val Asp Leu Leu
 315 320 325

TTA GGC GAT CCC ACT AAG GCA GAG AAA GAG CTA GAC TGG GTT AGG GAA 1061
 Leu Gly Asp Pro Thr Lys Ala Glu Lys Glu Leu Asp Trp Val Arg Glu
 330 335 340 345

TAC GAT TTA AAA GAG TTG GTT AAG GAC ATG TTA GAA TAC GAT TTA AAA 1109
 Tyr Asp Leu Lys Glu Leu Val Lys Asp Met Leu Glu Tyr Asp Leu Lys
 350 355 360

GAA TGC CAA AAA AAC CTT TAC TTG CAA GAT GGG GGT TAT ATT TTA AGG 1157
 Glu Cys Gln Lys Asn Leu Tyr Leu Gln Asp Gly Gly Tyr Ile Leu Arg
 365 370 375

AAT TTT TAT GAA TGAGATTATT TTAATCACTG GTGCCTATGG CATGGTGGGG CAGAA 1214
 Asn Phe Tyr Glu
 380

CACGGCGTTG TATTT 1229

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

Met Lys Glu Lys Ile Ala Leu Ile Thr Gly Val Thr Gly Gln Asp Gly
 1 5 10 15
 Ser Tyr Leu Ala Glu Tyr Leu Leu Asn Leu Gly Tyr Glu Val His Gly
 20 25 30
 Leu Lys Arg Arg Ser Ser Ser Ile Asn Thr Ser Arg Ile Asp His Leu
 35 40 45
 Tyr Glu Asp Leu His Ser Asp His Lys Arg Arg Phe Phe Leu His Tyr
 50 55 60
 Gly Asp Met Thr Asp Ser Ser Asn Leu Ile His Leu Ile Ala Thr Thr
 65 70 75 80
 Lys Pro Thr Glu Ile Tyr Asn Leu Ala Ala Gln Ser His Val Lys Val
 85 90 95
 Ser Phe Glu Thr Pro Glu Tyr Thr Ala Asn Ala Asp Gly Ile Gly Thr

AGG CGT TTT TTC TTA CAC TAT GGG GAT ATG ACC GAT AGC TCT AAT CTT	245
Arg Arg Phe Phe Leu His Tyr Gly Asp Met Thr Asp Ser Ser Asn Leu	
60 65 70	
ATC CAT TTA ATC GCT ACC ACT AAG CCT ACA GAG ATT TAT AAT TTA GCC	293
Ile His Leu Ile Ala Thr Lys Pro Thr Glu Ile Tyr Asn Leu Ala	
75 80 85	
GCT CAA AGC CAT GTA AAA GTC TCT TTT GAA ACC CCC GAA TAC ACC GCT	341
Ala Gln Ser His Val Lys Val Ser Phe Glu Thr Pro Glu Tyr Thr Ala	
90 95 100 105	
AAC GCT GAT GGT ATT GGC ACG CTA AGG ATT TTA GAA GCC ATG CGG ATT	389
Asn Ala Asp Gly Ile Gly Thr Leu Arg Ile Leu Glu Ala Met Arg Ile	
110 115 120	
TTA GGA TTA GAA AAG AAA ACG CGC TTT TAT CAA GCC AGC ACG AGC GAA	437
Leu Gly Leu Glu Lys Lys Thr Arg Phe Tyr Gln Ala Ser Thr Ser Glu	
125 130 135	
TTG TAT GGC GAA GTC TTA GAA ACC CCG CAA AAT GAA AAC ACC CCC TTT	485
Leu Tyr Gly Glu Val Leu Glu Thr Pro Gln Asn Glu Asn Thr Pro Phe	
140 145 150	
AAC CCA CGA AGC CCC TAT GCG GTC GCT AAA ATG TAT GCC TTT TAC ATC	533
Asn Pro Arg Ser Pro Tyr Ala Val Ala Lys Met Tyr Ala Phe Tyr Ile	
155 160 165	
ACC AAA AAT TAC AGA GAG GCC TAT AAC TTG TTT GCG GTT AAT GGC ATT	581
Thr Lys Asn Tyr Arg Glu Ala Tyr Asn Leu Phe Ala Val Asn Gly Ile	
170 175 180 185	
CTT TTT AAC CAT GAG AGC AGG GTA AGG GGC GAA ACT TTT GTA ACC CGT	629
Leu Phe Asn His Glu Ser Arg Val Arg Gly Glu Thr Phe Val Thr Arg	
190 195 200	
AAA ATC ACA CGA GCC GCT AGC GCG ATA GCG TAT AAC TTA ACG GAT TGC	677
Lys Ile Thr Arg Ala Ala Ser Ala Ile Ala Tyr Asn Leu Thr Asp Cys	
205 210 215	
TTG TAT TTA GGG AAT TTA GAC GCT AAA AGA GAC TGG GGG CAT GCC AAA	725
Leu Tyr Leu Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys	
220 225 230	
GAT TAC GTG AAA ATG ATG CAT TTA ATG CTC CAA GCG CCC ATC CCA CAA	773
Asp Tyr Val Lys Met Met His Leu Met Leu Gln Ala Pro Ile Pro Gln	
235 240 245	
GAT TAT GTG ATC GCC ACA GGA AAG ACC ACA AGC GTG CGC GAT TTT GTG	821
Asp Tyr Val Ile Ala Thr Gly Lys Thr Thr Ser Val Arg Asp Phe Val	
250 255 260 265	
AAA ATG AGC TTT GAA TTT ATC GGT ATC AAT TTA GAA TTT CAA AAT ACA	869
Lys Met Ser Phe Glu Phe Ile Gly Ile Asn Leu Glu Phe Gln Asn Thr	
270 275 280	

```

Asn Asn Asn Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg
      85                      90                      95
Ile Ile Thr Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly
      100                    105                    110
Ala Asp Ile Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg
      115                    120                    125
Asn Phe Gln Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn
      130                    135                    140
Gly Leu Leu Ile Gly Ile Thr Ser Ala Leu Asn Asn Arg Gly Asn Lys
      145                    150                    155                    160
Glu Gly Ala Thr Asn Phe Phe Gly Asp Tyr Leu Leu Met Gln Leu Met
      165                    170                    175
Arg Gln Ser Gly Met Gly Ile Asn Gln Val Val Asn Gln Ile Leu Arg
      180                    185                    190
Asp Lys Ser Lys Ile Ala Pro Ile Val Val Ile Arg Glu Gly Ser Arg
      195                    200                    205
Val Phe Ile Ser Pro Asn Thr Asp Ile Phe Phe Pro Ile Pro Arg Glu
      210                    215                    220
Asn Glu Val Ile Ala Glu Phe Leu Lys
      225                    230

```

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 27...1169
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

```

AAATAAAATT CAATAAAGGA AAAATA ATG AAA GAA AAA ATC GCT TTA ATC ACC      53
      Met Lys Glu Lys Ile Ala Leu Ile Thr
      1                      5

GGG GTT ACC GGG CAA GAC GGG AGC TAT CTG GCT GAA TAC TTG CTG AAT      101
Gly Val Thr Gly Gln Asp Gly Ser Tyr Leu Ala Glu Tyr Leu Leu Asn
      10                    15                    20                    25

TTG GGT TAT GAA GTG CAT GGG TTA AAA AGG CGC TCT TCT AGC ATC AAC      149
Leu Gly Tyr Glu Val His Gly Leu Lys Arg Arg Ser Ser Ser Ile Asn
      30                    35                    40

ACT TCT AGG ATC GAT CAT CTG TAT GAA GAT TTG CAT AGC GAT CAT AAA      197
Thr Ser Arg Ile Asp His Leu Tyr Glu Asp Leu His Ser Asp His Lys
      45                    50                    55

```

```

AAA GGC TAT AAC GGC TTG GTG GGG GAA TTG ATT GAA AGG AAT TTC CAG      442
Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg Asn Phe Gln
                120                      125                      130

CGC TAT GGC GTG CCG TTA CTG CTT TCT ACT CTC ACT AAC GGC CTA TTG      490
Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn Gly Leu Leu
                135                      140                      145

ATT GGG ATC ACT TCG GCT TTA AAC AAC AGA GGC AAT AAA GAA GGA GCC      538
Ile Gly Ile Thr Ser Ala Leu Asn Asn Arg Gly Asn Lys Glu Gly Ala
                150                      155                      160

ACC AAT TTC TTT GGG GAT TAT CTT TTA ATG CAA TTG ATG AGG CAA AGC      586
Thr Asn Phe Phe Gly Asp Tyr Leu Leu Met Gln Leu Met Arg Gln Ser
                165                      170                      175

GGC ATG GGG ATC AAT CAA GTA GTC AAT CAA ATT TTA AGA GAT AAG AGC      634
Gly Met Gly Ile Asn Gln Val Val Asn Gln Ile Leu Arg Asp Lys Ser
                180                      185                      190

AAA ATC GCT CCT ATT GTG GTG ATT AGA GAA GGG AGT AGG GTC TTC ATT      682
Lys Ile Ala Pro Ile Val Val Ile Arg Glu Gly Ser Arg Val Phe Ile
                200                      205                      210

TCG CCC AAT ACT GAC ATC TTT TTC CCT ATA CCC AGA GAG AAT GAA GTC      730
Ser Pro Asn Thr Asp Ile Phe Phe Pro Ile Pro Arg Glu Asn Glu Val
                215                      220                      225

ATC GCT GAG TTT TTG AAG TGA CTCAAAA ATCCCCAATT AAAAAACGCT      777
Ile Ala Glu Phe Leu Lys
                230

```

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

```

Met Asp Asn Pro Lys Gly Ile Asp Gly Phe Thr Asn Leu Lys Glu Lys
 1              5              10              15
Asp Ile Ala Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp
                20              25              30
Lys Met Ile Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala
                35              40              45
Gly Lys Val Ile Ala Gln Val Glu Ser Asp Ile Phe Ala His Met Gly
                50              55              60
Lys Ala Val Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Tyr Ser
        65              70              75              80

```

```

          325          330          335
Gln Lys Lys Val Lys Lys Asp Thr Ile Asn Thr Lys Asn Glu Ile
          340          345          350

```

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...748
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

```

CCCTTTCAAA CAAGGCCCTA AAAATTACGA AGAAAACCTG ATTTTCCCC ATG GAT AAC      58
                                     Met Asp Asn
                                     1

CCT AAA GGC ATT GAT GGT TTT ACT AAC CTT AAA GAA AAA GAC ATC GCC      106
Pro Lys Gly Ile Asp Gly Phe Thr Asn Leu Lys Glu Lys Asp Ile Ala
   5              10              15

ACT AAT GAA AAT AAG CTT TTA CGC ACC ATT ACA GCG GAT AAA ATG ATA      154
Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp Lys Met Ile
  20              25              30              35

CCC GCC TTT CTC ATC ACG CCT ATT TCT AGC CAG ATC GCT GGT AAA GTC      202
Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala Gly Lys Val
              40              45              50

ATC GCG CAG GTG GAG AGC GAT ATT TTT GCT CAC ATG GGC AAG GCC GTC      250
Ile Ala Gln Val Glu Ser Asp Ile Phe Ala His Met Gly Lys Ala Val
              55              60              65

TTA ATC CCC AAA GGC TCT AAA GTC ATA GGT TAT TAC AGC AAC AAT AAC      298
Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Tyr Ser Asn Asn Asn
  70              75              80

AAA ATG GGC GAA TAC CGC TTG GAT ATT GTA TGG AGC CGC ATC ATC ACT      346
Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg Ile Ile Thr
  85              90              95

CCC CAT GGC ATC AAT ATC ATG CTC ACT AAC GCT AAA GGG GCG GAC ATT      394
Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly Ala Asp Ile
 100              105              110              115

```


AATTTAATGA GAATTTT

1133

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

```

Met Lys Asn Asp Ala Tyr Glu Ile Ile Leu Ser Trp Phe Ile Thr Pro
 1           5           10           15
Leu Thr Ala Ile Leu Gly Arg Phe Ala Glu Phe Phe Leu Tyr Thr Leu
          20           25           30
His Ala Gln Leu Val Phe Asn Ser Val Val Ala Leu Ala Phe Met Leu
          35           40           45
Phe Ala Tyr Arg Ser Leu Lys Glu Gln Asn Phe Phe Ser Ala Ser Ala
          50           55           60
Leu Thr Glu Ala Leu Leu Phe Val Gly Phe Phe Ala Leu Phe Asn Tyr
          65           70           75           80
Ala Leu Lys Asn Pro Met His Phe Tyr Glu Phe Phe Gln Asn Ala Ile
          85           90           95
Phe Ile Ala Pro Asn Met Ile Ala Gln Ser Leu Ser Gln Ser Leu Ser
          100          105          110
Asn Phe Ser Asp His Ala Leu Ser Leu Asp Phe Ile Phe Asn His Gly
          115          120          125
Phe Tyr Ala Leu Ser Phe Ile Ser Asp Leu Ser His Asn Glu Met Ser
          130          135          140
Val Trp Leu Phe Leu Ser Val Leu Gln Gly Leu Phe Leu Ser Val Leu
          145          150          155          160
Phe Ala Ile Ile Ile Leu Val Tyr Leu Glu Val His Val Trp Cys Ser
          165          170          175
Leu Gly Val Leu Phe Leu Ala Phe Gly Phe Phe Lys Thr Trp Arg Ser
          180          185          190
Val Val Val Ile Cys Leu Lys Lys Cys Phe Ala Leu Gly Phe Tyr Lys
          195          200          205
Pro Phe Leu Leu Leu Val Gly Phe Leu Asn Val Ser Val Thr Lys Ala
          210          215          220
Leu Ile Asp Ala His Met Gln Glu Lys Gln Asp Leu Ser Leu Leu Leu
          225          230          235          240
Val Val Ala Leu Phe Leu Cys Cys Val Phe Ile Ile Gly Val Pro Phe
          245          250          255
Phe Ile Asn Ala Leu Phe Arg Val Gln Asn Ser Leu Lys Glu Thr Tyr
          260          265          270
Lys Leu Ala Thr Asn Leu Ser Ala Asn Leu Ser Gln Asn Ala Leu Asn
          275          280          285
Ser Leu Gln Tyr Ile Thr Thr Pro Pro Ala Ser Ser Ser Val Ser Ser
          290          295          300
Ser Met Ser Glu Ser Val Ser Lys Glu Lys Glu Thr His Ser Pro Thr
          305          310          315          320
Phe Lys Val Glu Thr Thr Gln Leu Asp Val Lys Ile Pro Asn Phe Lys

```

GCC CTT AGT TTC ATC AGC GAT TTG AGC CAT AAT GAA ATG TCT GTG TGG	489
Ala Leu Ser Phe Ile Ser Asp Leu Ser His Asn Glu Met Ser Val Trp	
135 140 145	
CTT TTT TTA AGC GTT TTG CAA GGG CTT TTT TTG AGC GTG CTG TTT GCA	537
Leu Phe Leu Ser Val Leu Gln Gly Leu Phe Leu Ser Val Leu Phe Ala	
150 155 160	
ATC ATC ATT TTA GTG TAT TTA GAA GTG CAT GTG TGG TGC TCT TTA GGG	585
Ile Ile Ile Leu Val Tyr Leu Glu Val His Val Trp Cys Ser Leu Gly	
165 170 175	
GTG CTG TTT TTA GCG TTT GGG TTT TTT AAA ACC TGG AGG AGC GTT GTG	633
Val Leu Phe Leu Ala Phe Gly Phe Phe Lys Thr Trp Arg Ser Val Val	
180 185 190	
GTT ATA TGC CTA AAA AAG TGC TTC GCT CTT GGG TTT TAC AAG CCT TTT	681
Val Ile Cys Leu Lys Lys Cys Phe Ala Leu Gly Phe Tyr Lys Pro Phe	
195 200 205 210	
TTG TTG TTG GTA GGG TTT TTG AAT GTG TCG GTT ACT AAG GCT TTA ATA	729
Leu Leu Leu Val Gly Phe Leu Asn Val Ser Val Thr Lys Ala Leu Ile	
215 220 225	
GAC GCT CAT ATG CAA GAA AAA CAA GAC TTA AGC CTT TTA TTG GTG GTA	777
Asp Ala His Met Gln Glu Lys Gln Asp Leu Ser Leu Leu Val Val	
230 235 240	
GCG TTA TTT TTG TGT TGC GTT TTT ATC ATC GGC GTG CCT TTT TTC ATC	825
Ala Leu Phe Leu Cys Cys Val Phe Ile Ile Gly Val Pro Phe Phe Ile	
245 250 255	
AAC GCT TTG TTT AGG GTG CAA AAC AGC CTT AAA GAA ACT TAC AAA CTC	873
Asn Ala Leu Phe Arg Val Gln Asn Ser Leu Lys Glu Thr Tyr Lys Leu	
260 265 270	
GCC ACC AAT TTG AGT GCC AAC CTC AGC CAA AAC GCC CTT AAT TCC TTA	921
Ala Thr Asn Leu Ser Ala Asn Leu Ser Gln Asn Ala Leu Asn Ser Leu	
275 280 285 290	
CAA TAC ATC ACG ACC CCA CCC GCT TCT TCT AGC GTT TCT TCT TCT ATG	969
Gln Tyr Ile Thr Thr Pro Pro Ala Ser Ser Ser Val Ser Ser Ser Met	
295 300 305	
AGT GAA AGC GTC TCT AAA GAA AAA GAA ACG CAT TCC CCC ACA TTT AAG	1017
Ser Glu Ser Val Ser Lys Glu Lys Glu Thr His Ser Pro Thr Phe Lys	
310 315 320	
GTA GAA ACC ACT CAA TTA GAT GTA AAA ATC CCA AAT TTC AAG CAA AAA	1065
Val Glu Thr Thr Gln Leu Asp Val Lys Ile Pro Asn Phe Lys Gln Lys	
325 330 335	
AAG GTT AAA AAG GAT ACA ATA AAT ACA AAA AAT GAA ATT TAAATAAATA GG	1116
Lys Val Lys Lys Asp Thr Ile Asn Thr Lys Asn Glu Ile	
340 345 350	

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1104
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

TAGTCTTGCG TAAAGGCTTT GAATTTTACA TTAAAGTCCG TTGAAGTATT G ATG AAA	57
Met Lys	
1	
AAT GAC GCT TAT GAA ATT ATT CTT TCT TGG TTT ATC ACG CCT CTC ACG	105
Asn Asp Ala Tyr Glu Ile Ile Leu Ser Trp Phe Ile Thr Pro Leu Thr	
5 10 15	
GCG ATT TTA GGG CGT TTC GCT GAA TTT TTT CTC TAC ACT TTG CAT GCG	153
Ala Ile Leu Gly Arg Phe Ala Glu Phe Phe Leu Tyr Thr Leu His Ala	
20 25 30	
CAA TTG GTG TTT AAT AGC GTG GTC GCT TTG GCG TTC ATG CTC TTT GCT	201
Gln Leu Val Phe Asn Ser Val Val Ala Leu Ala Phe Met Leu Phe Ala	
35 40 45 50	
TAT AGG AGT TTG AAA GAA CAG AAT TTC TTC AGC GCT AGC GCG CTA ACA	249
Tyr Arg Ser Leu Lys Glu Gln Asn Phe Phe Ser Ala Ser Ala Leu Thr	
55 60 65	
GAA GCG TTA TTG TTT GTG GGG TTT TTT GCA CTT TTC AAC TAC GCT TTA	297
Glu Ala Leu Leu Phe Val Gly Phe Phe Ala Leu Phe Asn Tyr Ala Leu	
70 75 80	
AAA AAT CCC ATG CAT TTT TAT GAA TTT TTC CAA AAC GCT ATT TTT ATT	345
Lys Asn Pro Met His Phe Tyr Glu Phe Phe Gln Asn Ala Ile Phe Ile	
85 90 95	
GCG CCT AAC ATG ATC GCG CAA AGC CTC TCT CAA AGC TTG AGT AAC TTT	393
Ala Pro Asn Met Ile Ala Gln Ser Leu Ser Gln Ser Leu Ser Asn Phe	
100 105 110	
TCT GAC CAT GCG CTT TCT TTA GAT TTT ATC TTT AAT CAT GGT TTT TAT	441
Ser Asp His Ala Leu Ser Leu Asp Phe Ile Phe Asn His Gly Phe Tyr	
115 120 125 130	

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

```

Met Phe His Lys Ala Leu Ile Thr Phe Ile Val Leu Trp Phe Phe Leu
 1             5             10             15
Asn Gly Leu Gly Ala Tyr Asp Phe Lys His Cys Gln Ala Phe Phe Lys
      20             25             30
Lys Ala Ser Leu Gln Lys Gly Gly Val Ala Leu Lys Glu Leu Pro Lys
      35             40             45
Gly Val Tyr Leu Tyr Tyr Ser Lys Thr Tyr Pro Lys His Ala Lys Val
      50             55             60
Ile Lys Ser Asp Pro Phe Val Gly Leu Tyr Leu Leu Gln Ser Ala Pro
65             70             75             80
Ser Glu Tyr Val Tyr Thr Leu Arg Asp Leu Asp Lys Asp Ala Leu Ile
      85             90             95
Arg Pro Met Ala Ser Ile Gly Asp Lys Glu Ala Leu Glu Thr Arg Leu
      100            105            110
Leu Val Gly Gln Arg Gly Tyr Glu Arg Tyr Ala Gln Ile Ser Gln Lys
      115            120            125
Thr Gln Lys Asn Gly Val Ile Ser Asn Ile Cys Tyr Gln Met Leu Gly
      130            135            140
Leu Gly Val Gly Gly Asn Gly Phe Ile Glu Thr Lys Phe Ile Lys Arg
145            150            155            160
Phe Leu Asn Gln Gln Glu Pro Tyr Tyr Gly Asp Ile Gly Val Arg Leu
      165            170            175
Glu Glu His His Lys Arg Leu Val Val Val Gln Phe Asp Pro Phe Phe
      180            185            190
Pro Lys Asn Pro Phe Leu Lys Asn Asp Glu Ile Leu Ala Ile Asn His
      195            200            205
Gln Lys Ile His Ser Leu Ala Glu Phe Glu Trp Val Val Ser Asn Leu
      210            215            220
Lys Tyr Gln Ser Leu Ala Lys Val Glu Ile Lys Arg Asn His Lys Val
225            230            235            240
Lys Glu Val Thr Leu Lys Val Asn Lys Arg Tyr Gly Gly Phe Leu Leu
      245            250            255
Lys Asp Thr Phe Leu Glu Arg Tyr Gly Ile Ala Leu Asp Glu Arg Phe
      260            265            270
Ile Ile Thr Lys Ile Gly Ala His Leu Pro Lys Gly Leu Asp Phe Leu
      275            280            285
Lys Leu Gly Asp Arg Ile Leu Trp Val Asn Tyr Lys Ser Val Ala Ser
      290            295            300
Asn Pro Lys Ala Leu Arg Glu Ala Leu Ser Ala Pro Lys Ile Glu Leu
305            310            315            320
Leu Val Leu Arg Lys Gly Phe Glu Phe Tyr Ile Lys Val Arg
      325            330

```

TCG CAA AAG ACT CAA AAA AAT GGC GTT ATC AGC AAT ATT TGC TAT CAA	435
Ser Gln Lys Thr Gln Lys Asn Gly Val Ile Ser Asn Ile Cys Tyr Gln	
130 135 140	
ATG TTA GGG CTA GGG GTA GGG GGG AAT GGC TTT ATA GAA ACG AAA TTT	483
Met Leu Gly Leu Gly Val Gly Gly Asn Gly Phe Ile Glu Thr Lys Phe	
145 150 155	
ATC AAG CGC TTT TTA AAC CAG CAA GAG CCT TAT TAT GGG GAT ATT GGG	531
Ile Lys Arg Phe Leu Asn Gln Gln Glu Pro Tyr Tyr Gly Asp Ile Gly	
160 165 170	
GTG CGT TTA GAA GAA CAT CAT AAG CGT TTA GTG GTA GTG CAA TTT GAT	579
Val Arg Leu Glu Glu His His Lys Arg Leu Val Val Val Gln Phe Asp	
175 180 185	
CCA TTT TTC CCT AAA AAC CCT TTT TTA AAA AAC GAT GAA ATC CTA GCG	627
Pro Phe Phe Pro Lys Asn Pro Phe Leu Lys Asn Asp Glu Ile Leu Ala	
190 195 200 205	
ATC AAC CAT CAA AAG ATC CAC TCA TTA GCG GAG TTT GAA TGG GTG GTG	675
Ile Asn His Gln Lys Ile His Ser Leu Ala Glu Phe Glu Trp Val Val	
210 215 220	
AGC AAT CTT AAA TAC CAA AGC CTT GCA AAA GTG GAA ATC AAA CGA AAC	723
Ser Asn Leu Lys Tyr Gln Ser Leu Ala Lys Val Glu Ile Lys Arg Asn	
225 230 235	
CAT AAA GTC AAA GAA GTA ACG CTC AAA GTC AAT AAG CGT TAT GGG GGG	771
His Lys Val Lys Glu Val Thr Leu Lys Val Asn Lys Arg Tyr Gly Gly	
240 245 250	
TTT TTA CTC AAA GAC ACT TTT TTA GAG CGC TAT GGC ATC GCT TTA GAT	819
Phe Leu Leu Lys Asp Thr Phe Leu Glu Arg Tyr Gly Ile Ala Leu Asp	
255 260 265	
GAG CGT TTT ATT ATC ACT AAA ATA GGC GCT CAT TTG CCC AAA GGC TTG	867
Glu Arg Phe Ile Ile Thr Lys Ile Gly Ala His Leu Pro Lys Gly Leu	
270 275 280 285	
GAT TTT TTA AAG CTT GGG GAT AGG ATT TTA TGG GTG AAT TAT AAA AGC	915
Asp Phe Leu Lys Leu Gly Asp Arg Ile Leu Trp Val Asn Tyr Lys Ser	
290 295 300	
GTG GCG TCC AAC CCA AAG GCT TTA AGA GAA GCG TTA AGC GCG CCT AAA	963
Val Ala Ser Asn Pro Lys Ala Leu Arg Glu Ala Leu Ser Ala Pro Lys	
305 310 315	
ATT GAA TTA TTA GTC TTG CGT AAA GGC TTT GAA TTT TAC ATT AAA GTC	1011
Ile Glu Leu Leu Val Leu Arg Lys Gly Phe Glu Phe Tyr Ile Lys Val	
320 325 330	
CGT TGAAGTATTG ATGAAAAATG ACGCTTATGA AATTATTCTT TCTTGTTT	1063
Arg	

Lys Asn Val Leu Thr Ser Gln Ile Phe Asp Gly Ala Tyr His Phe Lys
 580 585 590
 Ser

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1014
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

TGCTAAATTG TG ATG TTT CAC AAA GCC CTT ATT ACC TTT ATC GTT CTA TGG	51
Met Phe His Lys Ala Leu Ile Thr Phe Ile Val Leu Trp	
1 5 10	
TTT TTT TTG AAT GGC TTA GGG GCT TAT GAT TTC AAG CAT TGT CAA GCG	99
Phe Phe Leu Asn Gly Leu Gly Ala Tyr Asp Phe Lys His Cys Gln Ala	
15 20 25	
TTT TTT AAA AAA GCG AGC CTT CAA AAA GGA GGC GTG GCT TTA AAA GAA	147
Phe Phe Lys Lys Ala Ser Leu Gln Lys Gly Gly Val Ala Leu Lys Glu	
30 35 40 45	
TTG CCT AAA GGC GTG TAT TTG TAT TAT TCC AAA ACC TAT CCC AAA CAC	195
Leu Pro Lys Gly Val Tyr Leu Tyr Tyr Ser Lys Thr Tyr Pro Lys His	
50 55 60	
GCC AAA GTC ATC AAA TCC GAT CCC TTT GTA GGG TTG TAT TTG TTG CAA	243
Ala Lys Val Ile Lys Ser Asp Pro Phe Val Gly Leu Tyr Leu Leu Gln	
65 70 75	
AGC GCA CCA AGC GAG TAT GTT TAT ACC TTA AGG GAT TTA GAC AAA GAC	291
Ser Ala Pro Ser Glu Tyr Val Tyr Thr Leu Arg Asp Leu Asp Lys Asp	
80 85 90	
GCC CTT ATA AGG CCA ATG GCT AGC ATA GGG GAT AAA GAA GCC CTA GAA	339
Ala Leu Ile Arg Pro Met Ala Ser Ile Gly Asp Lys Glu Ala Leu Glu	
95 100 105	
ACG CGA TTA TTG GTG GGG CAA AGA GGC TAT GAG CGC TAC GCT CAA ATT	387
Thr Arg Leu Leu Val Gly Gln Arg Gly Tyr Glu Arg Tyr Ala Gln Ile	
110 115 120 125	

-1700-

```

CAA CTT GGC AAC ATC AGC CCT AGA CTA TCT AAA AGC ATA GTT ACC GCC      1593
Gln Leu Gly Asn Ile Ser Pro Arg Leu Ser Lys Ser Ile Val Thr Ala
500                               505                               510                               515

ATA GAG CAA GCA GAG GGC GTG AGA CTG AAT TAT GCG TTG ATT GAC AAA      1641
Ile Glu Gln Ala Glu Gly Val Arg Leu Asn Tyr Ala Leu Ile Asp Lys
                    520                               525                               530

ATC ACC TAT AAC TCA CTC CAC AAT ATC TTA AGT TTC ATT TTT GAT ATT      1689
Ile Thr Tyr Asn Ser Leu His Asn Ile Leu Ser Phe Ile Phe Asp Ile
                    535                               540                               545

GAT AAC CCT TTA AGC GAC CAA GTG TTT GAG AGA TTA GTC ATT GAA GTC      1737
Asp Asn Pro Leu Ser Asp Gln Val Phe Glu Arg Leu Val Ile Glu Val
                    550                               555                               560

CCA AGA GAA GCA CTT AAA AAT GTG AAG TTG CCA CAA ATC AAA AAT GTA      1785
Pro Arg Glu Ala Leu Lys Asn Val Lys Leu Pro Gln Ile Lys Asn Val
                    565                               570                               575

TTG ACT TCT CAA ATC TTT GAT GGC GCT TAC CAC TTT AAA AGT TAAACCATG  1836
Leu Thr Ser Gln Ile Phe Asp Gly Ala Tyr His Phe Lys Ser
580                               585                               590

CTCTTTTATCA GCGCAACTAA CACGAATGCC GGAAAAACCA CAT                        1879

```

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

```

Met Leu Leu Asn Tyr Asp Phe Leu Glu Phe Val Asp Glu Pro Lys Arg
 1             5             10             15
Asn Thr Ser Leu Thr Ala Ser Ile Asp Lys Ala Leu Ala Asp Arg Lys
      20             25             30
Leu Ala Arg Gln Asn Lys Pro Ser Val Arg Val Leu Gly Lys Ala Met
      35             40             45
Pro Leu Ser Lys Phe Leu Asp Ala Val Gly Asp Glu Ile Ser Arg Leu
      50             55             60
Lys Tyr Asp Met Ser His Lys Thr Ile Lys Gly Ser Thr Ile Glu Ser
65             70             75             80
Ser Asn Leu Ile Ser Ile Tyr Lys Lys Ile Ala Ser Gly Leu Pro Phe
      85             90             95
Gly Thr Ile Ser Ala Phe Arg Pro Phe Lys Asp Ala Phe Tyr Lys Asp
      100            105            110
Phe Thr Glu Lys Glu Gln Asn Ala Leu Ile Tyr Ala Tyr Lys Ser Gly
      115            120            125
Ala Asp Pro Lys Asn Ala Asp Ile Ile Ala Lys Tyr Trp Leu Ser Gln

```


Pro	Ser	Ser	Thr	Phe	Asp	Leu	Lys	Asn	His	Leu	Leu	Ile	Trp	Gly	Lys	
				280					285					290		
CAA	TTC	AGA	CAA	GTA	GCG	ATT	TGC	TAT	GGC	GGA	CAA	TTG	ATT	GCT	AAT	969
Gln	Phe	Arg	Gln	Val	Ala	Ile	Cys	Tyr	Gly	Gly	Gln	Leu	Ile	Ala	Asn	
			295					300					305			
AAG	AAT	AAG	ACT	TAT	AGG	ATA	GAT	TTG	ATA	AGT	TGC	AGA	CCT	GAT	AAT	1017
Lys	Asn	Lys	Thr	Tyr	Arg	Ile	Asp	Leu	Ile	Ser	Cys	Arg	Pro	Asp	Asn	
		310					315					320				
TTT	GGT	GAG	GTT	TGG	GCT	AAA	TTC	ACA	GGG	ATT	AAA	TTT	TCA	GTT	CCT	1065
Phe	Gly	Glu	Val	Trp	Ala	Lys	Phe	Thr	Gly	Ile	Lys	Phe	Ser	Val	Pro	
	325					330					335					
AGC	GAC	TTA	CCA	CAA	GCT	CTC	ACA	CGC	ATA	AAT	GAC	AGC	GTT	TAT	ACT	1113
Ser	Asp	Leu	Pro	Gln	Ala	Leu	Thr	Arg	Ile	Asn	Asp	Ser	Val	Tyr	Thr	
340					345					350					355	
TTT	CTC	TCT	AGG	AAT	AAA	GAG	GGT	ATC	GGT	CTT	AAT	AAA	CTC	GCT	CTC	1161
Phe	Leu	Ser	Arg	Asn	Lys	Glu	Gly	Ile	Gly	Leu	Asn	Lys	Leu	Ala	Leu	
			360						365					370		
AAT	AAA	GTC	GTT	AAG	ACA	GAA	TTA	AAA	GCG	ACT	TGT	ATG	CCC	TAT	GAT	1209
Asn	Lys	Val	Val	Lys	Thr	Glu	Leu	Lys	Ala	Thr	Cys	Met	Pro	Tyr	Asp	
		375						380					385			
TAC	TCT	AAA	TTG	GGT	ATA	GAG	ACT	ATT	GGC	GAG	GAC	ATT	AGA	AGC	AAT	1257
Tyr	Ser	Lys	Leu	Gly	Ile	Glu	Thr	Ile	Gly	Glu	Asp	Ile	Arg	Ser	Asn	
		390					395						400			
ATT	AAA	GCA	TTA	CAG	AAA	ATG	TCT	CGT	GGG	TAT	GGA	CAC	CCT	AAA	GAG	1305
Ile	Lys	Ala	Leu	Gln	Lys	Met	Ser	Arg	Gly	Tyr	Gly	His	Pro	Lys	Glu	
	405					410					415					
TTC	TTT	TTG	GAC	GCA	ATG	ATA	AAA	AAA	CAG	GAA	AAT	GCG	ATT	AAA	CGC	1353
Phe	Phe	Leu	Asp	Ala	Met	Ile	Lys	Lys	Gln	Glu	Asn	Ala	Ile	Lys	Arg	
420					425					430					435	
ATA	GAA	GCA	CGA	AAA	TGT	GCG	GTA	AGC	GAT	GAC	TTC	AAA	CAA	GGT	ATG	1401
Ile	Glu	Ala	Arg	Lys	Cys	Ala	Val	Ser	Asp	Asp	Phe	Lys	Gln	Gly	Met	
				440					445					450		
AAA	CGA	AAC	ATT	AAA	GTT	AAT	AAC	CTT	GTT	AAA	GCT	ATG	CGA	CAA	GGC	1449
Lys	Arg	Asn	Ile	Lys	Val	Asn	Asn	Leu	Val	Lys	Ala	Met	Arg	Gln	Gly	
			455					460					465			
AAA	AAA	GTG	AGT	AGG	ACA	TTG	ATT	GCT	AAA	GTG	CTT	GCT	AAC	ACC	ATA	1497
Lys	Lys	Val	Ser	Arg	Thr	Leu	Ile	Ala	Lys	Val	Leu	Ala	Asn	Thr	Ile	
		470					475						480			
GAC	ACC	GAT	GCG	GGT	TAT	TGC	TTC	ATT	TCG	CCG	ACA	GAT	TTA	GCG	ACA	1545
Asp	Thr	Asp	Ala	Gly	Tyr	Cys	Phe	Ile	Ser	Pro	Thr	Asp	Leu	Ala	Thr	
	485					490					495					

55					60					65						
ATG	AGC	CAC	AAG	ACT	ATT	AAA	GGC	TCT	ACA	ATT	GAG	AGT	TCT	AAT	CTT	297
Met	Ser	His	Lys	Thr	Ile	Lys	Gly	Ser	Thr	Ile	Glu	Ser	Ser	Asn	Leu	
		70					75					80				
ATC	AGC	ATT	TAT	AAA	AAG	ATT	GCG	AGC	GGA	CTA	CCT	TTT	GGG	ACT	ATC	345
Ile	Ser	Ile	Tyr	Lys	Lys	Ile	Ala	Ser	Gly	Leu	Pro	Phe	Gly	Thr	Ile	
		85				90					95					
TCG	GCG	TTT	AGA	CCT	TTT	AAA	GAC	GCT	TTT	TAT	AAA	GAC	TTT	ACC	GAA	393
Ser	Ala	Phe	Arg	Pro	Phe	Lys	Asp	Ala	Phe	Tyr	Lys	Asp	Phe	Thr	Glu	
100					105					110					115	
AAA	GAA	CAA	AAC	GCT	CTA	ATC	TAT	GCT	TAT	AAG	AGC	GGA	GCA	GAC	CCT	441
Lys	Glu	Gln	Asn	Ala	Leu	Ile	Tyr	Ala	Tyr	Lys	Ser	Gly	Ala	Asp	Pro	
				120					125					130		
AAA	AAT	GCG	GAC	ATA	ATA	GCC	AAA	TAT	TGG	TTA	AGT	CAA	TCT	GTG	GAT	489
Lys	Asn	Ala	Asp	Ile	Ile	Ala	Lys	Tyr	Trp	Leu	Ser	Gln	Ser	Val	Asp	
			135					140					145			
TTA	GAC	CCA	TAC	GAC	CCT	ATT	AAA	GTT	GTA	GAT	TTC	TTT	CAC	CCA	CAA	537
Leu	Asp	Pro	Tyr	Asp	Pro	Ile	Lys	Val	Val	Asp	Phe	Phe	His	Pro	Gln	
		150					155					160				
CCT	GAA	AAT	GGT	AAA	GAG	ACT	ACA	AAA	TTT	AAG	AAC	TAC	AAA	GAT	AGG	585
Pro	Glu	Asn	Gly	Lys	Glu	Thr	Thr	Lys	Phe	Lys	Asn	Tyr	Lys	Asp	Arg	
	165					170					175					
ATT	GAG	AAC	ATT	TAT	GCG	ACA	CTC	TAT	AAC	ACA	TTG	GGT	AGG	GGT	TAT	633
Ile	Glu	Asn	Ile	Tyr	Ala	Thr	Leu	Tyr	Asn	Thr	Leu	Gly	Arg	Gly	Tyr	
180					185					190					195	
GTG	GAT	AAA	TTT	TTT	AAA	AAA	GAA	GCC	ACA	ATG	AGG	GAC	TTT	ATG	TCT	681
Val	Asp	Lys	Phe	Phe	Lys	Lys	Glu	Ala	Thr	Met	Arg	Asp	Phe	Met	Ser	
				200					205					210		
AGC	GAT	AAA	TTT	GTT	GAG	AGA	TAC	CGC	TAC	ACT	AGA	AAA	GAA	AAT	ATG	729
Ser	Asp	Lys	Phe	Val	Glu	Arg	Tyr	Arg	Tyr	Thr	Arg	Lys	Glu	Asn	Met	
			215					220					225			
GCA	AGG	ACA	CAA	GCA	TTA	AAA	GAC	ATA	ATG	AAT	ATT	GAC	AGA	GAT	TTC	777
Ala	Arg	Thr	Gln	Ala	Leu	Lys	Asp	Ile	Met	Asn	Ile	Asp	Arg	Asp	Phe	
		230					235					240				
ATT	GGT	TAT	ATT	GAA	GTG	TTA	GGG	TAT	TGG	AAA	GAC	AAC	CCT	AAA	GAC	825
Ile	Gly	Tyr	Ile	Glu	Val	Leu	Gly	Tyr	Trp	Lys	Asp	Asn	Pro	Lys	Asp	
	245					250					255					
AAT	ATC	TTA	CCA	GAC	AAA	GAG	GTT	AGC	TTT	TTT	GTA	TTC	CAA	AAC	GAA	873
Asn	Ile	Leu	Pro	Asp	Lys	Glu	Val	Ser	Phe	Phe	Val	Phe	Gln	Asn	Glu	
260					265					270					275	
CCT	AGT	AGC	ACA	TTT	GAT	TTG	AAA	AAC	CAC	TTA	TTG	ATA	TGG	GGT	AAA	921

	195						200				205						
Glu	Leu	Thr	Leu	Phe	Asn	Ala	Thr	Ser	Cys	Ala	Thr	Tyr	Thr	Thr	Ala		
	210					215					220						
Ser	Leu	Glu	Cys	Ile	Leu	Asp	Ser	Ser	Phe	Lys	Asn	Asn	Ala	Tyr	Glu		
225	230					235					240						
Asn	Leu	Pro	Thr	Tyr	Leu	Thr	Lys	Ala	Gly	Ile	Lys	Val	Phe	Trp	Tyr		
	245					250					255						
Ser	Ala	Asn	Asp	Gly	Glu	Lys	Asn	Val	Lys	Val	Thr	Ser	Tyr	Leu	Lys		
	260					265					270						
Asn	Tyr	Glu	Leu	Ile	Gln	Lys	Cys	Pro	Asn	Cys	Glu	Ala	Ile	Ala	Pro		
	275					280					285						
Tyr	Asp	Glu	Ser	Leu	Leu	Tyr	Asn	Leu	Pro	Asp	Leu	Leu	Lys	Glu	His		
	290					295					300						
Ser	Asn	Glu	Asn	Val	Leu	Leu	Ile	Leu	His	Leu	Gln	Ala	Arg	Met	Ala		
305	310					315					320						
Gln	Thr	Thr	Thr	Thr	Lys	Cys	Leu										
	325																

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 49...1827
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

AAGCTCAAAG ATAAAGCGCT ACAATCTCGC TTAGAAAAAG GACACAAA													ATG	CTA	TTG	57
													Met	Leu	Leu	
													1			
AAT	TAC	GAT	TTT	TTA	GAA	TTT	GTT	GAT	GAG	CCG	AAA	AGA	AAC	ACT	TCT	105
Asn	Tyr	Asp	Phe	Leu	Glu	Phe	Val	Asp	Glu	Pro	Lys	Arg	Asn	Thr	Ser	
5		10					15									
TTG	ACA	GCA	TCT	ATT	GAT	AAA	GCG	TTA	GCG	GAC	AGG	AAG	TTA	GCT	AGA	153
Leu	Thr	Ala	Ser	Ile	Asp	Lys	Ala	Leu	Ala	Asp	Arg	Lys	Leu	Ala	Arg	
20	25					30			35							
CAA	AAT	AAA	CCT	AGC	GTT	AGG	GTG	CTT	GGT	AAG	GCG	ATG	CCC	TTA	AGC	201
Gln	Asn	Lys	Pro	Ser	Val	Arg	Val	Leu	Gly	Lys	Ala	Met	Pro	Leu	Ser	
40				45					50							
AAG	TTT	TTA	GAT	GCT	GTT	GGC	GAT	GAA	ATC	TCA	CGA	CTT	AAA	TAT	GAT	249
Lys	Phe	Leu	Asp	Ala	Val	Gly	Asp	Glu	Ile	Ser	Arg	Leu	Lys	Tyr	Asp	

TAT GAA TTG ATT CAA AAA TGC CCC AAT TGT GAA GCG ATC GCT CCT TAT 923
 Tyr Glu Leu Ile Gln Lys Cys Pro Asn Cys Glu Ala Ile Ala Pro Tyr
 275 280 285

 GAT GAA TCT TTA CTT TAT AAT TTG CCT GAC CTT TTA AAA GAA CAC TCT 971
 Asp Glu Ser Leu Leu Tyr Asn Leu Pro Asp Leu Leu Lys Glu His Ser
 290 295 300 305

 AAT GAA AAT GTC TTG CTC ATC TTA CAC TTG CAG GCT CGC ATG GCC CAA 1019
 Asn Glu Asn Val Leu Leu Ile Leu His Leu Gln Ala Arg Met Ala Gln
 310 315 320

 ACT ACG ACA ACA AAG TGC CTT TAAATTTTAG GGTGTTTAAG CCTTATTGCT CAAG 1074
 Thr Thr Thr Thr Lys Cys Leu
 325

 CGCTGATCTG TCTTCTT 1091

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

Met Met Val Val Val Leu Phe Cys Val Asn Gly Ala Leu Phe Leu Ala
 1 5 10 15
 Leu Gly Leu Ile Ser Ala Ser Leu Met Arg Trp Ser Ala Ile Val Phe
 20 25 30
 Ser Leu Leu Asn Ser Val Ala Phe Tyr Phe Ile Ser Ala Tyr Lys Val
 35 40 45
 Phe Leu Asn Lys Ser Met Met Gly Asn Val Leu Asn Thr Asn Thr His
 50 55 60
 Glu Val Leu Gly Phe Leu Ser Val Lys Leu Phe Val Phe Ile Val Val
 65 70 75 80
 Phe Gly Val Leu Pro Gly Tyr Val Ile Tyr Lys Ile Pro Leu Lys Asn
 85 90 95
 Ser Ser Lys Lys Ala Pro Phe Leu Ala Ile Leu Ala Leu Val Phe Ile
 100 105 110
 Phe Ile Ala Ser Ala Leu Ala Asn Thr Lys Asn Trp Leu Trp Phe Asp
 115 120 125
 Lys His Ala Lys Phe Ile Gly Gly Leu Ile Leu Pro Phe Ala Tyr Ser
 130 135 140
 Val Asn Ala Phe Arg Val Ser Ala Leu Lys Phe Phe Ala Pro Thr Ile
 145 150 155 160
 Lys Pro Leu Pro Leu Phe Ser Pro Asn His Ser His Ser Phe Val Val
 165 170 175
 Leu Val Ile Gly Glu Ser Ala Arg Lys His Asn Tyr Ala Leu Tyr Gly
 180 185 190
 Tyr Gln Lys Pro Thr Thr Pro Arg Leu Ser Lys Arg Leu Ala Asp Asn

Leu	Asn	Lys	Ser	Met	Met	Gly	Asn	Val	Leu	Asn	Thr	Asn	Thr	His	Glu	
50					55					60					65	
GTT	TTA	GGC	TTT	TTG	AGC	GTC	AAA	TTA	TTC	GTT	TTT	ATC	GTT	GTT	TTT	299
Val	Leu	Gly	Phe	Leu	Ser	Val	Lys	Leu	Phe	Val	Phe	Ile	Val	Val	Phe	
				70					75					80		
GGG	GTG	TTG	CCT	GGC	TAT	GTC	ATC	TAT	AAA	ATC	CCC	CTT	AAA	AAT	TCT	347
Gly	Val	Leu	Pro	Gly	Tyr	Val	Ile	Tyr	Lys	Ile	Pro	Leu	Lys	Asn	Ser	
			85					90					95			
TCT	AAA	AAA	GCG	CCC	TTT	TTA	GCG	ATC	TTG	GCG	TTA	GTG	TTT	ATC	TTT	395
Ser	Lys	Lys	Ala	Pro	Phe	Leu	Ala	Ile	Leu	Ala	Leu	Val	Phe	Ile	Phe	
		100					105					110				
ATC	GCT	AGC	GCT	TTA	GCT	AAC	ACT	AAA	AAT	TGG	CTG	TGG	TTT	GAC	AAG	443
Ile	Ala	Ser	Ala	Leu	Ala	Asn	Thr	Lys	Asn	Trp	Leu	Trp	Phe	Asp	Lys	
	115					120					125					
CAT	GCG	AAA	TTC	ATA	GGG	GGC	TTA	ATT	TTG	CCC	TTC	GCT	TAT	AGC	GTG	491
His	Ala	Lys	Phe	Ile	Gly	Gly	Leu	Ile	Leu	Pro	Phe	Ala	Tyr	Ser	Val	
130					135					140					145	
AAC	GCT	TTT	AGA	GTG	AGC	GCT	CTC	AAA	TTT	TTC	GCC	CCC	ACC	ATC	AAG	539
Asn	Ala	Phe	Arg	Val	Ser	Ala	Leu	Lys	Phe	Phe	Ala	Pro	Thr	Ile	Lys	
				150					155					160		
CCG	CTC	CCT	CTT	TTT	TCA	CCC	AAT	CAT	TCC	CAT	TCG	TTT	GTG	GTG	CTA	587
Pro	Leu	Pro	Leu	Phe	Ser	Pro	Asn	His	Ser	His	Ser	Phe	Val	Val	Leu	
			165					170					175			
GTC	ATT	GGC	GAA	AGC	GCT	AGG	AAA	CAT	AAT	TAC	GCC	CTT	TAT	GGC	TAT	635
Val	Ile	Gly	Glu	Ser	Ala	Arg	Lys	His	Asn	Tyr	Ala	Leu	Tyr	Gly	Tyr	
		180					185					190				
CAA	AAA	CCC	ACC	ACC	CCA	AGA	CTA	AGC	AAG	CGT	TTA	GCC	GAT	AAT	GAA	683
Gln	Lys	Pro	Thr	Thr	Pro	Arg	Leu	Ser	Lys	Arg	Leu	Ala	Asp	Asn	Glu	
	195					200					205					
CTC	ACT	CTT	TTC	AAC	GCC	ACT	TCT	TGC	GCC	ACT	TAC	ACG	ACA	GCG	AGT	731
Leu	Thr	Leu	Phe	Asn	Ala	Thr	Ser	Cys	Ala	Thr	Tyr	Thr	Thr	Ala	Ser	
210					215					220					225	
TTG	GAA	TGC	ATT	TTA	GAT	TCT	TCT	TTT	AAA	AAC	AAC	GCT	TAT	GAA	AAT	779
Leu	Glu	Cys	Ile	Leu	Asp	Ser	Ser	Phe	Lys	Asn	Asn	Ala	Tyr	Glu	Asn	
				230					235					240		
TTG	CCA	ACT	TAC	TTG	ACT	AAA	GCC	GGT	ATC	AAA	GTC	TTT	TGG	TAT	AGC	827
Leu	Pro	Thr	Tyr	Leu	Thr	Lys	Ala	Gly	Ile	Lys	Val	Phe	Trp	Tyr	Ser	
			245					250					255			
GCG	AAC	GAC	GGC	GAA	AAG	AAT	GTT	AAG	GTT	ACA	AGC	TAT	CTT	AAA	AAC	875
Ala	Asn	Asp	Gly	Glu	Lys	Asn	Val	Lys	Val	Thr	Ser	Tyr	Leu	Lys	Asn	
		260					265					270				

```

Leu Ser Val Ala Ile Pro Leu Ile Gln Arg Asp Ala Val Gly Leu Phe
65          70          75          80
Gln Val Ala Asn Ala Ser Ile Ala Thr Thr Leu Leu Thr His Thr Thr
          85          90          95
Lys Arg Ala Leu Asn His Val Thr Ile Asn Asp Gln Arg Leu Gly Glu
100        105        110
Arg Pro Tyr Gly Gly Asn Phe Asn Met Pro Ser Gly His Ser Ser Met
115        120        125
Val Gly Leu Ala Val Ala Phe Leu Met Arg Arg Tyr Ser Phe Lys Lys
130        135        140
Tyr Phe Trp Leu Leu Pro Leu Val Pro Leu Thr Met Leu Ala Arg Ile
145        150        155        160
Tyr Leu Asp Met His Thr Ile Gly Ala Val Leu Thr Gly Leu Gly Val
165        170        175
Gly Met Leu Cys Val Xaa Phe Leu Gln Ala Pro Lys Ser Leu Asn Gln
180        185        190
Lys Leu

```

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 57...1040
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

```

ATTTCCTTT GTTCGTTTAT GTTTATAAAG AAAGCAACCA GGTCAGTTTT ATCGCC ATG      59
                                     Met
                                     1

ATG GTT GTG GTG CTT TTT TGC GTT AAT GGC GCT CTT TTT TTG GCG TTA      107
Met Val Val Val Leu Phe Cys Val Asn Gly Ala Leu Phe Leu Ala Leu
          5          10          15

GGC TTG ATC TCT GCT TCT TTG ATG CGT TGG AGT GCG ATA GTT TTT AGC      155
Gly Leu Ile Ser Ala Ser Leu Met Arg Trp Ser Ala Ile Val Phe Ser
20          25          30

CTG CTC AAT TCC GTT GCT TTC TAT TTC ATT AGC GCT TAT AAG GTG TTT      203
Leu Leu Asn Ser Val Ala Phe Tyr Phe Ile Ser Ala Tyr Lys Val Phe
35          40          45

TTA AAT AAG AGC ATG ATG GGT AAT GTC TTA AAC ACC AAC ACG CAT GAA      251

```

55	60	65	70	
TTA ATC CAA AGA GAT GCG GTA GGG CTT TTT CAA GTC GCT AAC GCT TCT				294
Leu Ile Gln Arg Asp Ala Val Gly Leu Phe Gln Val Ala Asn Ala Ser	75	80	85	
ATC GCT ACA ACC CTT CTC ACG CAC ACC ACC AAA AGA GCC TTA AAC CAT				342
Ile Ala Thr Thr Leu Leu Thr His Thr Thr Lys Arg Ala Leu Asn His	90	95	100	
GTA ACA ATC AAC GAT CAG CGT TTG GGC GAG CGC CCT TAT GGA GGT AAT				390
Val Thr Ile Asn Asp Gln Arg Leu Gly Glu Arg Pro Tyr Gly Gly Asn	105	110	115	
TTC AAC ATG CCA AGC GGG CAT TCG TCT ATG GTG GGT TTG GCG GTG GCG				438
Phe Asn Met Pro Ser Gly His Ser Ser Met Val Gly Leu Ala Val Ala	120	125	130	
TTT TTA ATG CGC CGC TAT TCT TTT AAA AAA TAC TTT TGG CTC TTG CCC				486
Phe Leu Met Arg Arg Tyr Ser Phe Lys Lys Tyr Phe Trp Leu Leu Pro	135	140	145	150
CTA GTC CCT TTG ACC ATG CTC GCT CGC ATT TAT TTA GAC ATG CAC ACC				534
Leu Val Pro Leu Thr Met Leu Ala Arg Ile Tyr Leu Asp Met His Thr	155	160	165	
ATT GGC GCG GTG CTG ACC GGG CTT GGC GTT GGA ATG TTG TGC GTA ASC				582
Ile Gly Ala Val Leu Thr Gly Leu Gly Val Gly Met Leu Cys Val Xaa	170	175	180	
TTT TTA CAA GCC CCA AAA AGC CTT AAT CAA AAG CTT TAGTTTCTGT TTTTA				633
Phe Leu Gln Ala Pro Lys Ser Leu Asn Gln Lys Leu	185	190		

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

Met	Lys	Lys	Phe	Leu	Phe	Lys	Gln	Lys	Phe	Cys	Glu	Ser	Leu	Pro	Lys
1				5					10					15	
Ser	Phe	Ser	Lys	Thr	Leu	Leu	Ala	Leu	Ser	Leu	Gly	Leu	Ile	Leu	Leu
			20					25					30		
Gly	Ile	Phe	Ala	Pro	Phe	Pro	Lys	Val	Pro	Lys	Gln	Pro	Ser	Val	Pro
		35					40				45				
Leu	Met	Phe	His	Phe	Thr	Glu	His	Tyr	Ala	Arg	Phe	Ile	Pro	Thr	Ile
	50					55					60				

BNSDOCID: <WO 9843478A1 I >


```

AAC AAT CCT TTG ACT TCA AAA ATC CCT ATC GTG GTC AAT TCT TCT ATG      866
Asn Asn Pro Leu Thr Ser Lys Ile Pro Ile Val Val Asn Ser Ser Met
      270                      275                      280

AGC GGG AGT TCT AAT GAA GAC ATG GCC AGG AGT TTG AAG GCC GAT GAT      914
Ser Gly Ser Ser Asn Glu Asp Met Ala Arg Ser Leu Lys Ala Asp Asp
285                      290                      295                      300

TTC ATT TCC AAG TCT AAC CCC AAA GAC ATC CAG CGA GTG GTT AAG CAA      962
Phe Ile Ser Lys Ser Asn Pro Lys Asp Ile Gln Arg Val Val Lys Gln
      305                      310                      315

TTT TTG GAA TTA GCA TGAAAAATA CAGCACTATC CCCACCCCTT GCTACGTGTT A 1018
Phe Leu Glu Leu Ala
      320

GAGAGCGAAC GCTTAGAAAA AAACGC                                     1044

```

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

```

Met Ala Asp Ser Leu Ala Gly Ile Asp Gln Val Thr Ser Leu His Lys
  1           5           10           15
Asn Asn Glu Leu Gln Leu Leu Cys Phe Arg Leu Gly Lys Asn Lys Asp
      20           25           30
Leu Tyr Ala Val Asn Val Phe Lys Ile Arg Glu Val Val Lys Tyr His
      35           40           45
Gly Asn Leu Thr Ile Ile Ser His Glu Asn Asn Ser Leu Val Glu Gly
      50           55           60
Leu Ile Ile Ile Arg Glu Leu Thr Ile Pro Leu Ile Asp Met Lys Lys
      65           70           75           80
Trp Phe Tyr Tyr Asp Ser Gln Asn Lys Asn Lys Asp Leu Arg Pro Tyr
      85           90           95
Arg Ile Glu Lys Glu Lys Gly Glu Asp Asp Ile Val Met Ile Cys Glu
      100          105          110
Phe Ser Arg Trp Thr Ile Gly Val Arg Ile Tyr Glu Ala Asp Arg Ile
      115          120          125
Leu Ser Lys Lys Trp Thr Glu Met Glu Gln Ser Ala Gly Leu Gly Gly
      130          135          140
Ser Ala Gly Asn Asn Lys Leu Val Ser Arg Thr Arg Tyr Phe Asp Gly
      145          150          155          160
Arg Leu Val Gln Val Val Asp Ile Glu Lys Met Leu Ile Asp Val Phe
      165          170          175
Pro Trp Ile Glu Asp Glu Lys His Asn Asp Leu Glu Thr Leu Ser Lys
      180          185          190
Ile His Ser Asn Gln Cys Val Leu Leu Ala Asp Asp Ser Pro Ser Val

```

GTG AAA TAC CAT GGC AAT CTC ACC ATC ATT AGC CAC GAA AAC AAT TCG	194
Val Lys Tyr His Gly Asn Leu Thr Ile Ile Ser His Glu Asn Asn Ser	
45 50 55 60	
CTC GTT GAG GGG CTA ATC ATT ATA AGA GAA CTC ACC ATT CCC TTG ATT	242
Leu Val Glu Gly Leu Ile Ile Ile Arg Glu Leu Thr Ile Pro Leu Ile	
65 70 75	
GAT ATG AAA AAA TGG TTT TAT TAT GAC AGC CAA AAC AAA AAC AAG GAT	290
Asp Met Lys Lys Trp Phe Tyr Tyr Asp Ser Gln Asn Lys Asn Lys Asp	
80 85 90	
TTA CGC CCT TAT AGG ATA GAA AAA GAA AAA GGC GAA GAT GAT ATT GTT	338
Leu Arg Pro Tyr Arg Ile Glu Lys Glu Lys Gly Glu Asp Asp Ile Val	
95 100 105	
ATG ATT TGT GAG TTT TCT CGC TGG ACT ATA GGG GTT AGG ATC TAT GAA	386
Met Ile Cys Glu Phe Ser Arg Trp Thr Ile Gly Val Arg Ile Tyr Glu	
110 115 120	
GCG GAT AGG ATT TTG AGC AAG AAA TGG ACT GAA ATG GAG CAA AGC GCT	434
Ala Asp Arg Ile Leu Ser Lys Lys Trp Thr Glu Met Glu Gln Ser Ala	
125 130 135 140	
GGG CTA GGG GGA TCT GCA GGC AAT AAC AAA CTC GTG AGC CGC ACG CGC	482
Gly Leu Gly Gly Ser Ala Gly Asn Asn Lys Leu Val Ser Arg Thr Arg	
145 150 155	
TAT TTT GAT GGG CGC TTG GTG CAA GTG GTG GAT ATT GAA AAA ATG CTT	530
Tyr Phe Asp Gly Arg Leu Val Gln Val Val Asp Ile Glu Lys Met Leu	
160 165 170	
ATA GAC GTG TTC CCT TGG ATT GAA GAT GAA AAA CAC AAC GAT TTA GAG	578
Ile Asp Val Phe Pro Trp Ile Glu Asp Glu Lys His Asn Asp Leu Glu	
175 180 185	
ACG CTT TCT AAA ATC CAT TCT AAC CAA TGC GTT TTG CTT GCT GAT GAC	626
Thr Leu Ser Lys Ile His Ser Asn Gln Cys Val Leu Leu Ala Asp Asp	
190 195 200	
TCC CCA AGC GTT TTG AAA ACC ATG CAA ATG ATT TTA GAC AAG CTG GGC	674
Ser Pro Ser Val Leu Lys Thr Met Gln Met Ile Leu Asp Lys Leu Gly	
205 210 215 220	
GTC AAG CAT ATA GAT TTT ATC AAT GGT AAA ACC TTA CTA GAG CAT TTA	722
Val Lys His Ile Asp Phe Ile Asn Gly Lys Thr Leu Leu Glu His Leu	
225 230 235	
TTC AAC CCC ACA ACC GAT GTG AGT AAT ATT GGC CTG ATT ATT ACC GAT	770
Phe Asn Pro Thr Thr Asp Val Ser Asn Ile Gly Leu Ile Ile Thr Asp	
240 245 250	
TTG GAA ATG CCA GAG GCG AGC GGT TTT GAA GTG ATC AAG CAG GTT AAA	818
Leu Glu Met Pro Glu Ala Ser Gly Phe Glu Val Ile Lys Gln Val Lys	
255 260 265	

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

```

Met Ile Ile Leu Ser Ala Ser Val Lys Asn Leu Arg Glu Ile Ser Val
 1             5             10             15
Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Tyr Leu Ile Ser Val
      20             25             30
Phe Ala Pro Phe Ile Leu Leu Pro Trp Ile Asp Leu Leu Ser Ala Phe
      35             40             45
Leu Leu Tyr Leu Gly Phe Leu Ala Leu Phe Ser Val Leu Glu Phe Phe
 50             55             60
Asp Glu Asp Ile Ala Asp Ile Ile Val Ala Lys Ser Lys Ile Lys Thr
65             70             75             80
Lys Thr Lys Cys Tyr Arg Ala
      85

```

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 15...977
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

```

ATTAAGGGGA AGTC ATG GCT GAT AGT TTA GCG GGC ATT GAT CAA GTT ACG      50
      Met Ala Asp Ser Leu Ala Gly Ile Asp Gln Val Thr
        1             5             10

AGT TTG CAT AAA AAT AAC GAG TTA CAA TTG TTG TGT TTC AGG CTG GGT      98
Ser Leu His Lys Asn Asn Glu Leu Gln Leu Leu Cys Phe Arg Leu Gly
      15             20             25

AAA AAC AAG GAT TTG TAT GCG GTC AAT GTT TTT AAG ATC CGT GAA GTG      146
Lys Asn Lys Asp Leu Tyr Ala Val Asn Val Phe Lys Ile Arg Glu Val
      30             35             40

```

```

Asn His Leu Gln Tyr Ser Phe Glu Lys Ile Gln Asn Leu Leu Glu Glu
      245                      250                      255
Asp Ala Leu Gln Ala Lys Glu His Ala Asn Leu Ser Tyr Val Tyr Gln
      260                      265                      270
Ile Val Glu
      275

```

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...300
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

```

AGCTCCGAGT TTAGCGAATT GGTttATGGG AATTTTTTA ATG ATT ATC CTG TCA      54
                               Met Ile Ile Leu Ser
                               1           5

GCG AGC GTG AAG AAT TTG CGT GAA ATT TCG GTT AAA GAA AAA TTT TTA      102
Ala Ser Val Lys Asn Leu Arg Glu Ile Ser Val Lys Glu Lys Phe Leu
      10                      15                      20

TGG CTG AAC GCT AAG TCT TAT TTG ATT TCT GTT TTT GCG CCT TTT ATC      150
Trp Leu Asn Ala Lys Ser Tyr Leu Ile Ser Val Phe Ala Pro Phe Ile
      25                      30                      35

TTG CTC CCT TGG ATT GAT TTG TTG AGC GCT TTT TTA TTG TAT TTA GGG      198
Leu Leu Pro Trp Ile Asp Leu Leu Ser Ala Phe Leu Leu Tyr Leu Gly
      40                      45                      50

TTT TTA GCG CTC TTT AGC GTG CTG GAA TTT TTT GAT GAA GAC ATT GCA      246
Phe Leu Ala Leu Phe Ser Val Leu Glu Phe Phe Asp Glu Asp Ile Ala
      55                      60                      65

GAT ATT ATC GTG GCT AAA AGC AAA ATA AAG ACT AAA ACC AAA TGT TAT      294
Asp Ile Ile Val Ala Lys Ser Lys Ile Lys Thr Lys Thr Lys Cys Tyr
      70                      75                      80                      85

AGA GCG TAGAATGTTA GAAAAGCTTT TAAGCGCTAT CAAACAA      337
Arg Ala

```

```

Ile Val Ala Tyr Asn His Leu Gln Tyr Ser Phe Glu Lys Ile Gln Asn
      240                      245                      250

CTC TTA GAA GAG GAC GCC CTA CAA GCC AAA GAA CAC GCT AAT CTT TCT      817
Leu Leu Glu Glu Asp Ala Leu Gln Ala Lys Glu His Ala Asn Leu Ser
      255                      260                      265

TAT GTC TAT CAA ATC GTA GAA TAGTAAGGCT TTTACTACTCT TTGGCTTTGC TTTT      872
Tyr Val Tyr Gln Ile Val Glu
      270                      275

TTACCCTTT      881

```

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

```

Met Gln Glu Phe Leu Gly Phe Gly Val Val Gly Asn Phe Ala Gly His
 1           5           10           15
Leu Glu Gln Ala Gly Glu Ser His Ser Phe Ile Asn Met Lys Ser Glu
      20           25           30
Glu Lys Asp Ala Pro Lys Gly Leu Phe Pro Phe Tyr Ile Pro Tyr Glu
      35           40           45
Asn Cys Tyr Leu Gly Arg Cys Cys Ile Asp Asn His Lys Ile Ile Leu
      50           55           60
Pro Ser Asp Leu Asp Leu Arg Val Gln Ala Glu Pro Glu Ile Ala Leu
      65           70           75           80
Glu Cys Asp Val Lys Tyr Asp Glu Lys His Leu Val Ala Lys Leu Val
      85           90           95
Pro Asn Phe Phe Met Ala Phe Asn Asp Ala Ser Val Arg Asn Leu Asp
      100          105          110
Ala Ala Lys Leu Ser Gln Lys Lys Asn Phe Ser Pro Ala Ser Lys Gly
      115          120          125
Ile Gly Gln Lys Leu Pro Ile Asp Arg Phe Val Tyr Gly Gly Val Cys
      130          135          140
Asn Asn Phe Ser Ile Ala Ser Phe Leu Lys Tyr Asn Asn Val Trp His
      145          150          155          160
Ile Tyr Gly Glu Asn Ser Lys Leu Leu Lys Tyr Glu Phe Phe Tyr Gln
      165          170          175
Lys Leu Leu Asp Trp Ile Lys Asp Gln Leu Asn His Gln Gln Asp Gly
      180          185          190
Asp Ser Leu Glu Ala Leu Arg Pro Phe Leu Glu Arg His Asn Phe Pro
      195          200          205
Thr Lys Met Ile Phe Ala Ile Gly Ala Thr Pro Tyr Met Pro Phe Ala
      210          215          220
Gln Glu His Phe Leu Gln Lys Gly Asp Glu Val Val Ile Val Ala Tyr
      225          230          235          240

```

15	20	25	
ATG AAA AGC GAA GAA AAG GAC GCC CCT AAG GGG CTA TTC CCT TTT TAT			145
Met Lys Ser Glu Glu Lys Asp Ala Pro Lys Gly Leu Phe Pro Phe Tyr			
30	35	40	
ATC CCC TAT GAA AAT TGT TAT TTG GGG CGT TGT TGC ATT GAT AAC CAT			193
Ile Pro Tyr Glu Asn Cys Tyr Leu Gly Arg Cys Cys Ile Asp Asn His			
45	50	55	60
AAG ATT ATT TTG CCT AGT GAT CTA GAT TTA AGG GTG CAA GCA GAG CCA			241
Lys Ile Ile Leu Pro Ser Asp Leu Asp Leu Arg Val Gln Ala Glu Pro			
	65	70	75
GAA ATC GCT TTA GAA TGC GAT GTT AAA TAC GAT GAA AAA CAT TTG GTT			289
Glu Ile Ala Leu Glu Cys Asp Val Lys Tyr Asp Glu Lys His Leu Val			
	80	85	90
GCA AAG CTC GTG CCT AAT TTT TTC ATG GCG TTT AAT GAC GCT TCT GTG			337
Ala Lys Leu Val Pro Asn Phe Phe Met Ala Phe Asn Asp Ala Ser Val			
	95	100	105
CGC AAT TTA GAC GCC GCA AAA CTC TCC CAA AAA AAG AAT TTT TCA CCG			385
Arg Asn Leu Asp Ala Ala Lys Leu Ser Gln Lys Lys Asn Phe Ser Pro			
	110	115	120
GCT TCT AAA GGT ATA GGG CAG AAA TTG CCC ATT GAC AGG TTT GTT TAT			433
Ala Ser Lys Gly Ile Gly Gln Lys Leu Pro Ile Asp Arg Phe Val Tyr			
125	130	135	140
GGG GGG GTG TGT AAC AAT TTC TCT ATC GCG TCT TTT TTG AAA TAC AAT			481
Gly Gly Val Cys Asn Asn Phe Ser Ile Ala Ser Phe Leu Lys Tyr Asn			
	145	150	155
AAT GTT TGG CAC ATT TAT GGG GAA AAC AGC AAA TTG CTC AAA TAC GAG			529
Asn Val Trp His Ile Tyr Gly Glu Asn Ser Lys Leu Leu Lys Tyr Glu			
	160	165	170
TTT TTT TAT CAA AAG CTT TTA GAT TGG ATT AAA GAC CAA TTA AAC CAC			577
Phe Phe Tyr Gln Lys Leu Leu Asp Trp Ile Lys Asp Gln Leu Asn His			
	175	180	185
CAA CAA GAT GGC GAC TCT TTA GAG GCT CTA AGA CCT TTT TTA GAG CGC			625
Gln Gln Asp Gly Asp Ser Leu Glu Ala Leu Arg Pro Phe Leu Glu Arg			
	190	195	200
CAT AAT TTC CCC ACT AAA ATG ATT TTT GCA ATA GGG GCT ACC CCT TAT			673
His Asn Phe Pro Thr Lys Met Ile Phe Ala Ile Gly Ala Thr Pro Tyr			
205	210	215	220
ATG CCT TTT GCG CAA GAG CAT TTT TTG CAA AAA GGC GAT GAG GTG GTG			721
Met Pro Phe Ala Gln Glu His Phe Leu Gln Lys Gly Asp Glu Val Val			
	225	230	235
ATC GTT GCT TAC AAC CAT TTA CAA TAC AGT TTT GAA AAG ATT CAA AAC			769

```

          325          330          335
His Ser His Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile
          340          345          350
Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu
          355          360          365
Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser
          370          375          380
Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser
385          390          395          400
Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala
          405          410          415
Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp
          420          425          430
Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu
          435          440          445
Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn
          450          455          460
Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly
465          470          475          480
Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val
          485          490          495
Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu
          500          505          510
Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Ala Pro
          515          520          525
Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly
          530          535          540
Met Met
545

```

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 14...838
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

```

CTAGGAGGTT TGC ATG CAA GAG TTT TTA GGT TTT GGT GTG GTG GGG AAT      49
      Met Gln Glu Phe Leu Gly Phe Gly Val Val Gly Asn
          1              5              10

TTT GCA GGG CAT TTG GAG CAA GCA GGA GAG AGT CAT AGT TTT ATT AAC      97
Phe Ala Gly His Leu Glu Gln Ala Gly Glu Ser His Ser Phe Ile Asn

```

AAAATCCCCT AAAATCCCC CTTTCTAAAA TCTC

1724

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

```

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe
 1           5           10           15
Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro
          20           25           30
Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile
          35           40           45
Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro
          50           55           60
Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr
65           70           75           80
Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr
          85           90           95
Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro
          100          105          110
Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn
          115          120          125
Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr
          130          135          140
Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu
145          150          155          160
Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val
          165          170          175
Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met
          180          185          190
Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu
          195          200          205
Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys
          210          215          220
Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met
225          230          235          240
Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu
          245          250          255
Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile
          260          265          270
Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu
          275          280          285
Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu
          290          295          300
Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly
305          310          315          320
Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly

```


GTA GAT GGC AAA GGC CAT AGC CAT GAT GTC AAA GAC AGA GTC GCG CAA	1059
Val Asp Gly Lys Gly His Ser His Asp Val Lys Asp Arg Val Ala Gln	
335 340 345	
ATC AAA ACC CAA ATT GCA AGC ACG ACA AGC GAT TAT GAC AAA GAA AAA	1107
Ile Lys Thr Gln Ile Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys	
350 355 360	
TTG CAA GAA AGG TTG GCT AAA CTC TCT GGC GGT GTG GCT GTG ATT AAA	1155
Leu Gln Glu Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys	
365 370 375	
GTG GGC GCT GCG AGT GAA GTG GAA ATG AAA GAG AAA AAA GAC CGG GTT	1203
Val Gly Ala Ala Ser Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val	
380 385 390 395	
GAT GAT GCG TTG AGC GCG ACT AAA GCG GCT GTT GAA GAA GGT ATT GTG	1251
Asp Asp Ala Leu Ser Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val	
400 405 410	
ATT GGC GGC GGT GCG GCT CTC ATT CGC GCG GCT CAA AAA GTG CAT TTG	1299
Ile Gly Gly Gly Ala Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu	
415 420 425	
AAT TTG CAC GAT GAT GAA AAA GTG GGC TAT GAA ATC ATC ATG CGC GCC	1347
Asn Leu His Asp Asp Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala	
430 435 440	
ATT AAA GCC CCA TTA GCT CAA ATC GCT ATC AAT GCC GGT TAT GAT GGC	1395
Ile Lys Ala Pro Leu Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly	
445 450 455	
GGT GTG GTC GTG AAT GAA GTA GAA AAA CAC GAA GGG CAT TTT GGT TTT	1443
Gly Val Val Val Asn Glu Val Glu Lys His Glu Gly His Phe Gly Phe	
460 465 470 475	
AAC GCT AGC AAT GGC AAG TAT GTG GAT ATG TTT AAA GAA GGC ATT ATT	1491
Asn Ala Ser Asn Gly Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile	
480 485 490	
GAC CCC TTA AAA GTA GAA AGG ATC GCT TTA CAA AAT GCG GTT TCG GTT	1539
Asp Pro Leu Lys Val Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val	
495 500 505	
TCA AGC CTG CTT TTA ACC ACA GAA GCC ACC GTG CAT GAA ATC AAA GAA	1587
Ser Ser Leu Leu Leu Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu	
510 515 520	
GAA AAA GCG GCC CCA GCA ATG CCT GAT ATG GGT GGC ATG GGC GGT ATG	1635
Glu Lys Ala Ala Pro Ala Met Pro Asp Met Gly Gly Met Gly Gly Met	
525 530 535	
GGA GGC ATG GGT GGC ATG ATG TAAGCCCCCT TGCTTTT TAG TATCATCTGC TTTT	1690
Gly Gly Met Gly Gly Met Met	
540 545	

Ala Gly Ala Asn Pro Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala	
110 115 120	
GAA GCC ATT ATT AAT GAG CTT AAA AAA GCG AGC AAA AAA GTG GGC GGT	435
Glu Ala Ile Ile Asn Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly	
125 130 135	
AAA GAA GAA ATC ACC CAA GTG GCG ACC ATT TCT GCA AAC TCC GAT CAC	483
Lys Glu Glu Ile Thr Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His	
140 145 150 155	
AAT ATC GGG AAA CTC ATC GCT GAC GCT ATG GAA AAA GTG GGT AAA GAC	531
Asn Ile Gly Lys Leu Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp	
160 165 170	
GGC GTG ATC ACC GTT GAA GAA GCT AAG GGC ATT GAA GAT GAA CTA GAT	579
Gly Val Ile Thr Val Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp	
175 180 185	
GTT GTA GAA GGC ATG CAA TTT GAT AGA GGC TAC CTC TCC CCT TAT TTT	627
Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe	
190 195 200	
GTA ACA AAC GCT GAG AAA ATG ACC GCT CAA TTG GAT AAC GCT TAC ATC	675
Val Thr Asn Ala Glu Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile	
205 210 215	
CTT TTA ACG GAT AAA AAA ATC TCT AGC ATG AAA GAC ATT CTC CCG CTA	723
Leu Leu Thr Asp Lys Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu	
220 225 230 235	
CTA GAA AAA ACC ATG AAA GAG GGC AAA CCG CTT TTA ATC ATC GCT GAA	771
Leu Glu Lys Thr Met Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu	
240 245 250	
GAC ATT GAG GGC GAA GCT TTA ACG ACT CTA GTG GTG AAT AAA TTA AGA	819
Asp Ile Glu Gly Glu Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg	
255 260 265	
GGC GTG TTG AAT ATC GCA GCG GTT AAA GCT CCA GGC TTT GGG GAC AGA	867
Gly Val Leu Asn Ile Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg	
270 275 280	
AGA AAA GAA ATG CTC AAA GAC ATC GCT ATT TTA ACC GGC GGT CAA GTT	915
Arg Lys Glu Met Leu Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val	
285 290 295	
ATT AGC GAA GAA TTG GGC TTG AGT CTA GAA AAC GCT GAA GTG GAG TTT	963
Ile Ser Glu Glu Leu Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe	
300 305 310 315	
TTA GGC AAA GCC GGA AGG ATT GTG ATT GAC AAA GAC AAC ACC ACG ATC	1011
Leu Gly Lys Ala Gly Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile	
320 325 330	

```

Ser Phe Gly Val Leu Thr Thr Asp Asn Ile Glu Gln Ala Ile Glu Arg
      115                      120                      125
Ala Gly Ser Lys Ala Gly Asn Lys Gly Phe Glu Ala Met Ser Thr Leu
      130                      135                      140
Ile Glu Leu Leu Ser Leu Cys Gln Thr Leu Lys Gly
145                      150                      155

```

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1656
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

```

TATTATTAAG GATACAAA ATG GCA AAA GAA ATC AAA TTT TCA GAT AGC GCG      51
      Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala
      1                      5                      10

AGA AAC CTT TTA TTT GAA GGC GTG AGA CAA CTC CAT GAC GCT GTT AAA      99
Arg Asn Leu Leu Phe Glu Gly Val Arg Gln Leu His Asp Ala Val Lys
      15                      20                      25

GTA ACC ATG GGG CCA AGA GGC AGG AAC GTG TTG ATC CAA AAA AGC TAT      147
Val Thr Met Gly Pro Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr
      30                      35                      40

GGC GCT CCA AGC ATC ACT AAA GAT GGC GTG AGC GTG GCT AAA GAG ATT      195
Gly Ala Pro Ser Ile Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile
      45                      50                      55

GAA TTA AGT TGC CCG GTA GCT AAC ATG GGC GCT CAA CTC GTT AAA GAA      243
Glu Leu Ser Cys Pro Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu
      60                      65                      70                      75

GTA GCG AGC AAA ACC GCT GAT GCT GCC GGC GAT GGC ACG ACC ACA GCG      291
Val Ala Ser Lys Thr Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala
      80                      85                      90

ACC GTG CTG GCT TAT AGC ATT TTT AAA GAA GGT TTG AGG AAC ATC ACG      339
Thr Val Leu Ala Tyr Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr
      95                      100                      105

GCT GGG GCT AAC CCT ATT GAA GTG AAA CGA GGC ATG GAT AAA GCC GCT      387

```

```

TTG CCT TTT ATT TTA GAC AAA TTA TTA GAG AGC GAA AAA TAC GAT GGC      243
Leu Pro Phe Ile Leu Asp Lys Leu Leu Glu Ser Glu Lys Tyr Asp Gly
60                      65                      70                      75

GTG TGC GTT TTG GGA GCG ATC ATT AGA GGG GGG ACT CCG CAT TTT GAT      291
Val Cys Val Leu Gly Ala Ile Ile Arg Gly Gly Thr Pro His Phe Asp
80                      85                      90

TAT GTG AGC GCG GAA GCG ACT AAG GGT ATT GCC CAT GCG ATG CTT AAA      339
Tyr Val Ser Ala Glu Ala Thr Lys Gly Ile Ala His Ala Met Leu Lys
95                      100                      105

TAC AGC ATG CCG GTA AGC TTT GGC GTG CTG ACC ACG GAC AAT ATT GAA      387
Tyr Ser Met Pro Val Ser Phe Gly Val Leu Thr Thr Asp Asn Ile Glu
110                      115                      120

CAA GCG ATT GAA AGA GCG GGC AGT AAA GCC GGC AAT AAG GGC TTT GAA      435
Gln Ala Ile Glu Arg Ala Gly Ser Lys Ala Gly Asn Lys Gly Phe Glu
125                      130                      135

GCG ATG AGC ACC CTC ATT GAA TTG TTG AGC TTG TGC CAA ACT CTC AAG      483
Ala Met Ser Thr Leu Ile Glu Leu Leu Ser Leu Cys Gln Thr Leu Lys
140                      145                      150                      155

GGT TAAAATGGCG ACACGAACTC AAGCCAGGGG GGCTGTG      523
Gly

```

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

```

Met Gln Ile Ile Glu Gly Lys Leu Gln Leu Gln Gly Asn Glu Arg Val
1      5      10      15
Ala Ile Leu Thr Ser Arg Phe Asn His Ile Ile Thr Asp Arg Leu Gln
20     25     30
Glu Gly Ala Met Asp Cys Phe Lys Arg His Gly Gly Asp Glu Asp Leu
35     40     45
Leu Asp Ile Val Leu Val Pro Gly Ala Tyr Glu Leu Pro Phe Ile Leu
50     55     60
Asp Lys Leu Leu Glu Ser Glu Lys Tyr Asp Gly Val Cys Val Leu Gly
65     70     75     80
Ala Ile Ile Arg Gly Gly Thr Pro His Phe Asp Tyr Val Ser Ala Glu
85     90     95
Ala Thr Lys Gly Ile Ala His Ala Met Leu Lys Tyr Ser Met Pro Val
100    105    110

```

```

1           5           10           15
Asp Tyr Ala Lys Tyr Pro Arg Arg Ile Ala Glu Glu Leu Gln His Tyr
20           25           30
Gly Gly Asn Ser Phe Ala Asn Phe Arg Asp Glu Gly Val Leu Tyr
35           40           45
Lys Glu Ile Leu Cys Asp Ala Cys Asp His Leu Lys Val Asn Tyr Asn
50           55           60
Glu Glu Ser Ala Thr Ser Leu Ile Glu Gln Asn Met Leu Ser Lys Leu
65           70           75           80
Leu Lys Asp Ser Leu Glu Lys Met Ser Arg Arg Glu Ile Lys Glu Leu
85           90           95
Cys Asn Glu Leu Gly Met Thr Asn Ile Asp Lys Val Ile Gly Glu Asn
100          105          110
Lys Gln Val Leu Ile Ala Ser Thr Leu Thr Leu Phe Lys Ala Gly Gly
115          120          125
Ser His Ser Tyr Ala Leu Ala Val Ser Val Ala Asp Ala Met Val Arg
130          135          140
Gln Thr Leu Gly His Val Met Trp Trp Val Lys
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...486
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

```

TTATTTTAAA GGAATTTC ATG CAA ATC ATA GAA GGG AAA TTG CAA TTA CAA      51
      Met Gln Ile Ile Glu Gly Lys Leu Gln Leu Gln
      1           5           10

GGG AAT GAA AGA GTC GCT ATT TTA ACA TCG CGC TTC AAT CAT ATC ATC      99
Gly Asn Glu Arg Val Ala Ile Leu Thr Ser Arg Phe Asn His Ile Ile
      15           20           25

ACA GAC AGA TTG CAA GAA GGG GCG ATG GAC TGC TTT AAA AGG CAT GGG      147
Thr Asp Arg Leu Gln Glu Gly Ala Met Asp Cys Phe Lys Arg His Gly
      30           35           40

GGC GAT GAG GAT CTT TTA GAC ATC GTG CTG GTG CCT GGG GCT TAT GAA      195
Gly Asp Glu Asp Leu Leu Asp Ile Val Leu Val Pro Gly Ala Tyr Glu
      45           50           55

```

TCA ACA GAA TAT AAA AGA TAT GGC CAT GAT TAC GCC AAA TAC CCA AGA	102
Ser Thr Glu Tyr Lys Arg Tyr Gly His Asp Tyr Ala Lys Tyr Pro Arg	
10 15 20	
AGA ATC GCT GAA GAA TTG CAA CAT TAT GGG GGC AAT AGT TTT GCG AAT	150
Arg Ile Ala Glu Glu Leu Gln His Tyr Gly Gly Asn Ser Phe Ala Asn	
25 30 35	
TTT TTT AGA GAT GAA GGG GTC TTA TAC AAA GAG ATT TTG TGC GAT GCG	198
Phe Phe Arg Asp Glu Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Ala	
40 45 50 55	
TGC GAT CAT TTA AAG GTT AAT TAC AAT GAA GAA TCT GCA ACC TCT TTG	246
Cys Asp His Leu Lys Val Asn Tyr Asn Glu Glu Ser Ala Thr Ser Leu	
60 65 70	
ATT GAG CAA AAC ATG CTT TCT AAA CTC TTG AAA GAT AGT TTA GAA AAA	294
Ile Glu Gln Asn Met Leu Ser Lys Leu Leu Lys Asp Ser Leu Glu Lys	
75 80 85	
ATG AGT AGG AGA GAG ATT AAA GAA CTT TGC AAT GAA TTG GGC ATG ACA	342
Met Ser Arg Arg Glu Ile Lys Glu Leu Cys Asn Glu Leu Gly Met Thr	
90 95 100	
AAT ATT GAT AAA GTG ATT GGT GAA AAC AAA CAA GTC CTA ATC GCA TCT	390
Asn Ile Asp Lys Val Ile Gly Glu Asn Lys Gln Val Leu Ile Ala Ser	
105 110 115	
ACT TTA ACG CTG TTT AAA GCG GGT GGC TCT CAT TCT TAT GCG TTG GCT	438
Thr Leu Thr Leu Phe Lys Ala Gly Gly Ser His Ser Tyr Ala Leu Ala	
120 125 130 135	
GTA TCT GTT GCA GAT GCA ATG GTA AGA CAA ACT CTA GGG CAT GTT ATG	486
Val Ser Val Ala Asp Ala Met Val Arg Gln Thr Leu Gly His Val Met	
140 145 150	
TGG TGG GTA AAG TAGCACTTAA AAAAACTTTG GGC GTTTTGG CTGGCCCTAT TG GTT	543
Trp Trp Val Lys	
155	
GGGT	547

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

Met Asn Glu Asp Leu Thr Asn Ser Thr Glu Tyr Lys Arg Tyr Gly His

			100					105					110				
Arg	Gly	His	Val	Tyr	Ser	Leu	Phe	Ile	Asn	Glu	Lys	Gln	Thr	Cys	Met		
		115					120					125					
Pro	Leu	Ser	Val	Leu	Leu	Val	Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu		
	130					135					140						
Ala	Arg	Asp	Tyr	Glu	Asn	Ile	Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp		
145					150					155					160		
Ser	Phe	Gly	Glu	Ser	Phe	Asp	Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly		
			165					170					175				
Tyr	Pro	Gly	Gly	Pro	Ile	Val	Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Arg	His		
		180						185					190				
Pro	Asn	Glu	Pro	Leu	Met	Phe	Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn		
	195					200						205					
Leu	Ala	Phe	Ser	Phe	Ser	Gly	Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val		
	210					215					220						
Glu	Lys	Asn	Ala	Pro	Asn	Leu	Asn	Glu	Ala	Ile	Lys	Gln	Lys	Ile	Gly		
225					230					235					240		
Tyr	His	Phe	Gln	Ser	Ala	Ala	Ile	Glu	His	Leu	Ile	Gln	Gln	Thr	Lys		
			245					250					255				
Arg	Tyr	Phe	Lys	Ile	Lys	Arg	Pro	Lys	Ile	Phe	Gly	Ile	Val	Gly	Gly		
		260						265					270				
Ala	Ser	Gln	Asn	Leu	Ala	Leu	Arg	Lys	Ala	Phe	Glu	Asn	Leu	Cys	Asp		
	275					280						285					
Ala	Phe	Asp	Cys	Lys	Leu	Val	Leu	Ala	Pro	Leu	Glu	Phe	Cys	Ser	Asp		
	290					295					300						
Asn	Ala	Ala	Met	Ile	Gly	Arg	Ser	Ser	Leu	Glu	Ala	Tyr	Gln	Lys	Lys		
305					310					315					320		
Arg	Phe	Val	Pro	Leu	Glu	Lys	Ala	Asn	Ile	Ser	Pro	Arg	Thr	Leu	Leu		
			325					330						335			
Lys	Ser	Phe	Glu														
			340														

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...498
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

TGCACTTGTT	ATGATGAAGA	TGGCGCACTA	AGA	ATG	AAT	GAA	GAC	TTG	ACA	AAT							
				Met	Asn	Glu	Asp	Leu	Thr	Asn							
				1						5							

54

```

AAT GAA GCG ATC AAA CAA AAG ATT GGC TAT CAT TTT CAA AGT GCA GCG      774
Asn Glu Ala Ile Lys Gln Lys Ile Gly Tyr His Phe Gln Ser Ala Ala
      235                      240                      245

ATT GAG CAT TTA ATC CAG CAG ACT AAA CGC TAT TTT AAA ATC AAA CGC      822
Ile Glu His Leu Ile Gln Gln Thr Lys Arg Tyr Phe Lys Ile Lys Arg
      250                      255                      260

CCT AAA ATT TTT GGC ATT GTG GGG GGA GCG AGC CAA AAT TTG GCT TTA      870
Pro Lys Ile Phe Gly Ile Val Gly Gly Ala Ser Gln Asn Leu Ala Leu
      265                      270                      275

AGA AAG GCG TTT GAA AAT TTG TGC GAT GCG TTT GAT TGC AAG CTT GTT      918
Arg Lys Ala Phe Glu Asn Leu Cys Asp Ala Phe Asp Cys Lys Leu Val
      280                      285                      290                      295

TTA GCC CCT TTA GAA TTT TGC AGC GAC AAT GCC GCC ATG ATA GGG CGA      966
Leu Ala Pro Leu Glu Phe Cys Ser Asp Asn Ala Ala Met Ile Gly Arg
      300                      305                      310

TCC AGC CTA GAA GCT TAT CAA AAA AAG CGC TTT GTC CCT TTA GAA AAG      1014
Ser Ser Leu Glu Ala Tyr Gln Lys Lys Arg Phe Val Pro Leu Glu Lys
      315                      320                      325

GCT AAC ATT TCG CCA AGA ACG CTG TTA AAA AGT TTT GAG TGAATGGATA CA  1065
Ala Asn Ile Ser Pro Arg Thr Leu Leu Lys Ser Phe Glu
      330                      335                      340

AAAAGAAAGC GCATGATAAA AC                                          1087

```

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

```

Met Ile Leu Ser Ile Glu Ser Ser Cys Asp Asp Ser Ser Leu Ala Leu
 1           5           10           15
Thr Arg Ile Glu Asp Ala Gln Leu Ile Ala His Phe Lys Ile Ser Gln
      20           25           30
Glu Lys His His Ser Ser Tyr Gly Gly Val Val Pro Glu Leu Ala Ser
      35           40           45
Arg Leu His Ala Glu Asn Leu Pro Leu Leu Leu Glu Arg Ile Lys Ile
      50           55           60
Ser Leu Asn Lys Asp Phe Ser Lys Ile Lys Ala Ile Ala Ile Thr Asn
      65           70           75           80
Gln Pro Gly Leu Ser Val Thr Leu Ile Glu Gly Leu Met Met Ala Lys
      85           90           95
Ala Leu Ser Leu Ser Leu Asn Leu Pro Leu Ile Leu Glu Asp His Leu

```


TCT TGC GAT GAC AGC TCT TTA GCC CTT ACA AGA ATA GAG GAC GCT CAA	102
Ser Cys Asp Asp Ser Ser Leu Ala Leu Thr Arg Ile Glu Asp Ala Gln	
10 15 20	
CTC ATC GCT CAT TTT AAA ATC TCT CAA GAA AAG CAC CAT AGT TCT TAT	150
Leu Ile Ala His Phe Lys Ile Ser Gln Glu Lys His His Ser Ser Tyr	
25 30 35	
GGG GGC GTT GTG CCT GAG CTT GCA TCA CGT TTG CAT GCT GAG AAT TTG	198
Gly Gly Val Val Pro Glu Leu Ala Ser Arg Leu His Ala Glu Asn Leu	
40 45 50 55	
CCG CTT TTA TTA GAA CGC ATT AAA ATA AGC TTG AAT AAG GAT TTT TCC	246
Pro Leu Leu Leu Glu Arg Ile Lys Ile Ser Leu Asn Lys Asp Phe Ser	
60 65 70	
AAA ATT AAA GCC ATC GCT ATC ACT AAT CAG CCA GGT TTG AGC GTT ACT	294
Lys Ile Lys Ala Ile Ala Ile Thr Asn Gln Pro Gly Leu Ser Val Thr	
75 80 85	
TTA ATA GAA GGT TTG ATG ATG GCA AAA GCC TTG AGC TTG TCT TTG AAT	342
Leu Ile Glu Gly Leu Met Met Ala Lys Ala Leu Ser Leu Ser Leu Asn	
90 95 100	
TTG CCC TTG ATT TTA GAA GAT CAT TTG AGA GGG CAT GTG TAT TCG CTC	390
Leu Pro Leu Ile Leu Glu Asp His Leu Arg Gly His Val Tyr Ser Leu	
105 110 115	
TTT ATC AAT GAA AAA CAA ACC TGC ATG CCT TTA AGC GTG CTC TTA GTC	438
Phe Ile Asn Glu Lys Gln Thr Cys Met Pro Leu Ser Val Leu Leu Val	
120 125 130 135	
TCT GGG GGG CAT TCT TTG ATT TTA GAG GCT AGA GAT TAT GAG AAT ATT	486
Ser Gly Gly His Ser Leu Ile Leu Glu Ala Arg Asp Tyr Glu Asn Ile	
140 145 150	
AAA ATC GTT GCC ACG AGT TTA GAC GAT AGC TTT GGG GAG AGT TTT GAT	534
Lys Ile Val Ala Thr Ser Leu Asp Asp Ser Phe Gly Glu Ser Phe Asp	
155 160 165	
AAG GTT TCC AAA ATG CTT GAT TTA GGC TAT CCA GGA GGC CCT ATA GTG	582
Lys Val Ser Lys Met Leu Asp Leu Gly Tyr Pro Gly Gly Pro Ile Val	
170 175 180	
GAA AAA TTA GCC CTT GAT TAT AGG CAC CCA AAC GAG CCT TTA ATG TTC	630
Glu Lys Leu Ala Leu Asp Tyr Arg His Pro Asn Glu Pro Leu Met Phe	
185 190 195	
CCT ATC CCT TTA AAA AAC AGC CCG AAT CTG GCT TTT AGT TTT TCA GGT	678
Pro Ile Pro Leu Lys Asn Ser Pro Asn Leu Ala Phe Ser Phe Ser Gly	
200 205 210 215	
TTA AAA AAT GCG GTG CGT TTG GAG GTT GAA AAA AAC GCC CCC AAC TTG	726
Leu Lys Asn Ala Val Arg Leu Glu Val Glu Lys Asn Ala Pro Asn Leu	
220 225 230	

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

```

Met Leu Phe Asn Gly Leu Cys Leu Phe Glu Gln Ala Ser Leu Cys Phe
 1           5           10           15
Arg Lys Ala Ser Val Ser Met Lys Lys Leu Lys Gly Leu Phe Leu Ile
          20           25           30
Leu Leu Leu Trp Val Tyr Pro Leu Arg Ser Glu Pro Ile Asn Glu Gly
          35           40           45
Ala Tyr Ile Leu Glu Glu Ile Gly Asp Val Leu Arg Phe Leu Pro Ile
          50           55           60
Phe Val Gly Thr Val Ser Leu Ala Met Arg Asp Tyr Arg Gly Leu Gly
65           70           75           80
Glu Leu Ala Val Gly Thr Leu Val Thr Gln Gly Val Ile Tyr Gly Leu
          85           90           95
Lys Gly Ala Phe Ser Asn Ala His Lys Asp Gly Ala Arg Val Glu Phe
          100          105          110
Ala Lys Arg Pro Cys Cys Asn Ser Trp Arg Gly Met Pro Ser Gly His
          115          120          125
Ala Gly Gly Val Phe Ser Ala Ala Gly Phe Val Tyr Tyr Arg Tyr Gly
          130          135          140
Trp Lys Pro Ala Leu Pro Val Ile Ala Leu Ala Ile Leu Thr Asp Ala
145          150          155          160
Ser Arg Val Val Ala Arg Gln His Thr Ile Leu Gln Val Thr Ile Gly
          165          170          175
Ser Leu Ile Ala Trp Gly Phe Ala Tyr Leu Phe Thr Ser Arg Tyr Lys
          180          185          190
Pro Lys Gln Trp Met Leu Tyr Pro Glu Ile Ser Ser Asp Phe Lys Gly
          195          200          205
Ser Ser Arg Tyr Gly Val Ser Phe Ser Tyr Gln Trp
          210          215          220

```

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1053
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

```

TTCAAGCAAA AACACCACCC AAATATAAAG ATA ATG ATT TTA AGC ATT GAA AGT
                               Met Ile Leu Ser Ile Glu Ser
                               1           5

```

54

Pro	Ile	Asn	Glu	Gly	Ala	Tyr	Ile	Leu	Glu	Glu	Ile	Gly	Asp	Val	Leu		
45						50					55						
AGG	TTT	TTG	CCT	ATT	TTT	GTA	GGC	ACG	GTC	AGT	TTG	GCG	ATG	CGC	GAT	243	
Arg	Phe	Leu	Pro	Ile	Phe	Val	Gly	Thr	Val	Ser	Leu	Ala	Met	Arg	Asp		
60					65					70					75		
TAT	AGA	GGG	TTA	GGG	GAA	TTA	GCG	GTC	GGC	ACA	TTG	GTT	ACT	CAA	GGC	291	
Tyr	Arg	Gly	Leu	Gly	Glu	Leu	Ala	Val	Gly	Thr	Leu	Val	Thr	Gln	Gly		
				80					85					90			
GTG	ATT	TAT	GGC	CTT	AAA	GGA	GCT	TTT	AGC	AAC	GCC	CAT	AAA	GAT	GGG	339	
Val	Ile	Tyr	Gly	Leu	Lys	Gly	Ala	Phe	Ser	Asn	Ala	His	Lys	Asp	Gly		
			95					100					105				
GCT	AGA	GTG	GAA	TTT	GCT	AAA	CGC	CCG	TGC	TGT	AAT	TCT	TGG	AGA	GGC	387	
Ala	Arg	Val	Glu	Phe	Ala	Lys	Arg	Pro	Cys	Cys	Asn	Ser	Trp	Arg	Gly		
		110					115						120				
ATG	CCA	AGC	GGG	CAT	GCT	GGG	GGG	GTG	TTT	AGC	GCG	GCT	GGG	TTT	GTG	435	
Met	Pro	Ser	Gly	His	Ala	Gly	Gly	Val	Phe	Ser	Ala	Ala	Gly	Phe	Val		
		125				130					135						
TAT	TAC	CGC	TAT	GGG	TGG	AAG	CCG	GCT	CTT	CCT	GTG	ATC	GCT	CTT	GCA	483	
Tyr	Tyr	Arg	Tyr	Gly	Trp	Lys	Pro	Ala	Leu	Pro	Val	Ile	Ala	Leu	Ala		
140					145					150					155		
ATC	CTC	ACT	GAC	GCT	AGC	AGA	GTG	GTG	GCA	AGA	CAA	CAC	ACG	ATC	TTG	531	
Ile	Leu	Thr	Asp	Ala	Ser	Arg	Val	Val	Ala	Arg	Gln	His	Thr	Ile	Leu		
				160					165						170		
CAA	GTT	ACG	ATC	GGC	AGC	CTT	ATC	GCA	TGG	GGG	TTT	GCT	TAT	TTA	TTC	579	
Gln	Val	Thr	Ile	Gly	Ser	Leu	Ile	Ala	Trp	Gly	Phe	Ala	Tyr	Leu	Phe		
				175				180					185				
ACT	TCA	CGC	TAC	AAA	CCC	AAG	CAA	TGG	ATG	CTC	TAT	CCT	GAA	ATT	TCT	627	
Thr	Ser	Arg	Tyr	Lys	Pro	Lys	Gln	Trp	Met	Leu	Tyr	Pro	Glu	Ile	Ser		
			190				195					200					
AGC	GAT	TTT	AAG	GGC	AGT	AGC	CGC	TAT	GGG	GTG	AGC	TTT	TCT	TAT	CAA	675	
Ser	Asp	Phe	Lys	Gly	Ser	Ser	Arg	Tyr	Gly	Val	Ser	Phe	Ser	Tyr	Gln		
		205				210					215						
TGG	TAAAGGGATA	AAGTGCTAAA	AAAATTATTA	TTCATTGCAC	T											719	
Trp																	
220																	

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```

Phe Leu Gln Leu Leu Arg Ala Tyr Ala Val Phe Ser Asn Glu Gly Lys
 450                      455                      460
Leu Thr Thr Pro Tyr Leu Val Gln Arg Glu Thr Ala Pro Asn Gly Asp
465                      470                      475                      480
Ile Tyr Ile Pro Ser Pro Lys Pro Thr Phe Gln Val Ile Ser Pro Lys
                      485                      490                      495
Ser Ala Arg Lys Met Lys Glu Thr Leu Ile Lys Val Val Arg Tyr Gly
                    500                      505                      510
Thr Gly Lys Asn Ala Gln Phe Glu Gly Leu Tyr Ile Gly Gly Lys Thr
                    515                      520                      525
Gly Thr Ala Arg Val Ala Lys Asn Gly Ser Tyr Ser Ala Gln Ser Tyr
                    530                      535                      540
Asn Ser Ser Phe Phe Gly Phe Ala Glu Asp Glu Arg Gln Val Phe Thr
545                      550                      555                      560
Ile Gly Val Val Ile Leu Gly Ser His Gly Lys Glu Glu Tyr Tyr Ala
                      565                      570                      575
Ser Lys Ile Ala Ala Pro Ile Phe Lys Glu Ile Thr Glu Ile Leu Val
                    580                      585                      590
Arg Tyr Asn Tyr Leu Ser Pro Ser Ile Ala Ile Gln Asn Ala Leu Glu
                    595                      600                      605
Lys Asn Arg Phe Lys Ile Lys
 610                      615

```

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...678
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

```

TAGCCTAGTC TTTATCGC ATG CTA TTT AAT GGG CTA TGC TTA TTT GAA CAG      51
                Met Leu Phe Asn Gly Leu Cys Leu Phe Glu Gln
                  1                      5                      10

GCA AGT TTG TGC TTT AGA AAA GCG AGC GTT TCA ATG AAA AAG CTC AAA      99
Ala Ser Leu Cys Phe Arg Lys Ala Ser Val Ser Met Lys Lys Leu Lys
                  15                      20                      25

GGT CTT TTT TTG ATC CTG CTC TTA TGG GTC TAT CCT TTA AGG AGT GAG     147
Gly Leu Phe Leu Ile Leu Leu Leu Trp Val Tyr Pro Leu Arg Ser Glu
                  30                      35                      40

CCA ATC AAT GAG GGA GCA TAC ATT TTA GAA GAG ATT GGC GAT GTG CTT     195

```

1		5		10		15
Glu Thr Gln Lys Tyr Lys Gly Thr Val Thr Ala Leu Ile Phe Leu Leu						
	20			25		30
Leu Phe Phe Ile Phe Leu Met Val Ala Phe Lys Lys Ala Phe Phe Ala						
	35		40		45	
Gln Ala Asn Met Pro Asn Leu Val Met Ser Lys Gln Asp Thr Ala Ala						
	50	55		60		
Arg Gly Thr Ile Tyr Ser Gln Asp Asn Tyr Ser Leu Ala Thr Ser Gln						
65		70		75		80
Thr Leu Phe Lys Leu Gly Phe Asp Thr Arg Phe Leu Asn Pro Asp Lys						
	85		90		95	
Glu Asp Phe Phe Ile Asp Phe Leu Ser Ile Tyr Ser Asn Ile Pro Lys						
	100		105		110	
Lys Ser Leu Lys Asp Ala Ile Asn Thr Lys Gly Tyr Ile Ile Leu Ala						
	115		120		125	
Tyr Asp Leu Thr Pro Asn Met Ala Ala Asn Ile Arg Asp Leu Asn Lys						
	130	135		140		
Lys Phe Leu Ala Phe Gly Val Phe Gln Asn Phe Lys Asp Ala His Asp						
145		150		155		160
Lys Val Trp Gln Lys Gln Gly Leu Asn Ile Glu Val Ser Gly Val Ser						
	165		170		175	
Arg His Tyr Pro Tyr Gln Asn Ser Leu Glu Pro Ile Ile Gly Tyr Val						
	180		185		190	
Gln Lys Gln Glu Glu Asp Lys Leu Thr Leu Thr Thr Gly Lys Lys Gly						
	195		200		205	
Val Glu Lys Ser Gln Asp His Leu Leu Lys Ala Gln Gln Asn Gly Ile						
	210	215		220		
Arg Thr Gly Lys Arg Asp Val Ser Phe Asn Phe Ile Gln Asn His Ser						
225		230		235		240
Tyr Thr Glu Val Glu Arg Leu Asp Gly Tyr Glu Val Tyr Leu Ser Val						
	245		250		255	
Pro Leu Lys Leu Gln Arg Glu Ile Glu Thr Leu Leu Asp Lys Thr Lys						
	260		265		270	
Asp Lys Leu Lys Ala Lys Glu Ile Leu Val Gly Ile Ile Asn Pro Lys						
	275		280		285	
Ser Gly Glu Ile Leu Ser Leu Ala Ser Ser Lys Arg Phe Asn Pro Asn						
	290	295		300		
Ala Ile Lys Thr Ser Asp Tyr Glu Ser Leu Asn Leu Ser Val Ala Glu						
305		310		315		320
Lys Val Phe Glu Pro Gly Ser Thr Ile Lys Pro Ile Val Tyr Ser Leu						
	325		330		335	
Leu Leu Asp Lys Asn Leu Ile Asn Pro Lys Glu Arg Ile Asp Leu Asn						
	340		345		350	
His Gly Tyr Tyr Gln Leu Gly Lys Tyr Thr Ile Lys Asp Asp Phe Ile						
	355		360		365	
Pro Ser Lys Lys Ala Val Val Glu Asp Ile Leu Ile Gln Ser Ser Asn						
	370	375		380		
Val Gly Met Ile Lys Ile Ser Lys Asn Leu Asn Pro Lys Asp Phe Tyr						
385		390		395		400
Asn Gly Leu Leu Gly Tyr Gly Phe Ser Gln Lys Thr Gly Ile Asp Leu						
	405		410		415	
Ser Leu Glu Ala Thr Gly Lys Ile Pro Pro Leu Ser Ala Phe Lys Arg						
	420		425		430	
Glu Val Leu Lys Gly Ser Val Ser Tyr Gly Tyr Gly Leu Asn Ala Thr						
	435		440		445	

GAA GGC AAA TTG ACT ACC CCC TAT TTA GTG CAA CGA GAA ACC GCC CCT	1443
Glu Gly Lys Leu Thr Thr Pro Tyr Leu Val Gln Arg Glu Thr Ala Pro	
465 470 475	
AAT GGC GAT ATT TAC ATC CCT AGC CCC AAA CCC ACC TTT CAA GTC ATT	1491
Asn Gly Asp Ile Tyr Ile Pro Ser Pro Lys Pro Thr Phe Gln Val Ile	
480 485 490	
AGC CCA AAA AGC GCT AGG AAA ATG AAA GAA ACC TTA ATC AAA GTA GTG	1539
Ser Pro Lys Ser Ala Arg Lys Met Lys Glu Thr Leu Ile Lys Val Val	
495 500 505	
CGT TAT GGC ACA GGC AAA AAC GCT CAA TTT GAA GGG CTA TAC ATA GGG	1587
Arg Tyr Gly Thr Gly Lys Asn Ala Gln Phe Glu Gly Leu Tyr Ile Gly	
510 515 520 525	
GGC AAA ACC GGC ACG GCT AGG GTC GCT AAA AAC GGG AGT TAT AGC GCG	1635
Gly Lys Thr Gly Thr Ala Arg Val Ala Lys Asn Gly Ser Tyr Ser Ala	
530 535 540	
CAG TCC TAC AAC AGC TCT TTT TTT GGG TTT GCT GAA GAT GAA AGG CAG	1683
Gln Ser Tyr Asn Ser Ser Phe Phe Gly Phe Ala Glu Asp Glu Arg Gln	
545 550 555	
GTT TTT ACT ATC GGC GTG GTT ATC TTA GGT TCG CAT GGC AAG GAA GAA	1731
Val Phe Thr Ile Gly Val Val Ile Leu Gly Ser His Gly Lys Glu Glu	
560 565 570	
TAT TAC GCC AGC AAG ATT GCA GCC CCC ATT TTT AAA GAA ATC ACC GAA	1779
Tyr Tyr Ala Ser Lys Ile Ala Ala Pro Ile Phe Lys Glu Ile Thr Glu	
575 580 585	
ATT TTA GTG CGT TAC AAT TAT CTA TCG CCC TCT ATT GCG ATT CAA AAC	1827
Ile Leu Val Arg Tyr Asn Tyr Leu Ser Pro Ser Ile Ala Ile Gln Asn	
590 595 600 605	
GCG CTC GAG AAA AAC CGC TTT AAG ATA AAA TAAAAGGCTC TTTTCAACCC AAA	1880
Ala Leu Glu Lys Asn Arg Phe Lys Ile Lys	
610 615	
CTCCAAAAAA GGAGTCTTAA GTT	1903

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

Met Asp Asn Arg Asn Ile Asp Pro Tyr Phe Asn Pro Glu Gln Phe Leu

Asn	His	Ser	Tyr	Thr	Glu	Val	Glu	Arg	Leu	Asp	Gly	Tyr	Glu	Val	Tyr	
		240					245					250				
TTG	AGC	GTT	CCT	TTA	AAA	CTC	CAA	AGA	GAA	ATT	GAA	ACC	CTA	TTG	GAT	819
Leu	Ser	Val	Pro	Leu	Lys	Leu	Gln	Arg	Glu	Ile	Glu	Thr	Leu	Leu	Asp	
		255				260					265					
AAA	ACT	AAA	GAC	AAA	CTC	AAG	GCT	AAA	GAA	ATC	CTA	GTG	GGT	ATC	ATT	867
Lys	Thr	Lys	Asp	Lys	Leu	Lys	Ala	Lys	Glu	Ile	Leu	Val	Gly	Ile	Ile	
270					275					280					285	
AAC	CCT	AAA	AGC	GGG	GAA	ATT	TTA	TCG	CTA	GCT	TCA	AGC	AAG	CGC	TTC	915
Asn	Pro	Lys	Ser	Gly	Glu	Ile	Leu	Ser	Leu	Ala	Ser	Ser	Lys	Arg	Phe	
				290					295					300		
AAT	CCT	AAT	GCG	ATT	AAA	ACC	AGC	GAT	TAT	GAA	AGC	TTG	AAT	TTG	AGC	963
Asn	Pro	Asn	Ala	Ile	Lys	Thr	Ser	Asp	Tyr	Glu	Ser	Leu	Asn	Leu	Ser	
			305					310					315			
GTT	GCT	GAA	AAG	GTT	TTT	GAG	CCA	GGC	AGC	ACG	ATC	AAA	CCC	ATT	GTT	1011
Val	Ala	Glu	Lys	Val	Phe	Glu	Pro	Gly	Ser	Thr	Ile	Lys	Pro	Ile	Val	
		320					325					330				
TAT	TCC	TTG	CTG	TTA	GAC	AAG	AAT	TTG	ATC	AAC	CCC	AAA	GAA	CGC	ATT	1059
Tyr	Ser	Leu	Leu	Leu	Asp	Lys	Asn	Leu	Ile	Asn	Pro	Lys	Glu	Arg	Ile	
		335				340					345					
GAT	TTA	AAC	CAT	GGC	TAT	TAC	CAA	TTA	GGA	AAA	TAC	ACC	ATT	AAA	GAC	1107
Asp	Leu	Asn	His	Gly	Tyr	Tyr	Gln	Leu	Gly	Lys	Tyr	Thr	Ile	Lys	Asp	
350					355					360					365	
GAC	TTT	ATC	CCC	AGT	AAA	AAA	GCC	GTT	GTG	GAA	GAC	ATT	TTG	ATC	CAA	1155
Asp	Phe	Ile	Pro	Ser	Lys	Lys	Ala	Val	Val	Glu	Asp	Ile	Leu	Ile	Gln	
				370					375					380		
TCT	AGC	AAT	GTG	GGC	ATG	ATA	AAA	ATC	AGT	AAA	AAC	TTA	AAC	CCA	AAG	1203
Ser	Ser	Asn	Val	Gly	Met	Ile	Lys	Ile	Ser	Lys	Asn	Leu	Asn	Pro	Lys	
			385					390					395			
GAT	TTC	TAT	AAT	GGG	CTT	TTA	GGC	TAT	GGA	TTT	TCT	CAA	AAA	ACC	GGC	1251
Asp	Phe	Tyr	Asn	Gly	Leu	Leu	Gly	Tyr	Gly	Phe	Ser	Gln	Lys	Thr	Gly	
		400					405					410				
ATT	GAT	TTA	TCT	CTA	GAA	GCC	ACA	GGA	AAG	ATC	CCT	CCT	TTG	TCC	GCT	1299
Ile	Asp	Leu	Ser	Leu	Glu	Ala	Thr	Gly	Lys	Ile	Pro	Pro	Leu	Ser	Ala	
		415				420					425					
TTC	AAG	CGT	GAA	GTG	TTA	AAG	GGG	AGC	GTT	TCT	TAT	GGC	TAT	GGG	CTG	1347
Phe	Lys	Arg	Glu	Val	Leu	Lys	Gly	Ser	Val	Ser	Tyr	Gly	Tyr	Gly	Leu	
430					435					440					445	
AAC	GCG	ACT	TTT	TTG	CAG	CTT	TTA	AGG	GCT	TAT	GCG	GTG	TTT	TCT	AAT	1395
Asn	Ala	Thr	Phe	Leu	Gln	Leu	Leu	Arg	Ala	Tyr	Ala	Val	Phe	Ser	Asn	
				450					455					460		

15	20	25	
TTT TTA TTG CTT TTT TTT ATT TTT TTA ATG GTG GCT TTT AAA AAA GCT			147
Phe Leu Leu Leu Phe Phe Ile Phe Leu Met Val Ala Phe Lys Lys Ala			
30	35	40	45
TTT TTT GCC CAA GCC AAC ATG CCT AAT CTA GTG ATG AGC AAA CAA GAC			195
Phe Phe Ala Gln Ala Asn Met Pro Asn Leu Val Met Ser Lys Gln Asp			
50	55		60
ACT GCG GCT AGG GGG ACT ATC TAT AGT CAA GAC AAC TAC AGC CTA GCC			243
Thr Ala Ala Arg Gly Thr Ile Tyr Ser Gln Asp Asn Tyr Ser Leu Ala			
65	70		75
ACT TCA CAA ACC CTT TTC AAA CTG GGC TTT GAT ACA AGG TTT TTA AAC			291
Thr Ser Gln Thr Leu Phe Lys Leu Gly Phe Asp Thr Arg Phe Leu Asn			
80	85		90
CCG GAT AAA GAA GAT TTT TTC ATT GAT TTC CTT TCT ATT TAT AGC AAT			339
Pro Asp Lys Glu Asp Phe Phe Ile Asp Phe Leu Ser Ile Tyr Ser Asn			
95	100		105
ATC CCT AAA AAG TCC TTA AAA GAC GCC ATC AAT ACA AAA GGC TAT ATC			387
Ile Pro Lys Lys Ser Leu Lys Asp Ala Ile Asn Thr Lys Gly Tyr Ile			
110	115		125
ATT CTA GCC TAT GAT CTC ACG CCC AAT ATG GCT GCT AAT ATT AGA GAC			435
Ile Leu Ala Tyr Asp Leu Thr Pro Asn Met Ala Ala Asn Ile Arg Asp			
130	135		140
TTA AAT AAG AAA TTT TTA GCC TTT GGG GTT TTT CAA AAT TTC AAA GAC			483
Leu Asn Lys Lys Phe Leu Ala Phe Gly Val Phe Gln Asn Phe Lys Asp			
145	150		155
GCG CAC GAT AAG GTG TGG CAA AAG CAA GGG CTA AAC ATT GAA GTG AGC			531
Ala His Asp Lys Val Trp Gln Lys Gln Gly Leu Asn Ile Glu Val Ser			
160	165		170
GGC GTT TCT AGG CAT TAC CCT TAT CAA AAT AGC CTA GAG CCA ATC ATT			579
Gly Val Ser Arg His Tyr Pro Tyr Gln Asn Ser Leu Glu Pro Ile Ile			
175	180		185
GGC TAT GTG CAA AAA CAA GAA GAA GAC AAG CTC ACT TTA ACT ACC GGT			627
Gly Tyr Val Gln Lys Gln Glu Glu Asp Lys Leu Thr Leu Thr Thr Gly			
190	195		205
AAA AAA GGC GTT GAA AAA TCT CAA GAT CAC TTG CTT AAA GCC CAA CAA			675
Lys Lys Gly Val Glu Lys Ser Gln Asp His Leu Leu Lys Ala Gln Gln			
210	215		220
AAT GGC ATA AGA ACA GGC AAA AGA GAC GTG AGT TTT AAC TTT ATC CAA			723
Asn Gly Ile Arg Thr Gly Lys Arg Asp Val Ser Phe Asn Phe Ile Gln			
225	230		235
AAC CAC TCT TAT ACA GAG GTT GAA CGC CTT GAT GGC TAT GAG GTG TAT			771


```

225          230          235          240
Ser Gly Ile His Ala Thr Ile Ala Ala Val Ile Leu Ala Phe Met Ile
          245          250          255
Pro Val Lys Ile Pro Lys Asp Ser Lys Asn Val Glu Leu Leu Glu Leu
          260          265          270
Gly Lys Arg Tyr Ala Glu Thr Ser Ser Gly Ala Leu Leu Ser Lys Glu
          275          280          285
Gln Gln Glu Ile Leu His Ser Ile Glu Glu Lys Ala Ser Ala Leu Gln
          290          295          300
Ser Pro Leu Glu Arg Leu Glu His Phe Leu Ala Pro Ile Ser Gly Tyr
305          310          315          320
Phe Ile Met Pro Leu Phe Ala Phe Ala Asn Ala Gly Val Ser Val Asp
          325          330          335
Ser Ser Ile Asn Leu Glu Val Asp Lys Val Leu Leu Gly Val Ile Leu
          340          345          350
Gly Leu Cys Leu Gly Lys Pro Leu Gly Ile Phe Leu Ile Thr Phe Ile
          355          360          365
Ser Glu Lys Leu Lys Ile Thr Ala Arg Pro Lys Gly Ile Ser Trp Trp
          370          375          380
His Ile Leu Gly Ala Gly Leu Leu Ala Gly Ile Gly Phe Thr Met Ser
385          390          395          400
Met Phe Ile Ser Asn Leu Ala Phe Thr Ser Glu His Lys Asp Ala Met
          405          410          415
Glu Val Ala Lys Ile Ala Ile Leu Leu Gly Ser Leu Ile Ser Gly Ile
          420          425          430
Ile Gly Ala Leu Tyr Leu Phe Ala Leu Asp Lys Arg Ala Ala Leu Lys
          435          440          445
Lys

```

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1857
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

```

AAGTAAGTGC TT ATG GAT AAT AGG AAT ATT GAT CCT TAC TTC AAC CCA GAG      51
      Met Asp Asn Arg Asn Ile Asp Pro Tyr Phe Asn Pro Glu
          1          5          10

CAA TTT TTA GAA ACC CAA AAA TAC AAA GGC ACG GTT ACA GCA TTA ATC      99
Gln Phe Leu Glu Thr Gln Lys Tyr Lys Gly Thr Val Thr Ala Leu Ile

```

CAT AAA GAC GCT ATG GAA GTG GCA AAA ATT GCG ATT TTA CTC GGA TCT 1299
 His Lys Asp Ala Met Glu Val Ala Lys Ile Ala Ile Leu Leu Gly Ser
 415 420 425

TTG ATT TCT GGG ATC ATA GGG GCT TTG TAT TTA TTT GCG CTA GAC AAA 1347
 Leu Ile Ser Gly Ile Ile Gly Ala Leu Tyr Leu Phe Ala Leu Asp Lys
 430 435 440

AGA GCG GCT TTA AAG AAA TAGCTAAAAA TGCTATAATT TGAGATTAAA ACATCTTT 1403
 Arg Ala Ala Leu Lys Lys
 445

TAAGGAAATT AAATGGGACA AATT 1427

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

Met Gly Leu Lys Leu Lys Ile Leu Arg Leu Ser Met Asn Leu Lys Lys
 1 5 10 15
 Thr Glu Asn Ala Leu Ser Leu Thr Leu Lys Asn Phe Ile Lys Ser Glu
 20 25 30
 Ser Phe Gly Gly Ile Phe Leu Phe Leu Asn Ala Val Leu Ala Met Val
 35 40 45
 Val Ala Asn Ser Phe Leu Lys Glu Ser Tyr Phe Ala Leu Trp His Thr
 50 55 60
 Pro Phe Gly Phe Gln Ile Gly Asp Phe Phe Ile Gly Phe Ser Leu His
 65 70 75 80
 Asn Trp Ile Asp Asp Val Leu Met Ala Leu Phe Phe Leu Met Ile Gly
 85 90 95
 Leu Glu Ile Lys Arg Glu Leu Leu Phe Gly Glu Leu Ser Ser Phe Lys
 100 105 110
 Lys Ala Ser Phe Pro Val Ile Ala Ala Ile Gly Gly Met Ile Ala Pro
 115 120 125
 Gly Leu Ile Tyr Phe Phe Leu Asn Ala Asn Thr Pro Ser Gln His Gly
 130 135 140
 Phe Gly Ile Pro Met Ala Thr Asp Ile Ala Phe Ala Leu Gly Val Ile
 145 150 155 160
 Met Leu Leu Gly Lys Arg Val Pro Thr Ala Leu Lys Val Phe Leu Ile
 165 170 175
 Thr Leu Ala Val Ala Asp Asp Leu Gly Ala Ile Val Val Ile Ala Leu
 180 185 190
 Phe Tyr Thr Thr Asn Leu Lys Phe Ala Trp Leu Leu Gly Ala Leu Gly
 195 200 205
 Val Val Leu Val Leu Ala Val Leu Asn Arg Leu Asn Met Arg Ser Leu
 210 215 220
 Ile Pro Tyr Leu Leu Leu Gly Val Leu Leu Trp Phe Cys Val His Gln

GTG GTG ATC GCG CTC TTT TAT ACC ACG AAT TTA AAA TTC GCA TGG CTT	627
Val Val Ile Ala Leu Phe Tyr Thr Thr Asn Leu Lys Phe Ala Trp Leu	
190 195 200	
TTA GGG GCT TTA GGG GTG GTT CTT GTT TTA GCC GTA TTA AAC CGC CTG	675
Leu Gly Ala Leu Gly Val Val Leu Val Leu Ala Val Leu Asn Arg Leu	
205 210 215	
AAT ATG CGC TCG CTC ATC CCT TAC TTG CTT TTA GGG GTG TTG CTT TGG	723
Asn Met Arg Ser Leu Ile Pro Tyr Leu Leu Leu Gly Val Leu Leu Trp	
220 225 230 235	
TTT TGC GTG CAT CAA AGC GGT ATC CAT GCG ACG ATT GCT GCA GTG ATT	771
Phe Cys Val His Gln Ser Gly Ile His Ala Thr Ile Ala Ala Val Ile	
240 245 250	
CTA GCT TTT ATG ATA CCG GTG AAG ATC CCT AAA GAT TCT AAA AAT GTA	819
Leu Ala Phe Met Ile Pro Val Lys Ile Pro Lys Asp Ser Lys Asn Val	
255 260 265	
GAG CTT TTG GAA CTA GGC AAA CGA TAC GCA GAA ACG AGT TCA GGA GCG	867
Glu Leu Leu Glu Leu Gly Lys Arg Tyr Ala Glu Thr Ser Ser Gly Ala	
270 275 280	
CTT TTG AGT AAA GAG CAG CAA GAA ATC TTG CAT TCT ATT GAA GAA AAA	915
Leu Leu Ser Lys Glu Gln Gln Glu Ile Leu His Ser Ile Glu Glu Lys	
285 290 295	
GCG AGC GCC TTA CAA AGC CCC TTA GAA AGA TTG GAG CAT TTT CTA GCC	963
Ala Ser Ala Leu Gln Ser Pro Leu Glu Arg Leu Glu His Phe Leu Ala	
300 305 310 315	
CCC ATT AGC GGG TAT TTC ATC ATG CCC TTA TTC GCG TTT GCA AAC GCT	1011
Pro Ile Ser Gly Tyr Phe Ile Met Pro Leu Phe Ala Phe Ala Asn Ala	
320 325 330	
GGG GTG AGC GTT GAT TCT AGC ATC AAT TTA GAA GTG GAT AAG GTG CTT	1059
Gly Val Ser Val Asp Ser Ser Ile Asn Leu Glu Val Asp Lys Val Leu	
335 340 345	
TTA GGG GTT ATT TTA GGG CTT TGC TTG GGC AAA CCT TTA GGG ATT TTC	1107
Leu Gly Val Ile Leu Gly Leu Cys Leu Gly Lys Pro Leu Gly Ile Phe	
350 355 360	
TTA ATC ACT TTT ATA AGC GAA AAG CTT AAA ATC ACC GCA CGC CCT AAA	1155
Leu Ile Thr Phe Ile Ser Glu Lys Leu Lys Ile Thr Ala Arg Pro Lys	
365 370 375	
GGC ATC AGC TGG TGG CAT ATT TTA GGG GCT GGG CTT TTA GCA GGG ATT	1203
Gly Ile Ser Trp Trp His Ile Leu Gly Ala Gly Leu Leu Ala Gly Ile	
380 385 390 395	
GGC TTT ACC ATG TCT ATG TTT ATT TCT AAT CTG GCC TTC ACG AGC GAG	1251
Gly Phe Thr Met Ser Met Phe Ile Ser Asn Leu Ala Phe Thr Ser Glu	
400 405 410	

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 19...1365
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

AAGACTGCTT	GAAAAATT	ATG	GGT	CTG	AAA	TTA	AAA	ATT	TTA	AGG	TTG	TCT	51			
		Met	Gly	Leu	Lys	Leu	Lys	Ile	Leu	Arg	Leu	Ser				
		1				5					10					
ATG	AAT	CTC	AAA	AAA	ACA	GAA	AAC	GCG	CTC	AGT	TTG	ACG	CTT	AAG	AAC	99
Met	Asn	Leu	Lys	Lys	Thr	Glu	Asn	Ala	Leu	Ser	Leu	Thr	Leu	Lys	Asn	
			15					20					25			
TTC	ATT	AAA	AGC	GAG	TCT	TTT	GGA	GGG	ATT	TTC	CTC	TTT	TTA	AAC	GCT	147
Phe	Ile	Lys	Ser	Glu	Ser	Phe	Gly	Gly	Ile	Phe	Leu	Phe	Leu	Asn	Ala	
		30					35					40				
GTT	TTA	GCG	ATG	GTG	GTG	GCT	AAT	TCG	TTT	TTA	AAA	GAA	AGT	TAT	TTT	195
Val	Leu	Ala	Met	Val	Val	Ala	Asn	Ser	Phe	Leu	Lys	Glu	Ser	Tyr	Phe	
	45					50					55					
GCA	CTA	TGG	CAC	ACC	CCT	TTT	GGG	TTT	CAA	ATA	GGG	GAT	TTT	TTC	ATC	243
Ala	Leu	Trp	His	Thr	Pro	Phe	Gly	Phe	Gln	Ile	Gly	Asp	Phe	Phe	Ile	
60					65				70					75		
GGC	TTT	AGT	TTG	CAC	AAC	TGG	ATT	GAT	GAT	GTC	TTA	ATG	GCG	TTA	TTC	291
Gly	Phe	Ser	Leu	His	Asn	Trp	Ile	Asp	Asp	Val	Leu	Met	Ala	Leu	Phe	
				80				85					90			
TTT	TTA	ATG	ATA	GGC	TTA	GAA	ATC	AAA	CGA	GAA	TTG	TTG	TTT	GGG	GAA	339
Phe	Leu	Met	Ile	Gly	Leu	Glu	Ile	Lys	Arg	Glu	Leu	Leu	Phe	Gly	Glu	
			95					100					105			
TTA	TCC	AGT	TTC	AAA	AAA	GCT	TCT	TTT	CCT	GTG	ATT	GCG	GCC	ATA	GGG	387
Leu	Ser	Ser	Phe	Lys	Lys	Ala	Ser	Phe	Pro	Val	Ile	Ala	Ala	Ile	Gly	
		110					115					120				
GGC	ATG	ATA	GCC	CCA	GGA	TTG	ATT	TAT	TTT	TTT	CTT	AAC	GCT	AAC	ACG	435
Gly	Met	Ile	Ala	Pro	Gly	Leu	Ile	Tyr	Phe	Phe	Leu	Asn	Ala	Asn	Thr	
	125					130					135					
CCT	TCC	CAG	CAT	GGT	TTT	GGG	ATC	CCT	ATG	GCG	ACG	GAT	ATT	GCG	TTC	483
Pro	Ser	Gln	His	Gly	Phe	Gly	Ile	Pro	Met	Ala	Thr	Asp	Ile	Ala	Phe	
140					145				150					155		
GCT	TTA	GGC	GTG	ATC	ATG	CTT	TTA	GGC	AAG	AGG	GTG	CCA	ACC	GCT	TTA	531
Ala	Leu	Gly	Val	Ile	Met	Leu	Leu	Gly	Lys	Arg	Val	Pro	Thr	Ala	Leu	
			160					165					170			
AAG	GTT	TTT	TTA	ATC	ACT	CTA	GCG	GTG	GCT	GAT	GAC	TTG	GGG	GCT	ATT	579
Lys	Val	Phe	Leu	Ile	Thr	Leu	Ala	Val	Ala	Asp	Asp	Leu	Gly	Ala	Ile	
			175				180						185			

Ile Ile Lys Ala Arg Ile Thr Ala Ala Ile Val Ala Trp Ile Pro Leu
 180 185 190

GATGCACGCA AAACCAAAGC AACACCCCTA AAAGC

670

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

Met Ile Pro Glu Ile Lys Asp Pro Ser Lys Ile Ala Ile Phe Ala Thr
 1 5 10 15
 Ser Ile Ala Ser Leu Cys Ser Leu Val Lys Ala Arg Leu Glu Ile Asn
 20 25 30
 Ile Asp Met Val Lys Pro Ile Pro Ala Lys Ser Pro Ala Pro Lys Ile
 35 40 45
 Cys His Gln Leu Met Pro Leu Gly Arg Ala Val Ile Leu Ser Phe Ser
 50 55 60
 Leu Ile Lys Val Ile Lys Lys Ile Pro Lys Gly Leu Pro Lys Gln Ser
 65 70 75 80
 Pro Lys Ile Thr Pro Lys Ser Thr Leu Ser Thr Ser Lys Leu Met Leu
 85 90 95
 Glu Ser Thr Leu Thr Pro Ala Phe Ala Asn Ala Asn Lys Gly Met Met
 100 105 110
 Lys Tyr Pro Leu Met Gly Ala Arg Lys Cys Ser Asn Leu Ser Lys Gly
 115 120 125
 Leu Cys Lys Ala Leu Ala Phe Ser Ser Ile Glu Cys Lys Ile Ser Cys
 130 135 140
 Cys Ser Leu Leu Lys Ser Ala Pro Glu Leu Val Ser Ala Tyr Arg Leu
 145 150 155 160
 Pro Ser Ser Lys Ser Thr Phe Leu Glu Ser Leu Gly Ile Phe Thr
 165 170 175
 Gly Ile Ile Lys Ala Arg Ile Thr Ala Ala Ile Val Ala Trp Ile Pro
 180 185 190
 Leu

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

TAGCTATTTTC	TTTAAAGCCG	CTCTTTTGTC	TAGCGCAAAT	AAATACAAAG	CCCCT	ATG	58
						Met	
						1	
ATC CCA GAA ATC AAA GAT CCG AGT AAA ATC GCA ATT TTT GCC ACT TCC	106						
Ile Pro Glu Ile Lys Asp Pro Ser Lys Ile Ala Ile Phe Ala Thr Ser							
5 10 15							
ATA GCG TCT TTA TGC TCG CTC GTG AAG GCC AGA TTA GAA ATA AAC ATA	154						
Ile Ala Ser Leu Cys Ser Leu Val Lys Ala Arg Leu Glu Ile Asn Ile							
20 25 30							
GAC ATG GTA AAG CCA ATC CCT GCT AAA AGC CCA GCC CCT AAA ATA TGC	202						
Asp Met Val Lys Pro Ile Pro Ala Lys Ser Pro Ala Pro Lys Ile Cys							
35 40 45							
CAC CAG CTG ATG CCT TTA GGG CGT GCG GTG ATT TTA AGC TTT TCG CTT	250						
His Gln Leu Met Pro Leu Gly Arg Ala Val Ile Leu Ser Phe Ser Leu							
50 55 60 65							
ATA AAA GTG ATT AAG AAA ATC CCT AAA GGT TTG CCC AAG CAA AGC CCT	298						
Ile Lys Val Ile Lys Lys Ile Pro Lys Gly Leu Pro Lys Gln Ser Pro							
70 75 80							
AAA ATA ACC CCT AAA AGC ACC TTA TCC ACT TCT AAA TTG ATG CTA GAA	346						
Lys Ile Thr Pro Lys Ser Thr Leu Ser Thr Ser Lys Leu Met Leu Glu							
85 90 95							
TCA ACG CTC ACC CCA GCG TTT GCA AAC GCG AAT AAG GGC ATG ATG AAA	394						
Ser Thr Leu Thr Pro Ala Phe Ala Asn Ala Asn Lys Gly Met Met Lys							
100 105 110							
TAC CCG CTA ATG GGG GCT AGA AAA TGC TCC AAT CTT TCT AAG GGG CTT	442						
Tyr Pro Leu Met Gly Ala Arg Lys Cys Ser Asn Leu Ser Lys Gly Leu							
115 120 125							
TGT AAG GCG CTC GCT TTT TCT TCA ATA GAA TGC AAG ATT TCT TGC TGC	490						
Cys Lys Ala Leu Ala Phe Ser Ser Ile Glu Cys Lys Ile Ser Cys Cys							
130 135 140 145							
TCT TTA CTC AAA AGC GCT CCT GAA CTC GTT TCT GCG TAT CGT TTG CCT	538						
Ser Leu Leu Lys Ser Ala Pro Glu Leu Val Ser Ala Tyr Arg Leu Pro							
150 155 160							
AGT TCC AAA AGC TCT ACA TTT TTA GAA TCT TTA GGG ATC TTC ACC GGT	586						
Ser Ser Lys Ser Ser Thr Phe Leu Glu Ser Leu Gly Ile Phe Thr Gly							
165 170 175							
ATC ATA AAA GCT AGA ATC ACT GCA GCA ATC GTC GCA TGG ATA CCG CTT T	635						

1	5	10	15
Asn Tyr Gly Val	Ile Val Ser Ala Ile	Leu Ala Leu Leu	Ala Leu Gly
20	25	30	
Leu Leu Phe Phe	Lys Gly Phe Ser Leu Gly Ile	Asp Phe Ala Gly Gly	
35	40	45	
Ser Leu Val Gln Val	Arg Tyr Thr Gln Asn Ala Pro	Ile Lys Glu Val	
50	55	60	
Arg Asp Leu Phe Glu	Lys Glu Ala Arg Phe Lys Gly Val	Gln Val Ser	
65	70	75	80
Glu Phe Gly Ser Lys	Glu Glu Ile Leu Ile Lys Phe Pro	Phe Val Glu	
85	90	95	
Thr Ala Glu Asn Glu	Asp Leu Asn Ala Ile Val Ala Asn	Ile Leu Lys	
100	105	110	
Pro Ser Gly Asp Phe	Glu Ile Arg Lys Phe Asp Thr Val	Gly Pro Arg	
115	120	125	
Val Gly Ser Glu Leu	Lys Glu Lys Gly Ile Leu Ser Leu	Ile Leu Ala	
130	135	140	
Leu Ile Ala Ile Met	Val Tyr Val Ser Phe Arg Tyr Glu	Trp Arg Phe	
145	150	155	160
Ala Leu Ala Ser Val	Ile Ala Leu Val His Asp Val Ile	Leu Val Ala	
165	170	175	
Ser Ser Val Ile Val	Phe Lys Ile Asp Met Asn Leu Glu	Val Ile Ala	
180	185	190	
Ala Leu Leu Thr Leu	Ile Gly Tyr Ser Ile Asn Asp Thr	Ile Ile Ile	
195	200	205	
Phe Asp Arg Ile Arg	Glu Glu Met Xaa Ser Gln Lys Thr	Lys Asn Ala	
210	215	220	
Thr Gln Ala Ile Asp	Glu Ala Ile Ser Ser Thr Leu Thr	Arg Thr Leu	
225	230	235	240
Leu Thr Ser Leu Thr	Val Phe Phe Val Val Leu Ile Leu	Cys Val Phe	
245	250	255	
Gly Ser Lys Ile Ile	Ile Gly Phe Ser Leu Pro Met Leu	Ile Gly Thr	
260	265	270	
Ile Val Gly Thr Tyr	Ser Ser Ile Phe Ile Ala Pro Lys	Val Ala Leu	
275	280	285	
Leu Leu Gly Phe Asp	Met Asp Lys Tyr Tyr Glu Asn Glu	Thr Arg Lys	
290	295	300	
Ile Lys Lys Ala Gln	Glu Lys Glu Lys Met Arg Arg Leu	Tyr Glu Ser	
305	310	315	320
Gly Gln Val			

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...634

CAT GAT GTG ATT TTA GTG GCA AGC TCG GTG ATT GTT TTT AAG ATT GAT	579
His Asp Val Ile Leu Val Ala Ser Ser Val Ile Val Phe Lys Ile Asp	
170 175 180 185	
ATG AAT TTG GAA GTG ATT GCG GCC TTG CTC ACC TTG ATT GGG TAT TCC	627
Met Asn Leu Glu Val Ile Ala Ala Leu Thr Leu Ile Gly Tyr Ser	
190 195 200	
ATT AAT GAT ACG ATC ATT ATT TTT GAC AGG ATC AGA GAA GAG ATG CTY	675
Ile Asn Asp Thr Ile Ile Ile Phe Asp Arg Ile Arg Glu Glu Met Xaa	
205 210 215	
TCT CAA AAA ACC AAA AAC GCC ACT CAA GCC ATT GAT GAA GCC ATT TCT	723
Ser Gln Lys Thr Lys Asn Ala Thr Gln Ala Ile Asp Glu Ala Ile Ser	
220 225 230	
AGC ACG CTC ACG CGC ACG CTT TTA ACT TCT TTA ACC GTG TTT TTT GTG	771
Ser Thr Leu Thr Arg Thr Leu Leu Thr Ser Leu Thr Val Phe Phe Val	
235 240 245	
GTG TTG ATT TTG TGC GTG TTT GGG AGT AAG ATC ATC ATT GGC TTT TCA	819
Val Leu Ile Leu Cys Val Phe Gly Ser Lys Ile Ile Ile Gly Phe Ser	
250 255 260 265	
TTG CCC ATG TTA ATA GGC ACG ATT GTA GGG ACT TAT AGC TCT ATT TTC	867
Leu Pro Met Leu Ile Gly Thr Ile Val Gly Thr Tyr Ser Ser Ile Phe	
270 275 280	
ATC GCC CCT AAA GTG GCG TTA TTG TTA GGC TTT GAT ATG GAT AAA TAT	915
Ile Ala Pro Lys Val Ala Leu Leu Leu Gly Phe Asp Met Asp Lys Tyr	
285 290 295	
TAT GAG AAT GAG ACT AGA AAA ATT AAA AAA GCT CAA GAG AAA GAA AAA	963
Tyr Glu Asn Glu Thr Arg Lys Ile Lys Lys Ala Gln Glu Lys Glu Lys	
300 305 310	
ATG CGC CGT TTG TAT GAG AGC GGT CAA GTT TAAGGAGTTT CTATGGATTG GGG	1016
Met Arg Arg Leu Tyr Glu Ser Gly Gln Val	
315 320	
TCGGGTCGTT CATGTGCTG	1035

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

Met Glu Leu Phe Lys Arg Thr Arg Ile Leu Ser Phe Met Arg Tyr Ser

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 25...993
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

GAATAAAAGA GCTTAGGAGG TTTT ATG GAA TTA TTC AAA CGA ACT AGA ATC	51
Met Glu Leu Phe Lys Arg Thr Arg Ile	
1 5	
TTA AGC TTC ATG CGT TAT TCC AAT TAT GGG GTG ATC GTT TCA GCA ATT	99
Leu Ser Phe Met Arg Tyr Ser Asn Tyr Gly Val Ile Val Ser Ala Ile	
10 15 20 25	
TTA GCG CTT CTA GCG TTG GGG CTT TTG TTT TTC AAA GGG TTT TCT TTA	147
Leu Ala Leu Leu Ala Leu Gly Leu Leu Phe Phe Lys Gly Phe Ser Leu	
30 35 40	
GGG ATT GAT TTT GCG GGG GGG AGT TTG GTG CAA GTG CGC TAC ACT CAA	195
Gly Ile Asp Phe Ala Gly Gly Ser Leu Val Gln Val Arg Tyr Thr Gln	
45 50 55	
AAC GCC CCC ATT AAA GAA GTG CGC GAT CTG TTT GAA AAA GAA GCT CGC	243
Asn Ala Pro Ile Lys Glu Val Arg Asp Leu Phe Glu Lys Glu Ala Arg	
60 65 70	
TTC AAA GGC GTG CAA GTG AGC GAA TTT GGC TCT AAA GAA GAA ATT TTA	291
Phe Lys Gly Val Gln Val Ser Glu Phe Gly Ser Lys Glu Glu Ile Leu	
75 80 85	
ATC AAA TTC CCT TTT GTA GAA ACG GCT GAA AAT GAA GAT CTG AAC GCT	339
Ile Lys Phe Pro Phe Val Glu Thr Ala Glu Asn Glu Asp Leu Asn Ala	
90 95 100 105	
ATC GTG GCC AAC ATT CTA AAA CCC AGC GGC GAT TTT GAA ATC CGT AAA	387
Ile Val Ala Asn Ile Leu Lys Pro Ser Gly Asp Phe Glu Ile Arg Lys	
110 115 120	
TTT GAC ACC GTG GGC CCT AGA GTG GGG AGC GAA TTG AAA GAG AAA GGC	435
Phe Asp Thr Val Gly Pro Arg Val Gly Ser Glu Leu Lys Glu Lys Gly	
125 130 135	
ATT TTG TCG CTG ATT TTA GCA TTA ATA GCG ATC ATG GTT TAT GTG AGT	483
Ile Leu Ser Leu Ile Leu Ala Leu Ile Ala Ile Met Val Tyr Val Ser	
140 145 150	
TTC CGC TAT GAA TGG CGT TTT GCT TTA GCG AGC GTC ATT GCG CTT GTG	531
Phe Arg Tyr Glu Trp Arg Phe Ala Leu Ala Ser Val Ile Ala Leu Val	
155 160 165	

```

ATT GGG GTG ATC AAG CGT TTC GCT TCA GAG CTA TTG GCC AGC TCT TTA      195
Ile Gly Val Ile Lys Arg Phe Ala Ser Glu Leu Leu Ala Ser Ser Leu
              50                      55                      60

GCC ACC GTA TTG CAT CTC ATA CCG GCA TTT GTG TTT TTA CAG ATT TTA      243
Ala Thr Val Leu His Leu Ile Pro Ala Phe Val Phe Leu Gln Ile Leu
              65                      70                      75

AAT AAT TTG GTT ACC GCT TAC ATG CTC ATG ATC GGG GCG TTG ATT AGC      291
Asn Asn Leu Val Thr Ala Tyr Met Leu Met Ile Gly Ala Leu Ile Ser
              80                      85                      90

AAC GCT TTC AGT CTC ATC TTT TTG TTG ATT GAA AGC GTT GTA ACG AGC      339
Asn Ala Phe Ser Leu Ile Phe Leu Leu Ile Glu Ser Val Val Thr Ser
              95                      100                     105

GAA ACG GAT TAAGGGGTAG TGATGGATTT TATCAATATA GAAAAAAAT GGC      391
Glu Thr Asp
110

```

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

```

Met Asp Trp Gly Arg Val Val His Val Leu Phe Ser Leu Ile Ser Leu
 1              5              10              15
Thr Thr Ile Ala Gly Phe Leu Tyr Glu Pro Asn Thr Val Val Leu Phe
              20              25              30
Val Ala Leu Ala Leu Asn Leu Ile Ser Val Thr Leu Lys Ile Gly Val
              35              40              45
Ile Lys Arg Phe Ala Ser Glu Leu Leu Ala Ser Ser Leu Ala Thr Val
              50              55              60
Leu His Leu Ile Pro Ala Phe Val Phe Leu Gln Ile Leu Asn Asn Leu
65              70              75              80
Val Thr Ala Tyr Met Leu Met Ile Gly Ala Leu Ile Ser Asn Ala Phe
              85              90              95
Ser Leu Ile Phe Leu Leu Ile Glu Ser Val Val Thr Ser Glu Thr Asp
              100             105             110

```

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

```

Met Ala Ile Phe Asp Asn Asn Asn Lys Ser Ala Asn Ala Lys Thr Gly
 1           5           10           15
Pro Ala Thr Ile Ile Ala Gln Gly Thr Lys Ile Lys Gly Glu Leu His
          20           25           30
Leu Asp Tyr His Leu His Val Asp Gly Glu Leu Glu Gly Val Val His
          35           40           45
Ser Lys Ser Thr Val Val Ile Gly Gln Thr Gly Ser Val Val Gly Glu
          50           55           60
Ile Phe Thr Asn Lys Leu Val Val Ser Gly Lys Phe Thr Gly Thr Val
          65           70           75           80
Glu Ala Glu Val Val Glu Ile Met Pro Leu Gly His Leu Asp Gly Lys
          85           90           95
Ile Ser Ser Gln Glu Leu Val Val Glu Arg Lys Gly Ile Leu Ile Gly
          100          105          110
Glu Thr Arg Pro Lys Asn Ile Gln Gly Gly Ala Leu Leu Ile Asn Glu
          115          120          125
Gln Glu Lys Lys Ile Glu Asn Lys
          130          135

```

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...348
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

```

TAAGGAGTTT CT ATG GAT TGG GGT CGG GTC GTT CAT GTG CTG TTC AGC CTT      51
      Met Asp Trp Gly Arg Val Val His Val Leu Phe Ser Leu
          1           5           10

ATT TCT TTA ACC ACC ATT GCA GGG TTT TTG TAT GAG CCT AAT ACG GTG      99
Ile Ser Leu Thr Thr Ile Ala Gly Phe Leu Tyr Glu Pro Asn Thr Val
          15           20           25

GTG TTG TTT GTA GCG TTA GCT TTA AAC CTT ATT TCT GTT ACG CTT AAA      147
Val Leu Phe Val Ala Leu Ala Leu Asn Leu Ile Ser Val Thr Leu Lys
          30           35           40           45

```

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 22...429

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

CAATAAAGAA AGGAGCATCA G ATG GCA ATC TTT GAT AAC AAT AAT AAA TCG	51
Met Ala Ile Phe Asp Asn Asn Asn Lys Ser	
1 5 10	
GCT AAT GCA AAA ACA GGA CCA GCG ACT ATC ATC GCT CAA GGC ACA AAA	99
Ala Asn Ala Lys Thr Gly Pro Ala Thr Ile Ile Ala Gln Gly Thr Lys	
15 20 25	
ATA AAG GGG GAG CTT CAT TTA GAT TAC CAT TTG CAC GTA GAT GGC GAA	147
Ile Lys Gly Glu Leu His Leu Asp Tyr His Leu His Val Asp Gly Glu	
30 35 40	
TTA GAA GGG GTG GTG CAT TCT AAA AGC ACG GTG GTG ATC GGC CAA ACC	195
Leu Glu Gly Val Val His Ser Lys Ser Thr Val Val Ile Gly Gln Thr	
45 50 55	
GGC TCG GTA GTG GGT GAG ATT TTT ACT AAT AAA TTA GTG GTC AGT GGC	243
Gly Ser Val Val Gly Glu Ile Phe Thr Asn Lys Leu Val Val Ser Gly	
60 65 70	
AAG TTC ACT GGC ACG GTG GAG GCG GAA GTG GTA GAA ATC ATG CCT TTA	291
Lys Phe Thr Gly Thr Val Glu Ala Glu Val Val Glu Ile Met Pro Leu	
75 80 85 90	
GGG CAC CTT GAT GGC AAA ATC TCT AGC CAA GAG CTT GTG GTG GAA AGA	339
Gly His Leu Asp Gly Lys Ile Ser Ser Gln Glu Leu Val Val Glu Arg	
95 100 105	
AAG GGG ATT TTG ATT GGG GAA ACT CGC CCT AAG AAT ATT CAA GGG GGG	387
Lys Gly Ile Leu Ile Gly Glu Thr Arg Pro Lys Asn Ile Gln Gly Gly	
110 115 120	
GCG TTG TTA ATC AAT GAG CAA GAA AAG AAA ATT GAA AAT AAA TAGGGAATG	438
Ala Leu Leu Ile Asn Glu Gln Glu Lys Lys Ile Glu Asn Lys	
125 130 135	
ATCCAATCCA GCCTTTATAG AGCC	462

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

```

Thr Leu Phe Gly Val Leu Val Val Ser Gly Ile Phe Leu Leu Met Tyr
 50                      55                      60
Tyr Lys Pro Asp Ala Lys Met Ala Phe Asp Ser Val Asn Phe Thr Ile
65                      70                      75                      80
Met Gln Glu Val Ala Tyr Gly Trp Leu Trp Arg His Met His Ala Thr
                      85                      90                      95
Ala Ala Ser Met Ile Phe Val Ile Ile Tyr Ile His Met Phe Val Gly
                      100                      105                      110
Ile Tyr Tyr Gly Ser Tyr Lys Lys Gly Arg Glu Met Ile Trp Ile Ser
                      115                      120                      125
Gly Met Ile Leu Phe Val Val Phe Ser Ala Glu Ala Phe Ser Gly Tyr
                      130                      135                      140
Met Leu Pro Trp Gly Gln Met Ser Tyr Trp Ala Ala Ala Val Ile Thr
145                      150                      155                      160
Asn Leu Phe Gly Gly Ile Pro Phe Ile Gly Ala Asp Val Val Glu Trp
                      165                      170                      175
Ile Arg Gly Asn Tyr Val Val Ala Asp Ser Thr Leu Thr Arg Phe Phe
                      180                      185                      190
Met Leu His Val Phe Leu Leu Pro Ile Ala Ile Ile Leu Leu Val Gly
                      195                      200                      205
Val His Phe Tyr Ser Leu Arg Ile Pro His Val Asn Asn Gln Glu Gly
210                      215                      220
Glu Glu Ile Asp Phe Glu Leu Glu Glu Lys Lys Phe Ile Glu Gly Lys
225                      230                      235                      240
Lys Lys Glu Ser Lys Val Ile Pro Phe Trp Pro Val Phe Leu Ser Lys
                      245                      250                      255
Asp Ile Phe Val Val Cys Ala Phe Met Val Phe Phe Phe Tyr Leu Val
260                      265                      270
Cys Tyr His Tyr Asp Phe Ala Met Asp Pro Ile Asn Phe Glu Arg Ala
275                      280                      285
Asn Ser Leu Lys Thr Pro Pro His Ile Tyr Pro Glu Trp Tyr Phe Leu
290                      295                      300
Trp Ser Tyr Glu Val Leu Arg Gly Phe Phe Phe Ser Ala Asp Leu Gly
305                      310                      315                      320
Leu Met Ala Phe Gly Val Ala Gln Val Ile Phe Phe Leu Leu Pro Phe
                      325                      330                      335
Leu Asp Arg Ser Pro Val Val Ala Pro Ala His Lys Arg Pro Ala Phe
340                      345                      350
Met Val Trp Phe Trp Leu Val Ile Ile Asp Met Ile Val Leu Thr Ile
355                      360                      365
Tyr Gly Lys Leu Pro Pro Leu Gly Ile Gly Lys Tyr Ile Gly Leu Ala
370                      375                      380
Gly Ser Ile Thr Phe Leu Ala Leu Phe Phe Val Val Leu Pro Ile Ile
385                      390                      395                      400
Thr Ile Ala Glu Ser Lys Lys Gln Gly Gly Val Arg
                      405                      410

```

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Pro	Ile	Asn	Phe	Glu	Arg	Ala	Asn	Ser	Leu	Lys	Thr	Pro	Pro	His	Ile	
		285						290					295			
TAC	CCT	GAA	TGG	TAT	TTC	TTA	TGG	AGC	TAT	GAA	GTC	TTA	AGA	GGC	TTT	963
Tyr	Pro	Glu	Trp	Tyr	Phe	Leu	Trp	Ser	Tyr	Glu	Val	Leu	Arg	Gly	Phe	
		300					305					310				
TTC	TTT	AGC	GCT	GAT	TTA	GGG	CTA	ATG	GCC	TTT	GGC	GTG	GCG	CAA	GTG	1011
Phe	Phe	Ser	Ala	Asp	Leu	Gly	Leu	Met	Ala	Phe	Gly	Val	Ala	Gln	Val	
		315				320					325					
ATT	TTC	TTT	TTG	CTA	CCC	TTC	TTG	GAT	CGA	AGT	CCA	GTG	GTC	GCT	CCT	1059
Ile	Phe	Phe	Leu	Leu	Pro	Phe	Leu	Asp	Arg	Ser	Pro	Val	Val	Ala	Pro	
330					335				340					345		
GCG	CAC	AAA	CGG	CCG	GCG	TTT	ATG	GTG	TGG	TTT	TGG	CTT	GTA	ATC	ATT	1107
Ala	His	Lys	Arg	Pro	Ala	Phe	Met	Val	Trp	Phe	Trp	Leu	Val	Ile	Ile	
			350					355					360			
GAT	ATG	ATT	GTT	TTA	ACG	ATC	TAT	GGT	AAA	TTG	CCT	CCG	CTT	GGG	ATT	1155
Asp	Met	Ile	Val	Leu	Thr	Ile	Tyr	Gly	Lys	Leu	Pro	Pro	Leu	Gly	Ile	
		365					370						375			
GGT	AAA	TAC	ATT	GGC	TTA	GCG	GGT	TCA	ATC	ACT	TTT	TTG	GCC	CTT	TTC	1203
Gly	Lys	Tyr	Ile	Gly	Leu	Ala	Gly	Ser	Ile	Thr	Phe	Leu	Ala	Leu	Phe	
		380					385					390				
TTT	GTG	GTA	TTG	CCC	ATC	ATC	ACT	ATC	GCT	GAG	AGC	AAG	AAA	CAA	GGG	1251
Phe	Val	Val	Leu	Pro	Ile	Ile	Thr	Ile	Ala	Glu	Ser	Lys	Lys	Gln	Gly	
	395					400				405						
GGT	GTT	AGA	TGAAAGAGTT	TAAGATTCTA	ATCATCCTCA	TTGTGGTGGT	AGGCGTGAT									1309
Gly	Val	Arg														
410																
TTATTATGGG	GTGGA															1324

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

Met	Ala	Glu	Ile	Lys	Lys	Ala	Lys	Asn	Leu	Gly	Glu	Trp	Leu	Asp	Met	
1				5				10					15			
Arg	Leu	Gly	Thr	Asn	Lys	Leu	Val	Lys	Val	Leu	Met	Thr	Glu	Tyr	Trp	
			20					25					30			
Ile	Pro	Lys	Asn	Ile	Asn	Phe	Leu	Trp	Ala	Met	Gly	Val	Ile	Leu	Leu	
		35					40					45				

60	65	70	
GAT AGC GTG AAT TTC ACC ATC ATG CAA GAA GTG GCT TAT GGC TGG CTT			291
Asp Ser Val Asn Phe Thr Ile Met Gln Glu Val Ala Tyr Gly Trp Leu			
75	80	85	
TGG CGC CAC ATG CAT GCC ACG GCA GCG AGC ATG ATT TTT GTC ATC ATT			339
Trp Arg His Met His Ala Thr Ala Ala Ser Met Ile Phe Val Ile Ile			
90	95	100	105
TAT ATC CAC ATG TTT GTT GGC ATC TAT TAT GGC TCT TAC AAA AAG GGT			387
Tyr Ile His Met Phe Val Gly Ile Tyr Tyr Gly Ser Tyr Lys Lys Gly			
110	115	120	
CGT GAG ATG ATT TGG ATT AGC GGG ATG ATT TTG TTT GTG GTC TTT AGC			435
Arg Glu Met Ile Trp Ile Ser Gly Met Ile Leu Phe Val Val Phe Ser			
125	130	135	
GCG GAA GCC TTT AGC GGG TAT ATG CTG CCT TGG GGG CAG ATG AGT TAT			483
Ala Glu Ala Phe Ser Gly Tyr Met Leu Pro Trp Gly Gln Met Ser Tyr			
140	145	150	
TGG GCC GCA GCG GTT ATC ACG AAT TTA TTT GGA GGC ATT CCT TTC ATT			531
Trp Ala Ala Ala Val Ile Thr Asn Leu Phe Gly Gly Ile Pro Phe Ile			
155	160	165	
GGG GCT GAT GTG GTG GAG TGG ATT AGA GGC AAT TAT GTT GTG GCG GAT			579
Gly Ala Asp Val Val Glu Trp Ile Arg Gly Asn Tyr Val Val Ala Asp			
170	175	180	185
TCC ACT TTA ACG CGC TTT TTC ATG CTC CAT GTG TTT TTA CTG CCC ATT			627
Ser Thr Leu Thr Arg Phe Phe Met Leu His Val Phe Leu Leu Pro Ile			
190	195	200	
GCG ATC ATT CTA CTT GTT GGG GTG CAT TTT TAT TCT TTA CGC ATC CCG			675
Ala Ile Ile Leu Leu Val Gly Val His Phe Tyr Ser Leu Arg Ile Pro			
205	210	215	
CAT GTC AAT AAC CAA GAA GGC GAA GAG ATT GAC TTT GAA TTA GAA GAG			723
His Val Asn Asn Gln Glu Gly Glu Glu Ile Asp Phe Glu Leu Glu Glu			
220	225	230	
AAG AAA TTC ATT GAA GGC AAG AAA AAA GAA TCC AAA GTC ATT CCT TTT			771
Lys Lys Phe Ile Glu Gly Lys Lys Lys Glu Ser Lys Val Ile Pro Phe			
235	240	245	
TGG CCG GTG TTC TTG TCT AAA GAT ATT TTT GTG GTT TGC GCG TTC ATG			819
Trp Pro Val Phe Leu Ser Lys Asp Ile Phe Val Val Cys Ala Phe Met			
250	255	260	265
GTC TTT TTC TTT TAC TTG GTG TGT TAC CAC TAT GAT TTT GCG ATG GAT			867
Val Phe Phe Phe Tyr Leu Val Cys Tyr His Tyr Asp Phe Ala Met Asp			
270	275	280	
CCT ATC AAC TTT GAA AGG GCT AAC AGC CTT AAA ACG CCG CCT CAC ATT			915

```

          325          330          335
Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu
          340          345          350
Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser
          355          360          365
Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys
          370          375          380
Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser
385          390          395          400
Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met
          405          410          415
Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Glu Lys Ser Pro Phe Val
          420          425          430
Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp
          435          440          445
Lys Lys Thr Ala Phe Asn Ser Ser Glu
          450          455

```

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1260
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

```

TGGCTAAAGC GTAAGGAGAG TTTA ATG GCA GAG ATA AAA AAA GCG AAA AAT      51
          Met Ala Glu Ile Lys Lys Ala Lys Asn
          1                      5

TTA GGC GAA TGG CTG GAC ATG CGT CTT GGC ACT AAC AAG CTT GTT AAA      99
Leu Gly Glu Trp Leu Asp Met Arg Leu Gly Thr Asn Lys Leu Val Lys
10                      15                      20                      25

GTG CTA ATG ACA GAA TAT TGG ATC CCT AAA AAC ATC AAT TTT TTA TGG     147
Val Leu Met Thr Glu Tyr Trp Ile Pro Lys Asn Ile Asn Phe Leu Trp
          30                      35                      40

GCG ATG GGG GTG ATT TTA TTA ACC CTT TTT GGC GTG CTT GTG GTC TCA     195
Ala Met Gly Val Ile Leu Leu Thr Leu Phe Gly Val Leu Val Val Ser
          45                      50                      55

GGG ATT TTC TTG CTC ATG TAT TAC AAG CCT GAT GCG AAA ATG GCG TTT     243
Gly Ile Phe Leu Leu Met Tyr Tyr Lys Pro Asp Ala Lys Met Ala Phe

```


TTTCAAAT

1463

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

```

Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
 1           5           10           15
Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
          20          25          30
Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
          35          40          45
Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
          50          55          60
Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
65          70          75          80
His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
          85          90          95
Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
          100         105         110
Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
          115         120         125
Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
          130         135         140
Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
145         150         155         160
Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
          165         170         175
Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
          180         185         190
Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
          195         200         205
Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu
          210         215         220
Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile
225         230         235         240
Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp
          245         250         255
Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro
          260         265         270
Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu
          275         280         285
Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His
          290         295         300
Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser
305         310         315         320
Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys

```

Ser	Asp	Arg	Ser	Pro	Lys	Asn	Ile	Ala	Gly	Leu	Glu	Asp	Arg	Leu	Lys	
245						250					255					
TCG	CGC	TTT	GAA	TGG	GGG	ATA	ACC	GCT	AAA	GTC	ATG	CCC	CCT	GAT	TTA	871
Ser	Arg	Phe	Glu	Trp	Gly	Ile	Thr	Ala	Lys	Val	Met	Pro	Pro	Asp	Leu	
260					265					270					275	
GAA	ACC	AAA	CTT	TCC	ATT	GTC	AAA	CAA	AAA	TGC	CAG	CTC	AAT	CAA	ATC	919
Glu	Thr	Lys	Leu	Ser	Ile	Val	Lys	Gln	Lys	Cys	Gln	Leu	Asn	Gln	Ile	
				280					285					290		
ACT	TTG	CCT	GAA	GAG	GTG	ATG	GAA	TAC	ATC	GCC	CAA	CAC	ATC	AGC	GAC	967
Thr	Leu	Pro	Glu	Glu	Val	Met	Glu	Tyr	Ile	Ala	Gln	His	Ile	Ser	Asp	
			295					300					305			
AAT	ATC	CGC	CAA	ATG	GAA	GGC	GCG	ATC	ATT	AAA	ATC	AGC	GTG	AAC	GCG	1015
Asn	Ile	Arg	Gln	Met	Glu	Gly	Ala	Ile	Ile	Lys	Ile	Ser	Val	Asn	Ala	
		310					315					320				
AAC	TTG	ATG	AAC	GCT	TCC	ATT	GAT	TTG	AAC	CTC	GCT	AAA	ACC	GTT	TTA	1063
Asn	Leu	Met	Asn	Ala	Ser	Ile	Asp	Leu	Asn	Leu	Ala	Lys	Thr	Val	Leu	
	325					330					335					
GAA	GAT	TTG	CAA	AAA	GAT	CAT	GCT	GAA	GGT	TCA	AGC	TTG	GAA	AAT	ATC	1111
Glu	Asp	Leu	Gln	Lys	Asp	His	Ala	Glu	Gly	Ser	Ser	Leu	Glu	Asn	Ile	
340					345					350					355	
CTA	CTC	GCT	GTC	GCG	CAA	AGC	CTG	AAT	CTC	AAA	TCC	AGC	GAA	ATC	AAA	1159
Leu	Leu	Ala	Val	Ala	Gln	Ser	Leu	Asn	Leu	Lys	Ser	Ser	Glu	Ile	Lys	
				360					365					370		
GTC	TCT	TCG	CGC	CAA	AAA	AAT	GTC	GCT	TTG	GCG	AGG	AAA	TTA	GTC	GTG	1207
Val	Ser	Ser	Arg	Gln	Lys	Asn	Val	Ala	Leu	Ala	Arg	Lys	Leu	Val	Val	
			375					380					385			
TAT	TTC	GCC	AGG	CTT	TAT	ACC	CCT	AAC	CCC	ACG	CTC	TCG	CTC	GCT	CAA	1255
Tyr	Phe	Ala	Arg	Leu	Tyr	Thr	Pro	Asn	Pro	Thr	Leu	Ser	Leu	Ala	Gln	
		390					395					400				
TTT	TTG	GAT	TTA	AAG	GAT	CAT	TCA	AGC	ATT	TCT	AAA	ATG	TAT	TCT	GGC	1303
Phe	Leu	Asp	Leu	Lys	Asp	His	Ser	Ser	Ile	Ser	Lys	Met	Tyr	Ser	Gly	
	405					410					415					
GTT	AAA	AAA	ATG	CTT	GAA	GAA	GAA	AAA	AGC	CCT	TTT	GTC	TTA	AGC	CTT	1351
Val	Lys	Lys	Met	Leu	Glu	Glu	Glu	Lys	Ser	Pro	Phe	Val	Leu	Ser	Leu	
420					425					430					435	
AGA	GAA	GAA	ATC	AAA	AAC	CGC	TTG	AAC	GAA	TTG	AAC	GAC	AAA	AAA	ACC	1399
Arg	Glu	Glu	Ile	Lys	Asn	Arg	Leu	Asn	Glu	Leu	Asn	Asp	Lys	Lys	Thr	
				440					445					450		
GCT	TTC	AAT	TCA	AGT	GAA	TGAAAAAAGG	CTTATGAAAA	AGCGTTTCAT	TCACTTCT							1455
Ala	Phe	Asn	Ser	Ser	Glu											
				455												

20	25	30	35	
AAC CCT AAC GCA AGC AAG AGC GAT ATT GCC TTT TTT TAT GCC CCC AAC				199
Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr Ala Pro Asn	40	45	50	
CAA GTC TTA TGC ACC ACG ATT ACA GCT AAA TAC GGC GCG TTG CTT AAA				247
Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala Leu Leu Lys	55	60	65	
GAA ATT TTA AGC CAG AAT AAA GTC GGC ATG CAT TTA GCC CAC AGC GTG				295
Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala His Ser Val	70	75	80	
GAT GTG CGT ATT GAA GTA GCG CCT AAA ATC CAA ATT AAC GCC CAA TCT				343
Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn Ala Gln Ser	85	90	95	
AAT ATC AAT TAC AAA GCC ATA AAA ACG AGC GTC AAA GAC TCT TAC ACT				391
Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp Ser Tyr Thr	100	105	110	115
TTT GAA AAT TTT GTC GTA GGC TCA TGC AAT AAC ACC GTT TAT GAA ATC				439
Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val Tyr Glu Ile	120	125	130	
GCT AAA AAA GTC GCC CAA AGC GAT ACC CCC CCT TAT AAC CCG GTG CTT				487
Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn Pro Val Leu	135	140	145	
TTT TAT GGC GGC ACA GGG TTA GGC AAA ACG CAC ATT TTA AAC GCT ATC				535
Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu Asn Ala Ile	150	155	160	
GGC AAC CAT GCC CTA GAA AAG CAT AAA AAA GTC GTG TTA GTC ACT TCA				583
Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu Val Thr Ser	165	170	175	
GAA GAC TTT TTG ACA GAC TTT TTA AAG CAT TTA GAC AAC AAA ACC ATG				631
Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn Lys Thr Met	180	185	190	195
GAT TCT TTT AAA GCA AAA TAC CGC CAT TGC GAC TTT TTC TTG TTA GAT				679
Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe Leu Leu Asp	200	205	210	
GAC GCT CAA TTT TTG CAA GGA AAA CCC AAG CTA GAA GAA GAA TTT TTC				727
Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu Glu Phe Phe	215	220	225	
CAC ACC TTT AAC GAA TTG CAC GCC AAC AGC AAA CAA ATC GTA TTG ATT				775
His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile Val Leu Ile	230	235	240	
TCA GAC CGA TCG CCT AAA AAC ATC GCC GGC TTA GAA GAT CGC TTA AAA				823

```

225          230          235          240
Ile Ala Lys Asn His Gln Val Ile Val Val Tyr Pro Leu Val Asn Glu
          245          250          255
Ser Glu Lys Ile Pro Tyr Leu Ser Leu Ser Glu Gly Ala Ser Phe Trp
          260          265          270
Gln Lys Arg Phe Lys Lys Val Tyr Thr Thr Ser Gly Gln Asp Lys Asn
          275          280          285
Lys Glu Glu Val Ile Glu Glu Phe Arg Glu Ser Gly Ser Ile Leu Leu
          290          295          300
Ala Thr Thr Leu Ile Glu Val Gly Ile Ser Leu Pro Arg Leu Ser Val
305          310          315          320
Met Val Ile Leu Ala Pro Glu Arg Leu Gly Leu Ala Thr Leu His Gln
          325          330          335
Leu Arg Gly Arg Val Ser Arg Asn Gly Leu Lys Gly Tyr Cys Phe Leu
          340          345          350
Cys Thr Ile Gln Glu Glu Asn Glu Arg Leu Glu Lys Phe Ala Asp Glu
          355          360          365
Leu Asp Gly Phe Lys Ile Ala Glu Leu Asp Leu Glu Tyr Arg Lys Ser
          370          375          380
Gly Asp Leu Leu Gln Gly Gly Glu Gln Ser Gly Asn Ser Phe Glu Tyr
385          390          395          400
Ile Asp Leu Ala Lys Asp Glu Asn Ile Ile Ala Glu Val Lys Arg Asp
          405          410          415
Phe Leu Lys Ala Ala Ser Val Ser Arg Gly Thr Phe Glu Asn
          420          425          430

```

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...1417
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

```

TGTTATTCCT TTTTCATTCA CCACTTATTC ACGCTATAAT AACGCC ATG GAT ACC      55
                                     Met Asp Thr
                                     1

AAC AAC AAT ATT GAA AAA GAA ATC TTG GCG CTA GTC AAA CAA AAT CCT      103
Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys Gln Asn Pro
   5              10              15

AAA GTT AGT CTC ATA GAG TAT GAA AAT TAC TTT AGC CAA CTC AAA TAC      151
Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln Leu Lys Tyr

```

GAT TTA CTC CAG GGA GGG GAG CAG AGC GGG AAT AGT TTT GAA TAC ATT 1257
 Asp Leu Leu Gln Gly Gly Glu Gln Ser Gly Asn Ser Phe Glu Tyr Ile
 390 395 400

GAC TTA GCC AAA GAT GAA AAC ATT ATC GCT GAA GTG AAA CGG GAT TTT 1305
 Asp Leu Ala Lys Asp Glu Asn Ile Ile Ala Glu Val Lys Arg Asp Phe
 405 410 415

TTA AAG GCC GCT AGC GTT TCA CGG GGA ACA TTT GAA AAT TGAAAATTAA GG 1356
 Leu Lys Ala Ala Ser Val Ser Arg Gly Thr Phe Glu Asn
 420 425 430

CAGAATTGGG TAATTTAAAT CATTTAAAAA AAG 1389

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

Met Leu Phe Tyr Met Lys Asn Leu Glu Arg Lys Lys Leu Gln Phe Gly
 1 5 10 15
 Ala Lys Ile Ala Cys Pro Asn Asn Asn Glu Arg Leu Lys Ala Phe Ile
 20 25 30
 Ala Ser Leu Pro Phe Lys Leu Thr Arg Asp Gln Gln Asn Ala Ile Lys
 35 40 45
 Glu Ile Gln Asn Asp Leu Thr Ser Ser Ile Ala Cys Lys Arg Leu Ile
 50 55 60
 Ile Gly Asp Val Gly Cys Gly Lys Thr Met Val Ile Leu Ala Ser Met
 65 70 75 80
 Val Leu Thr Tyr Pro Asn Lys Thr Leu Leu Met Ala Pro Thr Ser Ile
 85 90 95
 Leu Ala Lys Gln Leu Tyr Asn Glu Ala Leu Lys Phe Leu Pro Pro Tyr
 100 105 110
 Phe Glu Val Glu Leu Leu Leu Gly Gly Ser Tyr Lys Lys Arg Ser Asn
 115 120 125
 His Leu Phe Glu Thr Ile Thr His Val Val Ile Gly Thr Gln Ala Leu
 130 135 140
 Leu Phe Asp Lys Arg Asp Leu Asn Glu Phe Ala Leu Val Ile Thr Asp
 145 150 155 160
 Glu Gln His Arg Phe Gly Thr Lys Gln Arg Tyr Gln Leu Glu Lys Met
 165 170 175
 Ala Ser Ser Lys Gly Asn Lys Pro His Ser Leu Gln Phe Ser Ala Thr
 180 185 190
 Pro Ile Pro Arg Thr Leu Ala Leu Ala Lys Ser Ala Phe Val Lys Thr
 195 200 205
 Thr Met Ile Arg Glu Ile Pro Tyr Pro Lys Glu Ile Glu Thr Leu Val
 210 215 220
 Leu His Lys Arg Asp Phe Lys Ile Val Met Glu Lys Ile Ser Glu Glu

Gln	His	Arg	Phe	Gly	Thr	Lys	Gln	Arg	Tyr	Gln	Leu	Glu	Lys	Met	Ala	
			165					170					175			
AGC	AGT	AAG	GGT	AAT	AAA	CCC	CAT	TCT	TTG	CAA	TTT	TCC	GCT	ACC	CCC	633
Ser	Ser	Lys	Gly	Asn	Lys	Pro	His	Ser	Leu	Gln	Phe	Ser	Ala	Thr	Pro	
		180					185					190				
ATT	CCT	CGC	ACG	CTC	GCC	CTA	GCC	AAA	AGC	GCG	TTT	GTG	AAA	ACG	ACC	681
Ile	Pro	Arg	Thr	Leu	Ala	Leu	Ala	Lys	Ser	Ala	Phe	Val	Lys	Thr	Thr	
	195					200					205					
ATG	ATT	AGA	GAA	ATC	CCT	TAT	CCT	AAA	GAG	ATT	GAA	ACT	CTA	GTC	TTG	729
Met	Ile	Arg	Glu	Ile	Pro	Tyr	Pro	Lys	Glu	Ile	Glu	Thr	Leu	Val	Leu	
210					215				220						225	
CAT	AAA	AGA	GAT	TTT	AAA	ATA	GTG	ATG	GAG	AAA	ATC	AGC	GAA	GAA	ATC	777
His	Lys	Arg	Asp	Phe	Lys	Ile	Val	Met	Glu	Lys	Ile	Ser	Glu	Glu	Ile	
			230					235						240		
GCT	AAA	AAC	CAT	CAA	GTC	ATT	GTC	GTC	TAT	CCG	CTG	GTG	AAT	GAG	AGC	825
Ala	Lys	Asn	His	Gln	Val	Ile	Val	Val	Tyr	Pro	Leu	Val	Asn	Glu	Ser	
			245					250					255			
GAA	AAA	ATC	CCG	TAT	TTA	TCG	CTC	AGT	GAG	GGG	GCG	AGT	TTT	TGG	CAA	873
Glu	Lys	Ile	Pro	Tyr	Leu	Ser	Leu	Ser	Glu	Gly	Ala	Ser	Phe	Trp	Gln	
	260						265					270				
AAA	CGC	TTT	AAA	AAG	GTT	TAT	ACC	ACT	TCA	GGG	CAA	GAT	AAA	AAT	AAA	921
Lys	Arg	Phe	Lys	Lys	Val	Tyr	Thr	Thr	Ser	Gly	Gln	Asp	Lys	Asn	Lys	
	275					280					285					
GAA	GAA	GTG	ATT	GAA	GAA	TTT	AGA	GAA	TCC	GGG	AGC	ATT	CTT	TTA	GCG	969
Glu	Glu	Val	Ile	Glu	Glu	Phe	Arg	Glu	Ser	Gly	Ser	Ile	Leu	Leu	Ala	
290					295				300						305	
ACT	ACG	CTC	ATT	GAG	GTG	GGC	ATT	TCT	TTA	CCA	CGA	TTG	AGC	GTG	ATG	1017
Thr	Thr	Leu	Ile	Glu	Val	Gly	Ile	Ser	Leu	Pro	Arg	Leu	Ser	Val	Met	
			310					315						320		
GTG	ATT	TTA	GCG	CCC	GAA	AGG	TTA	GGC	TTA	GCG	ACT	TTA	CAC	CAG	TTA	1065
Val	Ile	Leu	Ala	Pro	Glu	Arg	Leu	Gly	Leu	Ala	Thr	Leu	His	Gln	Leu	
		325					330						335			
AGG	GGG	CGC	GTT	TCT	CGT	AAC	GGC	TTG	AAA	GGC	TAT	TGT	TTT	TTA	TGC	1113
Arg	Gly	Arg	Val	Ser	Arg	Asn	Gly	Leu	Lys	Gly	Tyr	Cys	Phe	Leu	Cys	
		340					345					350				
ACG	ATC	CAA	GAA	GAA	AAC	GAA	CGA	TTA	GAA	AAG	TTT	GCT	GAT	GAA	TTG	1161
Thr	Ile	Gln	Glu	Glu	Asn	Glu	Arg	Leu	Glu	Lys	Phe	Ala	Asp	Glu	Leu	
	355					360					365					
GAC	GGC	TTT	AAA	ATC	GCT	GAA	TTG	GAT	TTA	GAA	TAC	AGA	AAA	AGC	GGG	1209
Asp	Gly	Phe	Lys	Ile	Ala	Glu	Leu	Asp	Leu	Glu	Tyr	Arg	Lys	Ser	Gly	
370					375				380						385	

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 55...1344
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

```

GAAACGAATA AAAATTTTCC TTCACAACAT TTAAATGCAT TAAAATACAT TGAA ATG      57
                                   Met
                                   1

CTT TTT TAT ATG AAA AAT TTA GAG CGC AAA AAA TTG CAA TTT GGC GCT      105
Leu Phe Tyr Met Lys Asn Leu Glu Arg Lys Lys Leu Gln Phe Gly Ala
              5                      10                      15

AAA ATC GCA TGC CCC AAT AAT AAC GAG CGC TTG AAA GCG TTT ATC GCT      153
Lys Ile Ala Cys Pro Asn Asn Asn Glu Arg Leu Lys Ala Phe Ile Ala
              20                      25                      30

TCT TTA CCC TTT AAA CTC ACA CGC GAT CAA CAA AAC GCC ATT AAA GAA      201
Ser Leu Pro Phe Lys Leu Thr Arg Asp Gln Gln Asn Ala Ile Lys Glu
              35                      40                      45

ATC CAA AAC GAT CTC ACT AGC TCC ATA GCG TGC AAG CGT TTG ATT ATA      249
Ile Gln Asn Asp Leu Thr Ser Ser Ile Ala Cys Lys Arg Leu Ile Ile
50                      55                      60                      65

GGC GAT GTG GGG TGC GGG AAA ACG ATG GTG ATT TTA GCG AGC ATG GTA      297
Gly Asp Val Gly Cys Gly Lys Thr Met Val Ile Leu Ala Ser Met Val
              70                      75                      80

TTA ACT TAC CCA AAT AAA ACC CTT TTA ATG GCG CCC ACT TCC ATT CTC      345
Leu Thr Tyr Pro Asn Lys Thr Leu Leu Met Ala Pro Thr Ser Ile Leu
              85                      90                      95

GCT AAA CAG CTT TAT AAC GAA GCC TTA AAA TTT TTA CCC CCT TAT TTT      393
Ala Lys Gln Leu Tyr Asn Glu Ala Leu Lys Phe Leu Pro Pro Tyr Phe
              100                      105                      110

GAA GTG GAA TTG CTG CTC GGC GGG AGT TAC AAG AAG CGA TCC AAT CAT      441
Glu Val Glu Leu Leu Leu Gly Gly Ser Tyr Lys Lys Arg Ser Asn His
              115                      120                      125

TTG TTT GAA ACA ATC ACG CAT GTG GTT ATC GGC ACG CAA GCG TTG TTG      489
Leu Phe Glu Thr Ile Thr His Val Val Ile Gly Thr Gln Ala Leu Leu
130                      135                      140                      145

TTT GAT AAG CGC GAT TTG AAT GAA TTC GCT CTA GTG ATC ACT GAT GAA      537
Phe Asp Lys Arg Asp Leu Asn Glu Phe Ala Leu Val Ile Thr Asp Glu
              150                      155                      160

CAG CAC CGA TTT GGC ACC AAG CAG CGC TAC CAA TTA GAA AAA ATG GCA      585

```

BNSDOCID: <WO 9843478A1 | >


```

GGG ATT AGA AGA GAT TTA TTA GAA GAA GAG CAA TCA AAT AAA AAA ACA      1110
Gly Ile Arg Arg Asp Leu Leu Glu Glu Glu Gln Ser Asn Lys Lys Thr
                               350                               355                               360

ATT ACA GAT TTA TTA ACA GAA TGG GGA CAA AAT CAA GAT GCT ACT AAT      1158
Ile Thr Asp Leu Leu Thr Glu Trp Gly Gln Asn Gln Asp Ala Thr Asn
                               365                               370                               375

GAA TTA AAT ATT TTA TTT AAT AAT TCT AGC GAT GAA AGT ATT TTT TCA      1206
Glu Leu Asn Ile Leu Phe Asn Asn Ser Ser Asp Glu Ser Ile Phe Ser
                               380                               385                               390

AAT CCT AAA CCT ACA AAA CTC ATC AAC CGA TTG ATT GAA TTA TCC ACC      1254
Asn Pro Lys Pro Thr Lys Leu Ile Asn Arg Leu Ile Glu Leu Ser Thr
                               395                               400                               405

AAC GAG GGC GAC ATC ATC TTA GAC TTT TTT GCC GGG AGC GGG ACA ACC      1302
Asn Glu Gly Asp Ile Ile Leu Asp Phe Phe Ala Gly Ser Gly Thr Thr
410                               415                               420                               425

GCG CAT GCG GTG TTA GAG AGT AAT AAG AGC GAT TAT CAA AAA TTA AGT      1350
Ala His Ala Val Leu Glu Ser Asn Lys Ser Asp Tyr Gln Lys Leu Ser
                               430                               435                               440

GAG GGG GGG GGG GGT TAT TTA ATG GTT TGAACGCCGC ATTTAAAGAA AGGCGCT  1404
Glu Gly Gly Gly Gly Tyr Leu Met Val
                               445                               450

TCATTCTCGT C                                                                1415

```

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

```

Met Gln Asn Lys Glu Ile Gly Glu Glu Lys Ser Val Asn Glu Lys Asn
 1                               5                               10                               15
Val Glu Val Phe Asn Arg Tyr Phe Pro Gly Cys Leu Ser Ile Glu Asn
                               20                               25                               30
Asp Asn Lys Leu Thr Leu Asp Thr Gly Lys Leu Lys Ala Leu Leu Gly
                               35                               40                               45
Asp Phe Ser Glu Ile Lys Glu Glu Gly Tyr Gly Leu Asp Phe Val Gly
                               50                               55                               60
Lys Lys Ile Ala Leu Asn Gln Ala Phe Lys Lys Asn His Lys Ile Leu
65                               70                               75                               80
Lys Pro Leu Asn Glu Ser Thr Ser Lys His Val Leu Ile Lys Gly Asp
                               85                               90                               95
Asn Leu Asp Ala Leu Lys Ile Leu Lys Gln Ser Tyr Ser Glu Lys Ile

```

Asn Thr Lys	Asn Glu Asn Phe Ile Tyr Gly Asp Asp Phe Ser Gln Ser	
125	130	135
AAT GAA GAG GTT TTA AAA ACA TTG GAT TAT TCT AAA GAA AAA TTG GAT	486	
Asn Glu Glu Val Leu Lys Thr Leu Asp Tyr Ser Lys Glu Lys Leu Asp		
140	145	150
TAC ATC AAG AAC CTT TTT GGG TCA AAA TGC CAT AGC GGG TGG CTT AGT	534	
Tyr Ile Lys Asn Leu Phe Gly Ser Lys Cys His Ser Gly Trp Leu Ser		
155	160	165
TTC ATG TAT CCC AGA TTG TTG CTC GCT AAA GAT TTG CTC AAA CAA GAC	582	
Phe Met Tyr Pro Arg Leu Leu Leu Ala Lys Asp Leu Leu Lys Gln Asp		
170	175	180
GGC GTG ATT TTC ATT TCT ATT GAC GAT AAC GAA TGC GCT CAA CTC AAA	630	
Gly Val Ile Phe Ile Ser Ile Asp Asp Asn Glu Cys Ala Gln Leu Lys		
190	195	200
CTT TTA TGC GAT GAA ATT TTT GGG GAG GGG AAT TTT GTG GCG TGT TTA	678	
Leu Leu Cys Asp Glu Ile Phe Gly Glu Gly Asn Phe Val Ala Cys Leu		
205	210	215
AAA TGG AAA AAG AAA AAA CAA CCA AGT TTT TTA TCA AAA GTA GCC GTA	726	
Lys Trp Lys Lys Lys Lys Gln Pro Ser Phe Leu Ser Lys Val Ala Val		
220	225	230
ATA TTA GAA TAT ATT TTA GTA TAT GCA AAA GAT TTT AGT CTA ATT GAT	774	
Ile Leu Glu Tyr Ile Leu Val Tyr Ala Lys Asp Phe Ser Leu Ile Asp		
235	240	245
AAG TTA GGT TTA GAT AAT GTA TCT GAT AGC GAT AAA CCT ATC ATT AAT	822	
Lys Leu Gly Leu Asp Asn Val Ser Asp Ser Asp Lys Pro Ile Ile Asn		
250	255	260
ACC TCT AAT AAT TTA TCA AAA AGA TAT TTT AAA AAA GGT ATT AGG GTT	870	
Thr Ser Asn Asn Leu Ser Lys Arg Tyr Phe Lys Lys Gly Ile Arg Val		
270	275	280
AAA TCT GAT TTA AAT TTT ATA AAG AGT GGA AAG TAT CAA AAT AAG ACA	918	
Lys Ser Asp Leu Asn Phe Ile Lys Ser Gly Lys Tyr Gln Asn Lys Thr		
285	290	295
ATG ACG ATT GAA TTT ATG AAT GAT ATT TTT ATT GAA AAT GGC AGA ACT	966	
Met Thr Ile Glu Phe Met Asn Asp Ile Phe Ile Glu Asn Gly Arg Thr		
300	305	310
AAA AAT GAT TTT GAA TGT ATA GGT AAA TTT AGA ACA GGA CAA GAA AAT	1014	
Lys Asn Asp Phe Glu Cys Ile Gly Lys Phe Arg Thr Gly Gln Glu Asn		
315	320	325
ATT AAT GAA TTT ATT GAA AAA GAT TTA ATT TTT ATA ACA AAA AAT TTA	1062	
Ile Asn Glu Phe Ile Glu Lys Asp Leu Ile Phe Ile Thr Lys Asn Leu		
330	335	340
		345

Tyr His Leu Thr Asp Glu Glu Ile Lys Ile Ile Glu Glu Gly Gln
 265 1270 1275 1

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1377
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

```

TTTAAATCAT TTAAAAAAG GATAGAG ATG CAA AAT AAA GAA ATT GGT GAA GAA      54
                Met Gln Asn Lys Glu Ile Gly Glu Glu
                  1                5

AAA AGC GTT AAT GAA AAA AAT GTA GAG GTT TTT AAT CGT TAT TTT CCC      102
Lys Ser Val Asn Glu Lys Asn Val Glu Val Phe Asn Arg Tyr Phe Pro
10                15                20                25

GGT TGC TTG AGT ATA GAA AAT GAT AAC AAG CTC ACG CTG GAT ACA GGA      150
Gly Cys Leu Ser Ile Glu Asn Asp Asn Lys Leu Thr Leu Asp Thr Gly
                30                35                40

AAA TTA AAA GCG TTA CTA GGG GAT TTT AGC GAG ATA AAA GAA GAG GGC      198
Lys Leu Lys Ala Leu Leu Gly Asp Phe Ser Glu Ile Lys Glu Glu Gly
                45                50                55

TAT GGG TTG GAT TTT GTG GGT AAG AAA ATC GCC TTA AAC CAA GCT TTT      246
Tyr Gly Leu Asp Phe Val Gly Lys Lys Ile Ala Leu Asn Gln Ala Phe
                60                65                70

AAG AAA AAT CAT AAG ATT TTA AAG CCC TTA AAC GAA TCC ACT AGC AAG      294
Lys Lys Asn His Lys Ile Leu Lys Pro Leu Asn Glu Ser Thr Ser Lys
                75                80                85

CAC GTT CTC ATC AAG GGC GAT AAT TTA GAC GCT CTC AAA ATC TTA AAA      342
His Val Leu Ile Lys Gly Asp Asn Leu Asp Ala Leu Lys Ile Leu Lys
90                95                100                105

CAA AGC TAT AGT GAA AAA ATC AAA ATG ATT TAC ATT GAC CCG CCT TAC      390
Gln Ser Tyr Ser Glu Lys Ile Lys Met Ile Tyr Ile Asp Pro Pro Tyr
                110                115                120

AAC ACG AAA AAC GAG AAT TTT ATC TAT GGC GAT GAT TTC TCG CAA TCC      438

```

										820			825			830		
Val	Leu	Asp	Asp	Glu	Gly	Asp	Phe	Ser	Gly	Phe	Asp	Cys	Ile	Ile	Gly			
		835					840					845						
Asn	Pro	Pro	Tyr	Ile	Arg	Gln	Glu	His	Ile	Lys	Asp	Leu	Lys	Pro	Leu			
	850					855					860							
Leu	Glu	Lys	Gln	Tyr	Gln	Asp	Phe	Tyr	Asn	Ser	Thr	Ala	Asp	Ile	Tyr			
865					870					875					880			
Thr	Tyr	Phe	Phe	Ala	Leu	Ala	Phe	His	Leu	Leu	Lys	Glu	Lys	Gly	Phe			
				885					890						895			
Ser	Ala	Phe	Ile	Thr	Ser	Asn	Lys	Tyr	Thr	Arg	Ala	Lys	Tyr	Gly	Ala			
			900					905					910					
Lys	Leu	Arg	Glu	Trp	Leu	Leu	Lys	Lys	Thr	Thr	Ile	Val	Ser	Tyr	Met			
	915						920					925						
Glu	Leu	Asn	Ala	Leu	Lys	Val	Phe	Glu	Ser	Ala	Ala	Val	Asp	Thr	Ser			
	930					935					940							
Ile	Ile	His	Phe	Ile	Lys	Gln	Thr	Pro	Ser	Lys	Glu	Ser	Glu	Phe	Lys			
945					950					955					960			
Tyr	Tyr	Glu	Pro	Thr	Pro	Asn	Asp	Lys	Asp	Asp	Leu	Lys	Ser	Thr	Pro			
				965					970						975			
His	Leu	Leu	Met	Lys	Gln	Asn	Val	Leu	Ser	Thr	Glu	Ser	Phe	Ile	Phe			
			980					985					990					
Ala	Asn	Ala	Thr	Leu	Leu	Asp	Leu	Arg	Asp	Lys	Ile	Glu	Ser	Val	Gly			
	995					1000					1005							
Thr	Pro	Leu	Lys	Asp	Trp	Asp	Ile	Gln	Ile	Asn	Tyr	Gly	Ile	Lys	Thr			
1010					1015					1020								
Gly	Ala	Asn	Glu	Ala	Phe	Ile	Ile	Pro	Thr	Glu	Lys	Arg	Glu	Glu	Ile			
025				1030					1035						1040			
Leu	Asn	Ala	Cys	Lys	Thr	Gln	Glu	Glu	Arg	Glu	Arg	Thr	Glu	Arg	Leu			
				1045				1050					1055					
Ile	Lys	Pro	Ile	Leu	Arg	Gly	Lys	Asp	Ile	Lys	Arg	Tyr	Ser	Tyr	Glu			
		1060					1065					1070						
Trp	Ala	His	Leu	Trp	Val	Ile	Asn	Thr	His	Asn	Gly	Tyr	Thr	Ser	Ser			
	1075					1080				1085								
Leu	Lys	Ser	Lys	Ile	Pro	Pro	Ile	Asp	Ile	Glu	Lys	Tyr	Pro	Ala	Ile			
	1090				1095					1100								
Lys	Ala	His	Leu	Asp	Ala	His	Tyr	Asp	Thr	Ile	Ala	Thr	Arg	Cys	Asp			
105				1110					1115						1120			
Gln	Gly	Asp	Thr	Pro	Tyr	His	Leu	Arg										

Pro	Leu	Pro	Leu	Leu	Lys	Tyr	Leu	Phe	Lys	Phe	Leu	Arg	Leu	Tyr	Lys
385					390					395					400
Phe	Thr	Thr	Thr	Pro	Lys	Asp	Ile	Lys	Asp	Asn	Thr	Asp	Thr	Ser	Glu
				405					410					415	
Ser	Arg	Leu	Ile	Asn	Pro	Ser	Val	Leu	Gly	Leu	Val	Phe	Glu	Lys	Leu
			420					425					430		
Asn	Gly	Tyr	Lys	Glu	Gly	Ser	Phe	Tyr	Thr	Pro	Ser	Phe	Ile	Thr	Ser
		435					440					445			
Tyr	Met	Cys	Lys	Glu	Ser	Ile	Thr	Pro	Ile	Val	Leu	Asp	Lys	Phe	Asn
	450					455					460				
Ala	Ile	Tyr	Gln	Trp	Asp	Cys	Glu	Asn	Leu	Lys	Ala	Leu	Arg	Gly	Glu
465					470					475					480
Ile	Asp	Arg	Asn	Phe	Ser	Asn	Glu	Lys	Ala	Lys	Glu	Tyr	Leu	Asn	Thr
			485						490					495	
Leu	Leu	Thr	Leu	Arg	Ile	Cys	Asp	Pro	Ala	Val	Gly	Ser	Gly	His	Phe
			500					505					510		
Leu	Val	Ser	Ala	Leu	Asn	Glu	Met	Val	Arg	Val	Ala	Tyr	Glu	Leu	Gly
	515						520					525			
Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Tyr	Asp	Leu	Lys	Leu	Glu	Asn	Asp	Glu
	530					535					540				
Ile	Ile	Ile	His	His	Thr	Pro	Thr	Gly	Glu	Ile	Phe	Asn	Tyr	Ile	Lys
545					550					555					560
Pro	Asp	Ser	Glu	Asn	Asp	Pro	His	His	His	Ile	Gln	Lys	Glu	Leu	Phe
			565						570					575	
Asn	Leu	Lys	Lys	Ser	Ile	Ile	Glu	Asn	Cys	Leu	Phe	Gly	Val	Asp	Ile
			580					585					590		
Asn	Pro	Asn	Ser	Cys	Glu	Ile	Thr	Lys	Leu	Arg	Leu	Trp	Ile	Glu	Leu
		595					600					605			
Leu	Lys	Tyr	Ser	Tyr	Tyr	Ile	Phe	Glu	Lys	Gly	Lys	Asn	Thr	Asn	Ala
	610					615					620				
Leu	Glu	Thr	Leu	Pro	Asn	Ile	Asp	Ile	Asn	Ile	Lys	Cys	Ala	Asn	Ser
625					630					635					640
Leu	Ile	Ser	Arg	Phe	Ala	Leu	Lys	Asp	Lys	Ala	Leu	Leu	Lys	Ser	Glu
			645						650					655	
Lys	Asn	Lys	Asn	Leu	Glu	Tyr	Ser	Ile	Ala	Glu	Tyr	Lys	Glu	Leu	Val
			660					665					670		
Lys	Ile	Tyr	Lys	Asp	Pro	Lys	Ile	Leu	Glu	Thr	Leu	Thr	His	Pro	Ile
	675						680					685			
Lys	Asp	Ser	Asn	Ala	Val	Arg	Lys	Tyr	Ala	Lys	Glu	Arg	Leu	Tyr	Gln
	690					695					700				
Glu	Leu	Lys	Gln	Asn	Pro	Asn	Lys	Asp	Phe	Lys	Lys	Ala	Leu	Asn	Asp
705					710					715					720
Arg	Ile	Glu	Lys	Ile	Lys	Lys	Ala	Phe	Lys	Leu	Thr	Leu	Asn	Pro	Pro
			725						730					735	
Pro	Lys	Glu	Leu	Lys	Phe	Lys	Lys	Phe	Leu	Lys	Glu	His	Leu	Glu	Leu
			740					745					750		
Tyr	Gly	Lys	Ser	Ile	Leu	Glu	Glu	Ala	Asn	Tyr	Asn	Gly	Leu	Glu	Leu
		755					760					765			
Glu	Ala	Leu	Ala	Leu	Glu	Lys	Gln	Met	Ala	Asn	Leu	Phe	Phe	Asp	Tyr
	770					775					780				
Arg	Pro	Tyr	Pro	Lys	Leu	Asp	Lys	Ser	Asp	Lys	Val	Val	Gly	Leu	Glu
785					790					795					800
His	Phe	Asn	Arg	Tyr	Val	Leu	Thr	Ser	Tyr	Lys	Asp	Leu	Gln	Asp	Glu
			805						810				815		
Asn	Glu	Arg	Tyr	Ala	Asn	Ala	Leu	Glu	Trp	Arg	Phe	Glu	Phe	Pro	Glu

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

```

Met Asp Tyr Lys Lys Leu Asp Leu Pro Asn Thr Asn Tyr Pro Asn Gln
 1           5           10           15
Glu Gln Leu Lys Ala Phe Glu Thr Ala Phe Asp Ala Phe Leu Glu Thr
          20           25           30
Asn Gln Gln Glu Asn Glu Asn His Gln Asn Asp Ala Phe Asn Asp Leu
          35           40           45
Leu Lys Gly Val Phe Lys Tyr Lys Val Lys Pro Thr Lys Lys Ile Asp
          50           55           60
Ser Thr Ile Leu Asn Glu Asn Asn Glu Val Glu Val Ile Ile Glu Phe
          65           70           75           80
Lys Ala Leu Lys Asn Pro Asn Glu Phe Ile Lys Lys Gly Asp Leu Asn
          85           90           95
Val Lys Ala Phe His Glu Ser Leu Leu Ser Tyr Leu Thr Glu Arg Lys
          100          105          110
Glu Gly Asn Asn Asn Leu Lys His Leu Ile Leu Ala Thr Ile Lys Glu
          115          120          125
Leu Tyr Ile Ile Asp Ala Asn Glu Phe Glu Val Phe Asn Lys Asp Lys
          130          135          140
Glu Ile Glu Asn Ala Phe Lys Asn Cys His Asp Arg Lys Gly Asn Asp
          145          150          155          160
Thr Arg Thr Lys Ala Phe Tyr Asp Ala Cys Gln Lys Arg Leu Asn Glu
          165          170          175
Phe Asp Arg Ser Leu Lys Tyr His Tyr Ile Pro Leu Lys Lys Glu Asn
          180          185          190
Leu Ala Leu Ile Tyr Gln Ala Leu Ser Pro Asn Phe Leu Leu Lys Ile
          195          200          205
Pro Lys Tyr Ser Asp Ala Asn Thr Leu Asn Lys Asp Phe Tyr Glu Glu
          210          215          220
Leu Leu Tyr Ile Leu Gly Leu Glu Glu Gln Asn Asp Lys Gly Lys Ile
          225          230          235          240
Leu Ile Lys Pro Ser Arg Thr Gln Asn Ser Leu Ser Asp Ala Leu Lys
          245          250          255
Lys Glu Tyr Lys Asn Leu Asp Asp Glu Glu Val Met Ala Leu Leu Ile
          260          265          270
Ala Trp Asn Asn Arg Ile Leu Phe Leu Arg Leu Leu Glu Ser Leu Leu
          275          280          285
Ile Ser Phe Lys His Phe Glu Asn Pro Phe Leu Thr Thr Glu Asn Phe
          290          295          300
Glu Asn Phe Asn Asp Leu Asn Thr Leu Phe Phe Glu Val Leu Ala Lys
          305          310          315          320
Lys Asn Ser Glu Arg Leu Pro Glu Ile Lys Glu Asp Lys Ile Leu Glu
          325          330          335
Lys Ile Pro Tyr Leu Asn Ser Ser Leu Phe Asp Lys Thr Pro Leu Glu
          340          345          350
Leu Lys Gly His Glu Ile Lys Leu Leu Asp Asn Lys Lys Leu Glu Ile
          355          360          365
Tyr Lys Asn Ser Val Leu Lys Lys His Lys Asp Tyr Gln Lys Glu Lys
          370          375          380

```

GAA AAA TAC CCC GCA ATT AAA GCG CAT TTA GAC GCT CAT TAC GAC ACT	3362
Glu Lys Tyr Pro Ala Ile Lys Ala His Leu Asp Ala His Tyr Asp Thr	
1100 1105 1110	
ATT GCA ACA CGA TGC GAT CAA GGA GAC ACC CCC TAT CAC TTA AGG AAT	3410
Ile Ala Thr Arg Cys Asp Gln Gly Asp Thr Pro Tyr His Leu Arg Asn	
1115 1120 1125 1130	
TGC GCG TAT TTA GAG GAT TTT GAA AAA GAG AAA ATT GTG TGG GCA AGT	3458
Cys Ala Tyr Leu Glu Asp Phe Glu Lys Glu Lys Ile Val Trp Ala Ser	
1135 1140 1145	
GTG GGA TTT GTT GAA TAT TGT ATG ATC CCA GGA TTA TTG ATA CTT GAT	3506
Val Gly Phe Val Glu Tyr Cys Met Ile Pro Gly Leu Leu Ile Leu Asp	
1150 1155 1160	
ACA AAT TAT TTT TTT GAA GTC AGT AAA TTT GGC AAT ACA AAA AAC TAT	3554
Thr Asn Tyr Phe Phe Glu Val Ser Lys Phe Gly Asn Thr Lys Asn Tyr	
1165 1170 1175	
TTG CTT GGA CTT TTA AAT TCA AAA TTG CTA ACT TTT TGG TTA AAA GCT	3602
Leu Leu Gly Leu Leu Asn Ser Lys Leu Leu Thr Phe Trp Leu Lys Ala	
1180 1185 1190	
AAA AAT ACA CCA TTA GGC GAT ATG GGA GCT TAT AGA AAT TAT AAG TAT	3650
Lys Asn Thr Pro Leu Gly Asp Met Gly Ala Tyr Arg Asn Tyr Lys Tyr	
1195 1200 1205 1210	
AAT ATT ATG GAG TTA CCG ATG GTA AAA ATA ACG GCA AAA AAT AAA AAA	3698
Asn Ile Met Glu Leu Pro Met Val Lys Ile Thr Ala Lys Asn Lys Lys	
1215 1220 1225	
ATC GCC GAT AAA ATC ATC GCT TTA GTG GAT AAA ATC CTA CAA GCA AAA	3746
Ile Ala Asp Lys Ile Ile Ala Leu Val Asp Lys Ile Leu Gln Ala Lys	
1230 1235 1240	
GAA AAA GAC CCT AAA GCC AAC ACC CAA AAG TTA GAA AAA GAA ATT GAC	3794
Glu Lys Asp Pro Lys Ala Asn Thr Gln Lys Leu Glu Lys Glu Ile Asp	
1245 1250 1255	
GCC TTA GTC TAT CAG CTC TAC CAC CTC ACC GAT GAA GAA ATT AAG ATC	3842
Ala Leu Val Tyr Gln Leu Tyr His Leu Thr Asp Glu Glu Ile Lys Ile	
1260 1265 1270	
ATT GAA GAG GGG CAG TGAATGGAAA AGTTATTTGA AAAGATATTG CATGAAATGA G	3898
Ile Glu Glu Gly Gln	
1275 1	
ATCAA	3903

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1279 amino acids

(B) TYPE: amino acid

AGC ACC GCT GAC ATT TAC ACC TAC TTT TTT GCC CTG GCT TTC CAC CTT	2690
Ser Thr Ala Asp Ile Tyr Thr Tyr Phe Phe Ala Leu Ala Phe His Leu	
875 880 885 890	
TTA AAA GAA AAG GGG TTT AGC GCT TTC ATC ACT TCT AAC AAA TAT ACG	2738
Leu Lys Glu Lys Gly Phe Ser Ala Phe Ile Thr Ser Asn Lys Tyr Thr	
895 900 905	
CGA GCC AAA TAC GGC GCT AAA TTG AGG GAA TGG CTG CTC AAA AAA ACC	2786
Arg Ala Lys Tyr Gly Ala Lys Leu Arg Glu Trp Leu Leu Lys Lys Thr	
910 915 920	
ACC ATC GTC AGC TAC ATG GAA CTA AAC GCC TTA AAA GTC TTT GAG AGC	2834
Thr Ile Val Ser Tyr Met Glu Leu Asn Ala Leu Lys Val Phe Glu Ser	
925 930 935	
GCT GCA GTG GAT ACC AGC ATC ATT CAT TTC ATC AAA CAA ACG CCC TCT	2882
Ala Ala Val Asp Thr Ser Ile Ile His Phe Ile Lys Gln Thr Pro Ser	
940 945 950	
AAA GAG AGC GAA TTT AAA TAT TAC GAA CCC ACC CCA AAC GAT AAA GAC	2930
Lys Glu Ser Glu Phe Lys Tyr Tyr Glu Pro Thr Pro Asn Asp Lys Asp	
955 960 965 970	
GAT TTG AAA AGC ACC CCA CAC CTT TTG ATG AAA CAA AAC GTG CTT TCA	2978
Asp Leu Lys Ser Thr Pro His Leu Leu Met Lys Gln Asn Val Leu Ser	
975 980 985	
ACA GAA AGC TTT ATT TTT GCC AAC GCC ACG CTT TTA GAT TTG AGG GAC	3026
Thr Glu Ser Phe Ile Phe Ala Asn Ala Thr Leu Leu Asp Leu Arg Asp	
990 995 1000	
AAA ATA GAG AGT GTT GGC ACC CCG CTT AAA GAC TGG GAC ATT CAA ATC	3074
Lys Ile Glu Ser Val Gly Thr Pro Leu Lys Asp Trp Asp Ile Gln Ile	
1005 1010 1015	
AAT TAT GGG ATA AAA ACC GGC GCG AAC GAA GCC TTT ATC ATT CCC ACT	3122
Asn Tyr Gly Ile Lys Thr Gly Ala Asn Glu Ala Phe Ile Ile Pro Thr	
1020 1025 1030	
GAA AAA AGA GAA GAG ATC TTA AAC GCT TGC AAG ACG CAA GAA GAA AGG	3170
Glu Lys Arg Glu Glu Ile Leu Asn Ala Cys Lys Thr Gln Glu Glu Arg	
1035 1040 1045 1050	
GAG CGC ACA GAG AGG CTT ATT AAG CCT ATT TTA AGA GGG AAA GAC ATT	3218
Glu Arg Thr Glu Arg Leu Ile Lys Pro Ile Leu Arg Gly Lys Asp Ile	
1055 1060 1065	
AAA AGG TAT TCT TAT GAG TGG GCG CAT TTG TGG GTT ATC AAC ACC CAT	3266
Lys Arg Tyr Ser Tyr Glu Trp Ala His Leu Trp Val Ile Asn Thr His	
1070 1075 1080	
AAC GGC TAC ACT TCT TCT CTC AAA TCC AAA ATC CCT CCC ATT GAT ATA	3314
Asn Gly Tyr Thr Ser Ser Leu Lys Ser Lys Ile Pro Pro Ile Asp Ile	
1085 1090 1095	

GCC TTG TTA AAA AGC GAA AAA AAT AAA AAC CTA GAA TAC TCT ATC GCT	2018
Ala Leu Leu Lys Ser Glu Lys Asn Lys Asn Leu Glu Tyr Ser Ile Ala	
655 660 665	
GAA TAC AAA GAA CTC GTT AAA ATC TAT AAA GAC CCT AAA ATC TTA GAA	2066
Glu Tyr Lys Glu Leu Val Lys Ile Tyr Lys Asp Pro Lys Ile Leu Glu	
670 675 680	
ACC CTA ACG CAC CCC ATA AAA GAC TCT AAC GCC GTT AGA AAA TAC GCT	2114
Thr Leu Thr His Pro Ile Lys Asp Ser Asn Ala Val Arg Lys Tyr Ala	
685 690 695	
AAA GAA CGC CTT TAT CAA GAA CTA AAA CAA AAT CCT AAC AAA GAT TTT	2162
Lys Glu Arg Leu Tyr Gln Glu Leu Lys Gln Asn Pro Asn Lys Asp Phe	
700 705 710	
AAA AAG GCT CTC AAT GAT AGG ATA GAG AAA ATT AAA AAA GCT TTT AAA	2210
Lys Lys Ala Leu Asn Asp Arg Ile Glu Lys Ile Lys Lys Ala Phe Lys	
715 720 725 730	
CTC ACT TTA AAC CCC CCT CCA AAA GAA TTA AAA TTT AAA AAA TTT TTA	2258
Leu Thr Leu Asn Pro Pro Pro Lys Glu Leu Lys Phe Lys Lys Phe Leu	
735 740 745	
AAA GAG CAT TTA GAA CTC TAT GGC AAG AGT ATC TTA GAA GAG GCA AAC	2306
Lys Glu His Leu Glu Leu Tyr Gly Lys Ser Ile Leu Glu Glu Ala Asn	
750 755 760	
TAC AAC GGC TTA GAA TTG GAA GCC CTA GCA TTA GAA AAG CAA ATG GCG	2354
Tyr Asn Gly Leu Glu Leu Glu Ala Leu Ala Leu Glu Lys Gln Met Ala	
765 770 775	
AAT CTT TTT TTT GAT TAT AGA CCC TAC CCC AAA CTA GAC AAA TCG GAT	2402
Asn Leu Phe Phe Asp Tyr Arg Pro Tyr Pro Lys Leu Asp Lys Ser Asp	
780 785 790	
AAA GTA GTA GGA CTA GAA CAT TTT AAC CGC TAT GTC CTA ACA TCT TAT	2450
Lys Val Val Gly Leu Glu His Phe Asn Arg Tyr Val Leu Thr Ser Tyr	
795 800 805 810	
AAA GAT TTA CAA GAT GAA AAC GAA CGC TAC GCT AAC GCT CTT GAA TGG	2498
Lys Asp Leu Gln Asp Glu Asn Glu Arg Tyr Ala Asn Ala Leu Glu Trp	
815 820 825	
CGC TTT GAA TTC CCT GAA GTT TTA GAT GAT GAG GGG GAT TTT TCA GGC	2546
Arg Phe Glu Phe Pro Glu Val Leu Asp Asp Glu Gly Asp Phe Ser Gly	
830 835 840	
TTT GAT TGC ATC ATT GGG AAT CCA CCT TAT ATC CGC CAA GAA CAC ATC	2594
Phe Asp Cys Ile Ile Gly Asn Pro Pro Tyr Ile Arg Gln Glu His Ile	
845 850 855	
AAA GAC TTA AAG CCT TTA TTA GAA AAG CAA TAC CAA GAT TTC TAT AAC	2642
Lys Asp Leu Lys Pro Leu Leu Glu Lys Gln Tyr Gln Asp Phe Tyr Asn	
860 865 870	

CTT GTT TTT GAA AAA CTC AAC GGC TAT AAA GAG GGG AGC TTT TAT ACC	1346
Leu Val Phe Glu Lys Leu Asn Gly Tyr Lys Glu Gly Ser Phe Tyr Thr	
430 435 440	
CCA AGC TTT ATC ACA AGC TAC ATG TGC AAA GAG AGC ATC ACG CCC ATC	1394
Pro Ser Phe Ile Thr Ser Tyr Met Cys Lys Glu Ser Ile Thr Pro Ile	
445 450 455	
GTG TTG GAT AAA TTC AAC GCC ATT TAT CAG TGG GAC TGC GAA AAT CTA	1442
Val Leu Asp Lys Phe Asn Ala Ile Tyr Gln Trp Asp Cys Glu Asn Leu	
460 465 470	
AAA GCG TTG CGA GGA GAA ATA GAC AGA AAT TTT TCA AAT GAA AAA GCT	1490
Lys Ala Leu Arg Gly Glu Ile Asp Arg Asn Phe Ser Asn Glu Lys Ala	
475 480 485 490	
AAA GAA TAC CTA AAC ACG CTT TTA ACC TTG CGT ATT TGC GAT CCG GCG	1538
Lys Glu Tyr Leu Asn Thr Leu Leu Thr Leu Arg Ile Cys Asp Pro Ala	
495 500 505	
GTG GGG AGC GGG CAT TTC TTG GTT TCA GCG CTC AAT GAA ATG GTG CGG	1586
Val Gly Ser Gly His Phe Leu Val Ser Ala Leu Asn Glu Met Val Arg	
510 515 520	
GTT GCT TAT GAG CTA GGA CTT ATT GCT TCC TTG TAT CGC TAC GAT CTT	1634
Val Ala Tyr Glu Leu Gly Leu Ile Ala Ser Leu Tyr Arg Tyr Asp Leu	
525 530 535	
AAA TTA GAA AAC GAT GAA ATC ATC ATT CAC CAC ACG CCA ACG GGT GAA	1682
Lys Leu Glu Asn Asp Glu Ile Ile Ile His His Thr Pro Thr Gly Glu	
540 545 550	
ATC TTT AAC TAC ATA AAA CCA GAT AGC GAA AAC GAC CCC CAC CAC CAC	1730
Ile Phe Asn Tyr Ile Lys Pro Asp Ser Glu Asn Asp Pro His His His	
555 560 565 570	
ATC CAA AAA GAA CTT TTT AAT CTT AAA AAA TCC ATT ATT GAA AAC TGC	1778
Ile Gln Lys Glu Leu Phe Asn Leu Lys Lys Ser Ile Ile Glu Asn Cys	
575 580 585	
CTT TTT GGC GTG GAT ATT AAC CCC AAT TCT TGC GAA ATC ACC AAG CTC	1826
Leu Phe Gly Val Asp Ile Asn Pro Asn Ser Cys Glu Ile Thr Lys Leu	
590 595 600	
AGG CTA TGG ATA GAG CTT TTA AAA TAC AGC TAT TAT ATT TTT GAA AAG	1874
Arg Leu Trp Ile Glu Leu Leu Lys Tyr Ser Tyr Tyr Ile Phe Glu Lys	
605 610 615	
GGC AAG AAC ACT AAC GCG CTT GAA ACC CTC CCC AAC ATT GAT ATT AAC	1922
Gly Lys Asn Thr Asn Ala Leu Glu Thr Leu Pro Asn Ile Asp Ile Asn	
620 625 630	
ATT AAG TGC GCT AAT TCG CTC ATT TCT AGG TTT GCC CTC AAA GAT AAA	1970
Ile Lys Cys Ala Asn Ser Leu Ile Ser Arg Phe Ala Leu Lys Asp Lys	
635 640 645 650	

Asn	Phe	Leu	Leu	Lys	Ile	Pro	Lys	Tyr	Ser	Asp	Ala	Asn	Thr	Leu	Asn	
		205					210					215				
AAA	GAT	TTT	TAT	GAA	GAA	TTG	CTT	TAC	ATT	TTA	GGG	TTA	GAA	GAG	CAA	722
Lys	Asp	Phe	Tyr	Glu	Glu	Leu	Leu	Tyr	Ile	Leu	Gly	Leu	Glu	Glu	Gln	
		220				225					230					
AAT	GAC	AAA	GGG	AAA	ATT	TTA	ATC	AAG	CCC	AGC	CGC	ACC	CAA	AAT	TCC	770
Asn	Asp	Lys	Gly	Lys	Ile	Leu	Ile	Lys	Pro	Ser	Arg	Thr	Gln	Asn	Ser	
		235			240					245					250	
CTA	AGC	GAT	GCT	TTA	AAA	AAG	GAA	TAC	AAA	AAT	TTA	GAC	GAT	GAA	GAA	818
Leu	Ser	Asp	Ala	Leu	Lys	Lys	Glu	Tyr	Lys	Asn	Leu	Asp	Asp	Glu	Glu	
				255					260					265		
GTC	ATG	GCG	TTG	CTC	ATC	GCT	TGG	AAT	AAC	CGC	ATC	TTG	TTT	TTA	CGG	866
Val	Met	Ala	Leu	Leu	Ile	Ala	Trp	Asn	Asn	Arg	Ile	Leu	Phe	Leu	Arg	
			270					275					280			
CTT	TTA	GAA	AGC	CTT	TTA	ATT	TCT	TTT	AAG	CAT	TTT	GAA	AAT	CCT	TTC	914
Leu	Leu	Glu	Ser	Leu	Leu	Ile	Ser	Phe	Lys	His	Phe	Glu	Asn	Pro	Phe	
		285					290					295				
TTA	ACC	ACA	GAA	AAC	TTT	GAA	AAT	TTC	AAC	GAT	TTA	AAC	ACG	CTC	TTT	962
Leu	Thr	Thr	Glu	Asn	Phe	Glu	Asn	Phe	Asn	Asp	Leu	Asn	Thr	Leu	Phe	
	300					305					310					
TTT	GAA	GTC	CTA	GCC	AAG	AAA	AAC	AGC	GAG	CGC	TTA	CCA	GAA	ATT	AAA	1010
Phe	Glu	Val	Leu	Ala	Lys	Lys	Asn	Ser	Glu	Arg	Leu	Pro	Glu	Ile	Lys	
	315				320					325					330	
GAA	GAC	AAG	ATT	TTA	GAA	AAA	ATC	CCT	TAT	TTG	AAT	TCC	AGT	TTG	TTT	1058
Glu	Asp	Lys	Ile	Leu	Glu	Lys	Ile	Pro	Tyr	Leu	Asn	Ser	Ser	Leu	Phe	
				335					340					345		
GAT	AAA	ACG	CCT	TTA	GAA	TTA	AAG	GGG	CAT	GAA	ATC	AAG	CTT	TTA	GAC	1106
Asp	Lys	Thr	Pro	Leu	Glu	Leu	Lys	Gly	His	Glu	Ile	Lys	Leu	Leu	Asp	
			350					355					360			
AAT	AAA	AAG	CTA	GAA	ATC	TAT	AAA	AAT	TCC	GTT	CTC	AAA	AAA	CAT	AAA	1154
Asn	Lys	Lys	Leu	Glu	Ile	Tyr	Lys	Asn	Ser	Val	Leu	Lys	Lys	His	Lys	
		365					370					375				
GAT	TAT	CAA	AAA	GAA	AAA	CCT	TTG	CCC	TTG	CTA	AAA	TAC	CTT	TTT	AAA	1202
Asp	Tyr	Gln	Lys	Glu	Lys	Pro	Leu	Pro	Leu	Leu	Lys	Tyr	Leu	Phe	Lys	
	380					385					390					
TTT	TTG	CGT	CTT	TAT	AAA	TTC	ACC	ACC	ACC	CCT	AAA	GAC	ATT	AAA	GAT	1250
Phe	Leu	Arg	Leu	Tyr	Lys	Phe	Thr	Thr	Thr	Pro	Lys	Asp	Ile	Lys	Asp	
	395				400					405					410	
AAT	ACC	GAT	ACC	AGC	GAA	AGC	CGT	TTG	ATT	AAC	CCT	AGC	GTT	TTA	GGG	1298
Asn	Thr	Asp	Thr	Ser	Glu	Ser	Arg	Leu	Ile	Asn	Pro	Ser	Val	Leu	Gly	
				415					420					425		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

AAGCGATGTA AGGAATTAAC	ATG GAT TAT AAA AAA TTA GAT TTA CCC AAC	50
	Met Asp Tyr Lys Lys Leu Asp Leu Pro Asn	
	1 5 10	
ACA AAC TAC CCA AAT CAA GAG CAA CTG AAA GCT TTT GAA ACC GCT TTT	98	
Thr Asn Tyr Pro Asn Gln Glu Gln Leu Lys Ala Phe Glu Thr Ala Phe		
	15 20 25	
GAC GCC TTT TTA GAA ACC AAC CAA CAA GAA AAT GAA AAT CAC CAA AAC	146	
Asp Ala Phe Leu Glu Thr Asn Gln Gln Glu Asn Glu Asn His Gln Asn		
	30 35 40	
GAC GCT TTT AAT GAT TTA TTG AAA GGC GTT TTT AAA TAC AAG GTT AAG	194	
Asp Ala Phe Asn Asp Leu Leu Lys Gly Val Phe Lys Tyr Lys Val Lys		
	45 50 55	
CCC ACC AAA AAA ATA GAC AGC ACT ATT CTT AAT GAA AAT AAC GAA GTG	242	
Pro Thr Lys Lys Ile Asp Ser Thr Ile Leu Asn Glu Asn Asn Glu Val		
	60 65 70	
GAG GTG ATC ATT GAA TTT AAA GCC CTT AAA AAC CCC AAC GAA TTT ATT	290	
Glu Val Ile Ile Glu Phe Lys Ala Leu Lys Asn Pro Asn Glu Phe Ile		
	75 80 85 90	
AAA AAG GGC GAT TTG AAT GTT AAA GCC TTT CAT GAA AGC CTT TTG TCT	338	
Lys Lys Gly Asp Leu Asn Val Lys Ala Phe His Glu Ser Leu Leu Ser		
	95 100 105	
TAT CTC ACA GAA AGA AAA GAG GGT AAT AAC AAC CTT AAG CAT CTT ATC	386	
Tyr Leu Thr Glu Arg Lys Glu Gly Asn Asn Asn Leu Lys His Leu Ile		
	110 115 120	
TTA GCC ACT ATT AAA GAG CTT TAT ATC ATT GAT GCA AAC GAA TTT GAG	434	
Leu Ala Thr Ile Lys Glu Leu Tyr Ile Ile Asp Ala Asn Glu Phe Glu		
	125 130 135	
GTT TTT AAT AAA GAT AAA GAA ATT GAA AAC GCC TTT AAA AAT TGC CAC	482	
Val Phe Asn Lys Asp Lys Glu Ile Glu Asn Ala Phe Lys Asn Cys His		
	140 145 150	
GAT AGA AAG GGT AAC GAT ACA CGC ACA AAA GCG TTT TAT GAT GCT TGC	530	
Asp Arg Lys Gly Asn Asp Thr Arg Thr Lys Ala Phe Tyr Asp Ala Cys		
	155 160 165 170	
CAA AAG CGC CTT AAT GAG TTT GAT CGT TCT TTG AAA TAC CAC TAT ATC	578	
Gln Lys Arg Leu Asn Glu Phe Asp Arg Ser Leu Lys Tyr His Tyr Ile		
	175 180 185	
CCC CTC AAA AAA GAA AAT TTA GCC CTA ATC TAT CAA GCC CTA AGC CCT	626	
Pro Leu Lys Lys Glu Asn Leu Ala Leu Ile Tyr Gln Ala Leu Ser Pro		
	190 195 200	
AAT TTT TTG CTC AAA ATT CCA AAA TAT TCT GAC GCT AAC ACG CTT AAC	674	

BNSDOCID: <WO__9843478A1_I_>

```

TAC ATC ACT CTC GCA CTC GCT CCA GCC AAA ATT TTA AGC GTT GAA ATC      915
Tyr Ile Thr Leu Ala Leu Ala Pro Ala Lys Ile Leu Ser Val Glu Ile
                290                      295                      300

AAA AAA ATC CCT ATA GAA GAA TTG AAT GCT GAA GAA AAA GAA TCC ATT      963
Lys Lys Ile Pro Ile Glu Glu Leu Asn Ala Glu Glu Lys Glu Ser Ile
                305                      310                      315

CAA GAG CGT TTT ATC GTC AAT AAC CAT TTG CAA AAG GCT AAA GTG CGT      1011
Gln Glu Arg Phe Ile Val Asn Asn His Leu Gln Lys Ala Lys Val Arg
                320                      325                      330

TTA TTG GAC ATT GAA AAA TCT AAG GCT ATC GGT AAG GGC GGG GTG AAT      1059
Leu Leu Asp Ile Glu Lys Ser Lys Ala Ile Gly Lys Gly Gly Val Asn
                335                      340                      345

GTG TGC TTA GCG TCC ATG CTT ACA GGC TAT CAC ATA GAG TTT GAA ACC      1107
Val Cys Leu Ala Ser Met Leu Thr Gly Tyr His Ile Glu Phe Glu Thr
                350                      355                      360                      365

ATT CCT AGC GTG AAA GAA AAC GCA GAA AAT GAA AGC GAA AAA GAA ACG      1155
Ile Pro Ser Val Lys Glu Asn Ala Glu Asn Glu Ser Glu Lys Glu Thr
                370                      375                      380

CCA AAA GTG GGG GTA GAA GCT TTA GAG TCT TTG TTT AAG AAT TAAGGGTAT      1206
Pro Lys Val Gly Val Glu Ala Leu Glu Ser Leu Phe Lys Asn
                385                      390                      395

CTAAAATTCA ATCTCTAAAA AAGCTTTTAA CT      1238

```

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

```

Met Glu Lys Ile Ser Asp Leu Ile Glu Cys Ile Ala Tyr Glu Lys Asn
 1                5                10                15
Leu Pro Lys Glu Met Ile Ser Lys Val Ile Gln Gly Cys Leu Leu Lys
                20                25                30
Met Ala Gln Asn Glu Leu Asp Pro Leu Ala Arg Tyr Leu Val Val Glu
                35                40                45
Glu Asn Lys Gln Leu Gln Leu Ile Gln Leu Val Glu Val Leu Glu Asp
                50                55                60
Gly Asp Glu Arg Leu Val Asn Asp Pro Ser Lys Tyr Ile Ser Leu Ser
                65                70                75                80
Lys Ala Lys Glu Met Asp Pro Ser Val Lys Ile Lys Asp Glu Leu Ser
                85                90                95
Tyr Ser Leu Ser Leu Glu Ser Met Lys Gln Gly Ala Ile Asn Arg Leu

```

TTA GAA GAT GGT GAT GAA AGA TTG GTT AAC GAC CCT TCT AAA TAC ATC	243
Leu Glu Asp Gly Asp Glu Arg Leu Val Asn Asp Pro Ser Lys Tyr Ile	
65 70 75	
AGC CTG TCT AAA GCC AAA GAA ATG GAT CCA AGC GTT AAG ATT AAA GAC	291
Ser Leu Ser Lys Ala Lys Glu Met Asp Pro Ser Val Lys Ile Lys Asp	
80 85 90	
GAA TTG TCC TAT AGC TTG AGT TTG GAG AGC ATG AAA CAA GGA GCG ATC	339
Glu Leu Ser Tyr Ser Leu Ser Leu Glu Ser Met Lys Gln Gly Ala Ile	
95 100 105	
AAC CGC CTT TTT AAA GAT TTG CAA TAC CAG TTA GAA AAA GCG TTA GAA	387
Asn Arg Leu Phe Lys Asp Leu Gln Tyr Gln Leu Glu Lys Ala Leu Glu	
110 115 120 125	
GAC AGC CAC TTT GAA GCG TTT CAA AAG CGT CTT AAC AGC GTT TTA ATG	435
Asp Ser His Phe Glu Ala Phe Gln Lys Arg Leu Asn Ser Val Leu Met	
130 135 140	
GGG CAA GTG ATT TTA GTG GAT CAC AAC CAA AAC ACC TTT ATT GAG ATT	483
Gly Gln Val Ile Leu Val Asp His Asn Gln Asn Thr Phe Ile Glu Ile	
145 150 155	
GAG CAG CAA TTT CAG GGC GTT CTT TCC ATG CGC CAT CGC ATC AAG GGC	531
Glu Gln Gln Phe Gln Gly Val Leu Ser Met Arg His Arg Ile Lys Gly	
160 165 170	
GAG AGT TTT AAA GTG GGC GAT AGC ATT AAA GCG GTT TTA ACG CAA GTC	579
Glu Ser Phe Lys Val Gly Asp Ser Ile Lys Ala Val Leu Thr Gln Val	
175 180 185	
AAA CGC ACG AAA AAA GGC TTA TTA TTA GAG CTG AGC CGC ACC ACC CCT	627
Lys Arg Thr Lys Lys Gly Leu Leu Leu Glu Leu Ser Arg Thr Thr Pro	
190 195 200 205	
AAA ATG CTT GAA GCT TTG TTG GAA TTG GAA GTC CCT GAA ATT AAA GAC	675
Lys Met Leu Glu Ala Leu Leu Glu Leu Glu Val Pro Glu Ile Lys Asp	
210 215 220	
AAA GAA ATT GAA ATC ATC CAT TGT GCG CGA ATC CCA GGC AAC AGA GCG	723
Lys Glu Ile Glu Ile Ile His Cys Ala Arg Ile Pro Gly Asn Arg Ala	
225 230 235	
AAA GTG AGC TTT TTT TCC CAT AAC GCT AGG ATT GAC CCC ATA GGC GCG	771
Lys Val Ser Phe Phe Ser His Asn Ala Arg Ile Asp Pro Ile Gly Ala	
240 245 250	
GCT GTG GGG GTT AAG GGC GTG CGC ATT AAT GCG ATC AGT AAC GAA TTG	819
Ala Val Gly Val Lys Gly Val Arg Ile Asn Ala Ile Ser Asn Glu Leu	
255 260 265	
AAT AAA GAA AAC ATT GAT TGC ATA GAA TAT TCT AAT GTG CCT GAA ATT	867
Asn Lys Glu Asn Ile Asp Cys Ile Glu Tyr Ser Asn Val Pro Glu Ile	
270 275 280 285	

```

Leu Lys Asn His Pro Leu Tyr Arg Val Leu Arg Val Gly Lys Ile Thr
                245                      250                      255
Leu Thr Leu Leu Phe Cys Ser Leu Lys Ala Trp Ile Asn His Gln Glu
                260                      265                      270
Asp Ile Thr Ile His Ala Leu Leu Asn Gln Thr Lys Asp Ala Leu Leu
                275                      280                      285
Gln Lys Ala Leu Lys Leu Tyr Ala Leu Leu Lys Pro Leu Glu Leu Asn
                290                      295                      300
Val Ser Ile Ala Ser Ser Phe Ser Lys Ile Gly Asn Leu Phe Gly Arg
305                      310                      315                      320
Glu Leu Glu Ser Phe Cys Val Lys Ile Gln Pro Lys Asn Thr Arg Ala
                325                      330                      335
Leu Asn Ser Glu Lys Leu Tyr Leu Lys Leu Phe Gln Lys Gly Val Ile
                340                      345                      350
Ala Arg Ile Ser Cys Glu Phe Val Cys Phe Glu Val Phe Ser Leu Asn
                355                      360                      365
Glu Lys Asp Phe Glu Lys Ile Ala Leu Val Leu Glu Glu Ile Leu Asn
                370                      375                      380
Lys Ala
385

```

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1197
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

```

AGGAACTTAA GA ATG GAA AAA ATC AGC GAT CTT ATA GAA TGC ATT GCG TAT      51
      Met Glu Lys Ile Ser Asp Leu Ile Glu Cys Ile Ala Tyr
        1                      5                      10

GAA AAA AAT TTG CCT AAA GAG ATG ATT TCA AAA GTG ATT CAA GGC TGT      99
Glu Lys Asn Leu Pro Lys Glu Met Ile Ser Lys Val Ile Gln Gly Cys
    15                      20                      25

TTG TTA AAA ATG GCG CAA AAT GAG TTA GAC CCC CTA GCA CGC TAC TTG     147
Leu Leu Lys Met Ala Gln Asn Glu Leu Asp Pro Leu Ala Arg Tyr Leu
    30                      35                      40                      45

GTG GTT GAA GAA AAC AAG CAG CTC CAG CTT ATC CAG TTG GTA GAA GTT     195
Val Val Glu Glu Asn Lys Gln Leu Gln Leu Ile Gln Leu Val Glu Val
        50                      55                      60

```


Ser Glu Lys Leu Tyr Leu Lys Leu Phe Gln Lys Gly Val Ile Ala Arg
 340 345 350

ATT TCA TGC GAA TTC GTG TGC TTT GAA GTC TTT AGC TTG AAT GAA AAA 1161
 Ile Ser Cys Glu Phe Val Cys Phe Glu Val Phe Ser Leu Asn Glu Lys
 355 360 365 370

GAT TTT GAA AAA ATC GCT CTG GTT TTA GAA GAA ATT CTT AAT AAA GCT T 1210
 Asp Phe Glu Lys Ile Ala Leu Val Leu Glu Glu Ile Leu Asn Lys Ala
 375 380 385

AAAAATTCGC TATAATA 1227

(2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

Met Ala Lys Glu Thr Leu Glu Ile Thr Pro Asp Leu Leu Lys Asn Pro
 1 5 10 15

Tyr Gln Lys Ile Ile Asn Ala Ser Ala Ser Val Phe Asp Glu Lys His
 20 25 30

Gly Arg Ser Phe Phe Ser Thr Gln Phe Tyr Glu Lys Ile Glu Pro Tyr
 35 40 45

Leu Lys Glu Val Leu Thr His Pro Ile Asp Leu Glu Cys Asp Leu Asn
 50 55 60

Thr Ala Lys Lys Lys Asn Arg Leu Thr Pro Leu Lys Gln Leu Phe Lys
 65 70 75 80

Ala Cys Phe Asn Thr Glu Glu Ile Leu Ile Val Asn Asn Asn Thr Ser
 85 90 95

Ala Ile Phe Leu Ile Ala Asn Ala Leu Ala Gln Glu Lys Glu Ile Ile
 100 105 110

Val Ser Tyr Gly Glu Leu Val Gly Gly Asp Phe Asn Leu Lys Asp Ile
 115 120 125

Leu Leu Asn Ser Gly Ala Arg Leu His Leu Val Gly Asn Ile Asn Arg
 130 135 140

Ala Tyr Leu Arg Asp Tyr Arg Leu Ala Leu Asn Glu Asn Ser Lys Ile
 145 150 155 160

Leu Phe Lys Thr His Asn Pro His Phe Lys Lys Asp Thr Pro Phe Lys
 165 170 175

Asp Leu Gln Thr Leu Ala Lys Glu His Asp Leu Ile Asp Tyr Tyr Asn
 180 185 190

Leu Gly Asp Val Asp Leu Ser Asn Arg Val Ala Leu Glu Glu Ile Leu
 195 200 205

Ala Leu Lys Pro Ser Leu Leu Ser Phe Ser Ala Asp Lys Phe Phe Asn
 210 215 220

Ser Ala Gln Ala Gly Ile Ile Met Gly Gln Lys Glu Arg Val Glu Ala
 225 230 235 240

115	120	125	130	
AAT AGT GGG GCT AGG CTG CAT TTA GTG GGG AAT ATT AAT CGC GCT TAT				489
Asn Ser Gly Ala Arg Leu His Leu Val Gly Asn Ile Asn Arg Ala Tyr	135	140	145	
TTA AGG GAT TAC CGC TTA GCC TTG AAT GAA AAC AGC AAA ATA CTC TTT				537
Leu Arg Asp Tyr Arg Leu Ala Leu Asn Glu Asn Ser Lys Ile Leu Phe	150	155	160	
AAA ACC CAC AAC CCC CAT TTT AAA AAA GAC ACG CCC TTT AAA GAT TTA				585
Lys Thr His Asn Pro His Phe Lys Lys Asp Thr Pro Phe Lys Asp Leu	165	170	175	
CAA ACT CTT GCT AAA GAG CAT GAT CTC ATT GAT TAT TAC AAT TTA GGG				633
Gln Thr Leu Ala Lys Glu His Asp Leu Ile Asp Tyr Tyr Asn Leu Gly	180	185	190	
GAT GTG GAT TTG TCA AAC AGA GTG GCT TTG GAA GAA ATT TTA GCC CTA				681
Asp Val Asp Leu Ser Asn Arg Val Ala Leu Glu Glu Ile Leu Ala Leu	195	200	205	210
AAA CCA TCG CTT TTA AGC TTT AGC GCG GAT AAA TTC TTT AAC AGT GCG				729
Lys Pro Ser Leu Leu Ser Phe Ser Ala Asp Lys Phe Phe Asn Ser Ala	215	220	225	
CAA GCG GGC ATT ATT ATG GGG CAA AAA GAA CGG GTT GAA GCG TTA AAA				777
Gln Ala Gly Ile Ile Met Gly Gln Lys Glu Arg Val Glu Ala Leu Lys	230	235	240	
AAC CAC CCC CTT TAT AGA GTT TTA AGG GTG GGT AAA ATC ACG CTC ACC				825
Asn His Pro Leu Tyr Arg Val Leu Arg Val Gly Lys Ile Thr Leu Thr	245	250	255	
TTG CTT TTT TGC AGC CTA AAA GCA TGG ATA AAT CAT CAA GAA GAC ATT				873
Leu Leu Phe Cys Ser Leu Lys Ala Trp Ile Asn His Gln Glu Asp Ile	260	265	270	
ACA ATC CAT GCG TTA TTG AAC CAA ACT AAA GAC GCA TTA TTG CAA AAA				921
Thr Ile His Ala Leu Leu Asn Gln Thr Lys Asp Ala Leu Leu Gln Lys	275	280	285	290
GCC CTC AAA CTC TAC GCT CTT TTA AAG CCT TTA GAA TTG AAT GTG AGC				969
Ala Leu Lys Leu Tyr Ala Leu Leu Lys Pro Leu Glu Leu Asn Val Ser	295	300	305	
ATA GCC TCT AGC TTT TCT AAA ATA GGG AAT TTG TTT GGT AGG GAA TTA				1017
Ile Ala Ser Ser Phe Ser Lys Ile Gly Asn Leu Phe Gly Arg Glu Leu	310	315	320	
GAA TCC TTT TGC GTG AAA ATC CAG CCC AAA AAC ACC CGT GCT TTA AAT				1065
Glu Ser Phe Cys Val Lys Ile Gln Pro Lys Asn Thr Arg Ala Leu Asn	325	330	335	
AGT GAG AAA CTT TAT TTA AAG CTT TTC CAA AAA GGC GTT ATC GCA AGG				1113

115

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1209
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

```

TAAAATAACG CTTATTTTAA ACTCTCAAAA AAGGAATCAA ACGCACTCAT C ATG GCT      57
                                     Met Ala
                                     1

AAA GAA ACG CTT GAA ATA ACC CCG GAT CTT TTG AAA AAC CCT TAT CAA      105
Lys Glu Thr Leu Glu Ile Thr Pro Asp Leu Leu Lys Asn Pro Tyr Gln
      5                      10                      15

AAA ATC ATC AAT GCG AGC GCG AGC GTT TTT GAT GAA AAG CAT GGG CGA      153
Lys Ile Ile Asn Ala Ser Ala Ser Val Phe Asp Glu Lys His Gly Arg
      20                      25                      30

TCG TTT TTT AGC ACG CAA TTT TAT GAA AAA ATT GAA CCT TAT TTA AAA      201
Ser Phe Phe Ser Thr Gln Phe Tyr Glu Lys Ile Glu Pro Tyr Leu Lys
      35                      40                      45                      50

GAA GTT TTA ACC CAT CCC ATT GAT TTA GAA TGC GAT CTA AAC ACC GCT      249
Glu Val Leu Thr His Pro Ile Asp Leu Glu Cys Asp Leu Asn Thr Ala
                        55                      60                      65

AAA AAA AAG AAC CGC TTA ACC CCT TTA AAA CAG CTT TTT AAA GCG TGT      297
Lys Lys Lys Asn Arg Leu Thr Pro Leu Lys Gln Leu Phe Lys Ala Cys
      70                      75                      80

TTT AAC ACC GAA GAA ATT TTG ATT GTG AAT AAT AAC ACC AGC GCG ATT      345
Phe Asn Thr Glu Glu Ile Leu Ile Val Asn Asn Asn Thr Ser Ala Ile
      85                      90                      95

TTC CTC ATC GCT AAC GCT TTA GCG CAA GAA AAA GAA ATC ATT GTT TCT      393
Phe Leu Ile Ala Asn Ala Leu Ala Gln Glu Lys Glu Ile Ile Val Ser
      100                      105                      110

TAT GGC GAA TTA GTG GGG GGG GAT TTT AAC CTT AAA GAT ATT TTA TTA      441
Tyr Gly Glu Leu Val Gly Gly Asp Phe Asn Leu Lys Asp Ile Leu Leu

```

-1624-

10	15	20	
CGC TTA AAA CCC CAA AAA ATA AGC GTG AAT TTG GAT CTT TTC TAC ACG			150
Arg Leu Lys Pro Gln Lys Ile Ser Val Asn Leu Asp Leu Phe Tyr Thr			
25	30	35	40
CAA TTA CCC AAT AAG GTT TAT TTA GAC TAC ATG GAA ATT CAA GAG CTT			198
Gln Leu Pro Asn Lys Val Tyr Leu Asp Tyr Met Glu Ile Gln Glu Leu			
	45	50	55
ATT CAA AAG ATG ATG CAA GAA AAC CAA TAC CTT CTC ATT GAA GAC GCC			246
Ile Gln Lys Met Met Gln Glu Asn Gln Tyr Leu Leu Ile Glu Asp Ala			
	60	65	70
CTG AAA GAT TTG AGC CAT GCT TTA AAA ACG CGC TAC AAG GAG ATC ACT			294
Leu Lys Asp Leu Ser His Ala Leu Lys Thr Arg Tyr Lys Glu Ile Thr			
	75	80	85
GAA CTT TAT TTA AAA ATC AGC AAG TTA GAG ATT TCT CCC AAT TCT CAA			342
Glu Leu Tyr Leu Lys Ile Ser Lys Leu Glu Ile Ser Pro Asn Ser Gln			
	90	95	100
GTG GGA GCG AGC GTG AAA ATC CGC TAT GAA AGC AAT CTT TAGCCTCTTT TT			393
Val Gly Ala Ser Val Lys Ile Arg Tyr Glu Ser Asn Leu			
	105	110	115
CCTTCTTATT G			404

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

Met	Lys	Thr	Lys	Gln	Gly	Val	His	Ile	His	Asn	Leu	Val	Phe	Glu	Ala
1				5					10					15	
Ile	Leu	Gly	Ile	Leu	Glu	Phe	Glu	Arg	Leu	Lys	Pro	Gln	Lys	Ile	Ser
		20						25					30		
Val	Asn	Leu	Asp	Leu	Phe	Tyr	Thr	Gln	Leu	Pro	Asn	Lys	Val	Tyr	Leu
		35					40					45			
Asp	Tyr	Met	Glu	Ile	Gln	Glu	Leu	Ile	Gln	Lys	Met	Met	Gln	Glu	Asn
		50				55					60				
Gln	Tyr	Leu	Leu	Ile	Glu	Asp	Ala	Leu	Lys	Asp	Leu	Ser	His	Ala	Leu
		65			70					75				80	
Lys	Thr	Arg	Tyr	Lys	Glu	Ile	Thr	Glu	Leu	Tyr	Leu	Lys	Ile	Ser	Lys
				85					90					95	
Leu	Glu	Ile	Ser	Pro	Asn	Ser	Gln	Val	Gly	Ala	Ser	Val	Lys	Ile	Arg
			100					105					110		
Tyr	Glu	Ser	Asn	Leu											

BNSDOCID: <WO 9843478A1_I_>

GCA GTA TTT TTG AGC AAA TTG TTT GGG TTG GAT TAT AGT TTG CAA TGG	433
Ala Val Phe Leu Ser Lys Leu Phe Gly Leu Asp Tyr Ser Leu Gln Trp	
125 130 135 140	
ATG GTC GCT ATC GCT AGC ATT TTA GGG CAT TGC TAT TCG CCT TTT TTG	481
Met Val Ala Ile Ala Ser Ile Leu Gly His Cys Tyr Ser Pro Phe Leu	
145 150 155	
AAT TTC AAT GGA GGT AAG GGC GTT TCT ACG ATC ATG GGC TCT GTG GTG	529
Asn Phe Asn Gly Gly Lys Gly Val Ser Thr Ile Met Gly Ser Val Val	
160 165 170	
TTG CTC ATC CCT ATT GAA AGT CTC ATC GGC TTA ACG GTG TGG TTT TTT	577
Leu Leu Ile Pro Ile Glu Ser Leu Ile Gly Leu Thr Val Trp Phe Phe	
175 180 185	
GTG GGT AAG GTG CTT AAA ATC TCT TCA CTC GCT AGC ATT CTA GGG GTA	625
Val Gly Lys Val Leu Lys Ile Ser Ser Leu Ala Ser Ile Leu Gly Val	
190 195 200	
GGC ACA GCG ACT GTT CTT ATC TTT TTT GTG CCT TAT ATG CAT ATC CCA	673
Gly Thr Ala Thr Val Leu Ile Phe Phe Val Pro Tyr Met His Ile Pro	
205 210 215 220	
GAC AGC GTC AAT ATC CTT AAA GAA GTC GGC ACG CAA ACG CCG ATG GTG	721
Asp Ser Val Asn Ile Leu Lys Glu Val Gly Thr Gln Thr Pro Met Val	
225 230 235	
CTT ATT TTT ATT TTC ACC CTT ATC AAG CAT GCG GGT AAT ATT TTT AAT	769
Leu Ile Phe Ile Phe Thr Leu Ile Lys His Ala Gly Asn Ile Phe Asn	
240 245 250	
TTA TTG GCC GGC AAG GAA AAG AAA GTC TTA TGAAAACTAA ACAAGGCGTT CAT	822
Leu Leu Ala Gly Lys Glu Lys Lys Val Leu	
255 260	
A	823

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

Met	Ala	Arg	Ser	Phe	Lys	His	Ser	Gln	Tyr	Pro	Lys	Ile	Phe	Lys	Pro
1				5				10					15		
Leu	Tyr	Pro	Asn	Asn	Leu	Thr	Leu	Ser	Leu	Lys	Lys	Gln	His	Val	Ile
			20				25					30			
Met	Ile	Ala	Ile	Leu	Phe	Glu	Arg	Val	Phe	Met	Glu	Ser	Val	Leu	Asn

325 330 335
 Ala Leu Leu Trp Ile Glu Asn Ser
 340

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 14...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

ACGATTTTAA AAA ATG GCT AGA AGT TTC AAG CAT TCT CAA TAT CCT AAA	49
Met Ala Arg Ser Phe Lys His Ser Gln Tyr Pro Lys	
1 5 10	
ATT TTT AAG CCA CTA TAC CCT AAC AAC TTA ACG CTT TCA CTT AAA AAG	97
Ile Phe Lys Pro Leu Tyr Pro Asn Asn Leu Thr Leu Ser Leu Lys Lys	
15 20 25	
CAA CAT GTT ATA ATG ATC GCT ATT TTA TTT GAA AGG GTA TTT ATG GAA	145
Gln His Val Ile Met Ile Ala Ile Leu Phe Glu Arg Val Phe Met Glu	
30 35 40	
AGC GTT TTA AAT TTC CTA ACC AAT ATC AAT GTG ATT TTC ACC CTT TTG	193
Ser Val Leu Asn Phe Leu Thr Asn Ile Asn Val Ile Phe Thr Leu Leu	
45 50 55 60	
GGC TAT TTG ATT GGG GGG ATT CCT TTT GGC TAT GCG TTA ATG AAA ATC	241
Gly Tyr Leu Ile Gly Gly Ile Pro Phe Gly Tyr Ala Leu Met Lys Ile	
65 70 75	
TTT TAC GGC ATG GAT ATT ACT AAA ATC GGA TCG GGG GGC ATT GGC GCA	289
Phe Tyr Gly Met Asp Ile Thr Lys Ile Gly Ser Gly Gly Ile Gly Ala	
80 85 90	
ACG AAT GTC TTG CGT GCT TTA CAA AGT AAG GGC GTG AGT AAC GCT AAA	337
Thr Asn Val Leu Arg Ala Leu Gln Ser Lys Gly Val Ser Asn Ala Lys	
95 100 105	
CAA ATG GCC CTA TTA GTT TTA ATC TTG GAT CTC TTC AAA GGC ATG TTT	385
Gln Met Ala Leu Leu Val Leu Ile Leu Asp Leu Phe Lys Gly Met Phe	
110 115 120	

AAGATTATAC CAGCCTTTGA ACGCTTATTC TTACAACAGC GATTC

1108

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

```

Met Arg Leu Tyr Glu Ser Leu Leu Glu Met Cys Leu Asn Lys Ala Trp
 1           5           10           15
Glu His Gln Thr Leu Ala Leu Glu Asn Pro Ser Val Ala Cys Met Val
          20           25           30
Leu Asp Lys Asn His Glu Ile Leu Ser Leu Glu Thr His Lys Lys Ala
          35           40           45
Lys Thr Pro His Ala Glu Val Leu Ala Ala Gln Ser Ala Leu Lys Ile
          50           55           60
Leu Arg Pro Ser Leu Lys Asn Asp Leu Glu Lys Leu Glu Asp Pro Lys
          65           70           75           80
Thr Leu Ser Asp Phe Leu Lys Thr His His Asp Asn Ala Phe Thr Asp
          85           90           95
Cys Val Phe Leu Ile Thr Leu Glu Pro Cys Asn Ser Tyr Gly Lys Thr
          100          105          110
Pro Ala Cys Ser Glu Leu Leu Glu Ile Leu Lys Pro Lys Arg Val Val
          115          120          125
Ile Ala Thr Glu Glu Asn Glu Ala Lys Lys Gly Gly Leu Ala Arg Leu
          130          135          140
Gln Lys Ala Arg Ile Glu Thr Ile Ile Cys His Asn Leu Glu Asn Lys
          145          150          155          160
Ala Lys Asp Leu Leu Leu Pro Phe Arg Val Met Glu Gln Lys Gly Arg
          165          170          175
Phe Asn Leu Phe Lys Leu Ala Leu Arg Met Asn Gly Asp Tyr His His
          180          185          190
Gly Lys Ile Thr Gly Gln Lys Ser Val Ile Phe Thr His Asn Gln Arg
          195          200          205
Ala Ile Cys Asp Thr Leu Ile Val Ser Gly Lys Thr Ile Arg Thr Asp
          210          215          220
Asn Pro Leu Leu Asp Ala Arg Phe Cys Asp Ser Phe Tyr Gln Asn Lys
          225          230          235          240
Asn Pro Asn Ile Ala Ile Leu Ser Lys Arg Ser Ile Asp Pro Asn Ser
          245          250          255
Lys Val Phe Ser Ala Pro Asn Arg Leu Val Asn Thr Phe His Asp Pro
          260          265          270
Lys Asp Leu Pro Leu Glu Lys Gly Phe Asn Phe Ile Glu Gly Gly Trp
          275          280          285
Glu Leu Phe Glu Ser Leu Arg Asp Lys Ile Asp Ala Leu Leu Leu His
          290          295          300
Ser His Ala Ser Met Ile Gly Glu Ala Phe Lys Ala Leu Ala Leu Lys
          305          310          315          320
Thr Pro Phe Lys Gly Arg Leu Leu His Ala Gln Ile Leu Glu Asn Glu

```


Ile Leu Lys Pro Lys Arg Val Val Ile Ala Thr Glu Glu Asn Glu Ala	
125 130 135	
AAA AAA GGG GGT TTA GCA AGG CTA CAA AAG GCT CGT ATT GAA ACA ATA	486
Lys Lys Gly Gly Leu Ala Arg Leu Gln Lys Ala Arg Ile Glu Thr Ile	
140 145 150	
ATT TGC CAC AAT TTA GAA AAC AAA GCT AAA GAC TTG CTC TTG CCT TTT	534
Ile Cys His Asn Leu Glu Asn Lys Ala Lys Asp Leu Leu Leu Pro Phe	
155 160 165	
AGG GTA ATG GAA CAA AAG GGG CGT TTT AAT TTG TTC AAA CTC GCT TTA	582
Arg Val Met Glu Gln Lys Gly Arg Phe Asn Leu Phe Lys Leu Ala Leu	
170 175 180	
AGA ATG AAT GGG GAT TAC CAT CAT GGC AAG ATC ACC GGG CAA AAA AGC	630
Arg Met Asn Gly Asp Tyr His His Gly Lys Ile Thr Gly Gln Lys Ser	
185 190 195 200	
GTT ATT TTC ACG CAC AAC CAG CGA GCA ATA TGC GAC ACG CTT ATT GTT	678
Val Ile Phe Thr His Asn Gln Arg Ala Ile Cys Asp Thr Leu Ile Val	
205 210 215	
TCT GGG AAA ACC ATA AGA ACG GAC AAC CCC TTA TTG GAC GCT CGC TTT	726
Ser Gly Lys Thr Ile Arg Thr Asp Asn Pro Leu Leu Asp Ala Arg Phe	
220 225 230	
TGC GAC AGC TTT TAT CAA AAT AAA AAC CCC AAT ATC GCT ATT TTA TCC	774
Cys Asp Ser Phe Tyr Gln Asn Lys Asn Pro Asn Ile Ala Ile Leu Ser	
235 240 245	
AAG CGC TCA ATT GAC CCT AAT TCA AAA GTT TTT TCT GCG CCT AAT CGT	822
Lys Arg Ser Ile Asp Pro Asn Ser Lys Val Phe Ser Ala Pro Asn Arg	
250 255 260	
TTA GTT AAC ACT TTC CAT GAC CCC AAA GAT TTA CCC CTA GAG AAG GGG	870
Leu Val Asn Thr Phe His Asp Pro Lys Asp Leu Pro Leu Glu Lys Gly	
265 270 275 280	
TTT AAT TTC ATT GAA GGG GGG TGG GAA TTG TTT GAG AGC TTG AGG GAT	918
Phe Asn Phe Ile Glu Gly Gly Trp Glu Leu Phe Glu Ser Leu Arg Asp	
285 290 295	
AAA ATA GAC GCG TTG CTT TTG CAT TCG CAT GCG TCT ATG ATT GGC GAA	966
Lys Ile Asp Ala Leu Leu Leu His Ser His Ala Ser Met Ile Gly Glu	
300 305 310	
GCG TTT AAG GCA CTC GCT CTA AAA ACC CCT TTT AAA GGA CGG TTG TTG	1014
Ala Phe Lys Ala Leu Ala Leu Lys Thr Pro Phe Lys Gly Arg Leu Leu	
315 320 325	
CAT GCG CAA ATC TTA GAA AAT GAA GCC CTT TTA TGG ATA GAA AAC TCT T	1063
His Ala Gln Ile Leu Glu Asn Glu Ala Leu Leu Trp Ile Glu Asn Ser	
330 335 340	

Glu Lys Ile Ser Ala Ile
100

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1062
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

AGGCTTTTGTG CTCTGCCTT TTTTCCCATC	ATG AGA CTT TAT GAG AGT TTA TTA	54
	Met Arg Leu Tyr Glu Ser Leu Leu	
	1 5	
GAA ATG TGC TTG AAT AAG GCA TGG GAG CAT CAA ACC CTA GCC TTA GAA	102	
Glu Met Cys Leu Asn Lys Ala Trp Glu His Gln Thr Leu Ala Leu Glu		
10 15 20		
AAC CCA AGC GTA GCT TGC ATG GTG TTG GAT AAA AAC CAT GAG ATC TTG	150	
Asn Pro Ser Val Ala Cys Met Val Leu Asp Lys Asn His Glu Ile Leu		
25 30 35 40		
AGT TTA GAA ACC CAC AAA AAA GCC AAA ACC CCG CAT GCA GAA GTC TTA	198	
Ser Leu Glu Thr His Lys Lys Ala Lys Thr Pro His Ala Glu Val Leu		
45 50 55		
GCC GCC CAA TCA GCG CTA AAG ATT TTA CGC CCC AGT TTG AAA AAC GAT	246	
Ala Ala Gln Ser Ala Leu Lys Ile Leu Arg Pro Ser Leu Lys Asn Asp		
60 65 70		
TTA GAA AAG TTA GAA GAC CCT AAA ACT TTA AGC GAT TTT TTA AAA ACG	294	
Leu Glu Lys Leu Glu Asp Pro Lys Thr Leu Ser Asp Phe Leu Lys Thr		
75 80 85		
CAC CAC GAT AAC GCT TTT ACA GAC TGC GTT TTT TTA ATC ACC TTA GAG	342	
His His Asp Asn Ala Phe Thr Asp Cys Val Phe Leu Ile Thr Leu Glu		
90 95 100		
CCA TGC AAT TCT TAT GGC AAA ACC CCG GCT TGT AGC GAA TTG TTA GAA	390	
Pro Cys Asn Ser Tyr Gly Lys Thr Pro Ala Cys Ser Glu Leu Leu Glu		
105 110 115 120		
ATT TTA AAG CCT AAA AGA GTG GTC ATT GCC ACA GAA GAA AAC GAA GCT	438	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

```

TCAAATTCTT CATAA ATG ATT TTT TCT TTT AAA AGG ACT TCT TTT TGC GTG      51
      Met Ile Phe Ser Phe Lys Arg Thr Ser Phe Cys Val
            1             5             10

AGC GTG CCG GTT TTG TCT ATA AAG ATT TTT TTC ACT TTA GCC AGA GTT      99
Ser Val Pro Val Leu Ser Ile Lys Ile Phe Phe Thr Leu Ala Arg Val
      15             20             25

TCT AAA AAC AAC GCT TCT TTA AAC ACG ATC AAA GGG TTT TTA AAC ACC      147
Ser Lys Asn Asn Ala Ser Leu Asn Thr Ile Lys Gly Phe Leu Asn Thr
      30             35             40

CCT ATC ACT AAC GCA ATG GGC GTA GCC AGA GCG AAC GCG CAA GGG CAG      195
Pro Ile Thr Asn Ala Met Gly Val Ala Arg Ala Asn Ala Gln Gly Gln
      45             50             55             60

CTG ATG ACT AGC ACG CTA ATA CAC ACC ATT AAG GCT TTT TCA AAA TTA      243
Leu Met Thr Ser Thr Leu Ile His Thr Ile Lys Ala Phe Ser Lys Leu
            65             70             75

CCC CCC AAA CCA AAT TGC CAT AAC AAA AAG CTT ACA AAG GCT AAA AAC      291
Pro Pro Lys Pro Asn Cys His Asn Lys Lys Leu Thr Lys Ala Lys Asn
            80             85             90

AAC ACC GCT TTA GAA AAA ATA TCC GCA ATT TGATTCGCGC TACTCTCAAT T      342
Asn Thr Ala Leu Glu Lys Ile Ser Ala Ile
      95             100

```

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

```

Met Ile Phe Ser Phe Lys Arg Thr Ser Phe Cys Val Ser Val Pro Val
  1             5             10             15
Leu Ser Ile Lys Ile Phe Phe Thr Leu Ala Arg Val Ser Lys Asn Asn
      20             25             30
Ala Ser Leu Asn Thr Ile Lys Gly Phe Leu Asn Thr Pro Ile Thr Asn
      35             40             45
Ala Met Gly Val Ala Arg Ala Asn Ala Gln Gly Gln Leu Met Thr Ser
      50             55             60
Thr Leu Ile His Thr Ile Lys Ala Phe Ser Lys Leu Pro Pro Lys Pro
      65             70             75             80
Asn Cys His Asn Lys Lys Leu Thr Lys Ala Lys Asn Asn Thr Ala Leu
            85             90             95

```

70	75	80	
CGC TCC CTT AAA AAG CCC ACC CCA AAC ACC GCG CCC ACC ACA ATA TGC			343
Arg Ser Leu Lys Lys Pro Thr Pro Asn Thr Ala Pro Thr Thr Ile Cys			
85	90	95	
GTA GAG CTT ACG GGC AAG CCT AAT TGAGAGGCTA AAAGCACGGT GATGACT			394
Val Glu Leu Thr Gly Lys Pro Asn			
100	105		

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

Met	Glu	Arg	Leu	Ile	Thr	Ser	Ser	Leu	Tyr	Thr	Phe	Leu	Ser	Asp	Phe
1				5					10					15	
Phe	Ser	Phe	Phe	Asn	Ser	Lys	Ala	Met	Ala	Val	Phe	Leu	Leu	Phe	
			20				25					30			
Phe	Lys	Leu	Ser	Ser	Met	Ser	Asp	Phe	Ser	Phe	Lys	Leu	Ala	Leu	Ser
		35					40					45			
Lys	Arg	Ser	Lys	Lys	Pro	Ser	Ile	Ser	Ser	Lys	Ser	Ser	Pro	Lys	Cys
	50					55					60				
Ala	Ala	Thr	Met	Leu	Ser	Leu	Ile	Leu	Ala	Lys	Arg	Leu	Leu	Asp	Cys
65					70					75				80	
Ser	Leu	Lys	Arg	Ser	Leu	Lys	Lys	Pro	Thr	Pro	Asn	Thr	Ala	Pro	Thr
			85						90					95	
Thr	Ile	Cys	Val	Glu	Leu	Thr	Gly	Lys	Pro	Asn					
			100					105							

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...321
- (D) OTHER INFORMATION:

BNSDOCID: <WO__984347BA1_I_>

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

```

Met Gly Arg Asn Gln Gly Ala Tyr Leu Asp Pro Ser Glu Ser Ile Leu
 1           5           10           15
Met Leu Met Val Ala Phe Leu Leu Val Leu Leu Asn Ala Phe Phe Val
          20           25           30
Leu Ser Glu Phe Ala Leu Val Lys Val Arg Lys Thr Arg Leu Glu Glu
          35           40           45
Leu Val Lys Ile Gly Asn Ser Asn Ala Lys Leu Ala Leu Lys Met Ser
          50           55           60
Gln Arg Leu Asp Thr Tyr Leu Ser Ala Thr Gln Leu Gly Ile Thr Leu
          65           70           75           80
Ser Ser Leu Ala Leu Gly Trp Val Gly Glu Pro Ala Ile Ala Lys Leu
          85           90           95
Leu Ala Ala Leu Phe Glu Ser Met Asp Leu Arg Glu Asn Pro Ile Phe
          100          105          110
Ile His Ser Met Ser Val Val Ile Ala Phe Leu Ser Ile Thr Phe Leu
          115          120          125
His Val Val Leu Gly Glu Ile Val Pro Lys Ser Leu Ala Ile Ala Lys
          130          135          140
Ser Glu Lys Ala Thr Leu Phe Ala Ala Arg Pro Leu His Val Phe Trp
          145          150          155          160
Val Val Phe Tyr Pro Val Val Arg Leu Phe Asp Val Ile Ala His Phe
          165          170          175
Phe Leu Lys Lys Met Gly Ile Asn Pro Lys Glu His Asp Gly Thr His
          180          185          190
Ser Glu Glu Glu Leu Lys Ile Ile Val Gly Glu Ser Leu Arg Glu Gly
          195          200          205
Ile Ile Asp Ser Val Glu Gly Glu Ile Ile Lys Asn Ala Val Asp Phe
          210          215          220
Ser Asp Thr Ser Ala Lys Glu Ile Met Thr Pro Arg Lys Asp Met Val
          225          230          235          240
Cys Leu Asp Glu Glu Asn Ser Tyr Glu Glu Asn Ile Asp Ile Val Leu
          245          250          255
Lys Gly His Phe Thr Arg Tyr Pro Tyr Cys Lys Gly Ser Lys Asp Asn
          260          265          270
Ile Ile Gly Met Val His Ile Arg Asp Leu Leu Ser Arg Ser Ile Phe
          275          280          285
Thr Pro Lys Met His Asp Phe Asn Gln Ile Val Arg Lys Met Ile Ile
          290          295          300
Val Pro Glu Ser Ala Ser Ile Ser Gln Ile Leu Ile Lys Met Lys Lys
          305          310          315          320
Glu Gln Ile His Thr Ala Leu Val Ile Asp Glu Tyr Gly Gly Thr Ala
          325          330          335
Gly Leu Leu Thr Met Glu Asp Ile Ile Glu Glu Ile Met Gly Glu Ile
          340          345          350
Ser Asp Glu Tyr Asp Leu Lys Gln Glu Gly Ile Asn Lys Leu Glu Glu

```

TTG GAT GAA GAA AAC AGC TAT GAA GAA AAT ATA GAC ATT GTT TTA AAA	827
Leu Asp Glu Glu Asn Ser Tyr Glu Glu Asn Ile Asp Ile Val Leu Lys	
245 250 255	
GGC CAT TTC ACG CGC TAC CCT TAT TGC AAG GGT TCT AAG GAT AAC ATT	875
Gly His Phe Thr Arg Tyr Pro Tyr Cys Lys Gly Ser Lys Asp Asn Ile	
260 265 270	
ATC GGC ATG GTG CAT ATT AGG GAT TTG CTT TCG CGC TCT ATT TTT ACC	923
Ile Gly Met Val His Ile Arg Asp Leu Leu Ser Arg Ser Ile Phe Thr	
275 280 285	
CCC AAA ATG CAT GAT TTC AAT CAA ATC GTT AGG AAA ATG ATC ATC GTC	971
Pro Lys Met His Asp Phe Asn Gln Ile Val Arg Lys Met Ile Ile Val	
290 295 300 305	
CCC GAA AGC GCT TCC ATT TCT CAA ATC CTT ATT AAA ATG AAA AAA GAG	1019
Pro Glu Ser Ala Ser Ile Ser Gln Ile Leu Ile Lys Met Lys Lys Glu	
310 315 320	
CAA ATC CAT ACC GCT TTG GTG ATT GAT GAA TAC GGC GGC ACA GCC GGG	1067
Gln Ile His Thr Ala Leu Val Ile Asp Glu Tyr Gly Gly Thr Ala Gly	
325 330 335	
TTG CTC ACT ATG GAA GAC ATC ATT GAA GAG ATC ATG GGC GAG ATT AGC	1115
Leu Leu Thr Met Glu Asp Ile Ile Glu Glu Ile Met Gly Glu Ile Ser	
340 345 350	
GAC GAA TAC GAC TTA AAA CAA GAG GGC ATA AAC AAG CTT GAA GAG GGC	1163
Asp Glu Tyr Asp Leu Lys Gln Glu Gly Ile Asn Lys Leu Glu Glu Gly	
355 360 365	
GTG TTT GAA TTA GAG GGC ATG CTG GAT TTA GAG AGC GTA GAA GAA GCG	1211
Val Phe Glu Leu Glu Gly Met Leu Asp Leu Glu Ser Val Glu Glu Ala	
370 375 380 385	
CTT CAC ATT GAA TTT GAT AAA GAA TGC GAG CAG GTA ACG CTT GGG GGC	1259
Leu His Ile Glu Phe Asp Lys Glu Cys Glu Gln Val Thr Leu Gly Gly	
390 395 400	
TAT GTT TTT AGC TTG TTA GAG CGC ATG CCT ATG GAG GGA GAT ACA ATC	1307
Tyr Val Phe Ser Leu Leu Glu Arg Met Pro Met Glu Gly Asp Thr Ile	
405 410 415	
GTT TCG CAT GGG TAT TCT TTT GAA GTC TTA AGC GTG GAT GGG GCT AGG	1355
Val Ser His Gly Tyr Ser Phe Glu Val Leu Ser Val Asp Gly Ala Arg	
420 425 430	
ATA AAA CGC TTA AAA GCG GTT AAA CAA GAT CAG GGA GAA AAT GAA GCA T	1404
Ile Lys Arg Leu Lys Ala Val Lys Gln Asp Gln Gly Glu Asn Glu Ala	
435 440 445	
GAAAAAACA ACCCTCTTTG TATTGGGCTT ATTATTTAA	1443

(2) INFORMATION FOR SEQ ID NO:1106:

Leu	Met	Val	Ala	Phe	Leu	Leu	Val	Leu	Leu	Asn	Ala	Phe	Phe	Val	Leu		
		20						25						30			
TCA	GAG	TTT	GCC	CTT	GTG	AAA	GTG	CGT	AAA	ACC	CGC	TTA	GAA	GAG	CTG	203	
Ser	Glu	Phe	Ala	Leu	Val	Lys	Val	Arg	Lys	Thr	Arg	Leu	Glu	Glu	Leu		
		35				40					45						
GTT	AAA	ATC	GGT	AAT	TCC	AAC	GCT	AAA	CTC	GCT	TTA	AAG	ATG	AGT	CAA	251	
Val	Lys	Ile	Gly	Asn	Ser	Asn	Ala	Lys	Leu	Ala	Leu	Lys	Met	Ser	Gln		
		50			55					60					65		
AGA	CTA	GAC	ACT	TAT	TTG	AGC	GCG	ACG	CAG	TTA	GGC	ATC	ACC	CTT	TCT	299	
Arg	Leu	Asp	Thr	Tyr	Leu	Ser	Ala	Thr	Gln	Leu	Gly	Ile	Thr	Leu	Ser		
				70					75					80			
TCA	TTA	GCT	TTA	GGC	TGG	GTG	GGT	GAG	CCC	GCT	ATC	GCA	AAA	TTG	TTA	347	
Ser	Leu	Ala	Leu	Gly	Trp	Val	Gly	Glu	Pro	Ala	Ile	Ala	Lys	Leu	Leu		
			85					90					95				
GCC	GCG	CTG	TTT	GAG	TCT	ATG	GAT	TTG	AGA	GAA	AAT	CCT	ATT	TTT	ATC	395	
Ala	Ala	Leu	Phe	Glu	Ser	Met	Asp	Leu	Arg	Glu	Asn	Pro	Ile	Phe	Ile		
		100					105					110					
CAT	TCA	ATG	AGC	GTG	GTC	ATA	GCG	TTT	TTA	AGC	ATC	ACT	TTT	TTG	CAT	443	
His	Ser	Met	Ser	Val	Val	Ile	Ala	Phe	Leu	Ser	Ile	Thr	Phe	Leu	His		
		115				120					125						
GTC	GTG	TTG	GGC	GAG	ATT	GTG	CCT	AAA	TCT	TTA	GCG	ATC	GCT	AAA	TCT	491	
Val	Val	Leu	Gly	Glu	Ile	Val	Pro	Lys	Ser	Leu	Ala	Ile	Ala	Lys	Ser		
		130			135					140					145		
GAA	AAA	GCC	ACC	CTT	TTT	GCC	GCA	CGC	CCT	TTG	CAT	GTG	TTT	TGG	GTG	539	
Glu	Lys	Ala	Thr	Leu	Phe	Ala	Ala	Arg	Pro	Leu	His	Val	Phe	Trp	Val		
				150					155					160			
GTG	TTT	TAT	CCG	GTG	GTG	CGT	TTG	TTT	GAT	GTG	ATC	GCT	CAT	TTT	TTT	587	
Val	Phe	Tyr	Pro	Val	Val	Arg	Leu	Phe	Asp	Val	Ile	Ala	His	Phe	Phe		
			165					170					175				
TTG	AAA	AAG	ATG	GGC	ATC	AAT	CCT	AAA	GAG	CAT	GAC	GGC	ACG	CAT	TCT	635	
Leu	Lys	Lys	Met	Gly	Ile	Asn	Pro	Lys	Glu	His	Asp	Gly	Thr	His	Ser		
		180					185					190					
GAA	GAA	GAG	TTA	AAA	ATC	ATT	GTG	GGC	GAG	AGT	TTG	AGA	GAG	GGC	ATT	683	
Glu	Glu	Glu	Leu	Lys	Ile	Ile	Val	Gly	Glu	Ser	Leu	Arg	Glu	Gly	Ile		
		195				200					205						
ATT	GAT	TCA	GTG	GAG	GGC	GAA	ATC	ATT	AAA	AAC	GCA	GTG	GAT	TTT	TCT	731	
Ile	Asp	Ser	Val	Glu	Gly	Glu	Ile	Ile	Lys	Asn	Ala	Val	Asp	Phe	Ser		
		210			215					220					225		
GAC	ACG	AGC	GCT	AAA	GAA	ATC	ATG	ACC	CCA	CGA	AAA	GAC	ATG	GTG	TGT	779	
Asp	Thr	Ser	Ala	Lys	Glu	Ile	Met	Thr	Pro	Arg	Lys	Asp	Met	Val	Cys		
				230					235					240			

Phe	Leu	Glu	Asn	Lys	Lys	Ala	Leu	Arg	Leu	Val	Asp	Val	Ala	Cys	Gly
50						55					60				
Thr	Gly	Asp	Met	Leu	Val	Ala	Trp	Gln	Lys	Ser	Ala	Leu	Asn	Cys	Gly
65					70					75					80
Ile	Glu	Phe	Lys	Glu	Cys	Leu	Gly	Ile	Asp	Pro	Ser	Asn	Asn	Met	Leu
			85						90					95	
Glu	Leu	Ala	Ile	Lys	Lys	Cys	Glu	Glu	Leu	Glu	Asn	Lys	Ala	Ser	Phe
			100					105					110		
Ile	Gln	Ala	Gln	Ala	Lys	Asp	Leu	Lys	Gly	Val	Glu	Asn	Asn	Ser	Val
	115						120					125			
Asp	Ile	Leu	Ser	Ile	Ala	Tyr	Gly	Leu	Arg	Asn	Val	Val	Glu	Arg	Gln
	130					135					140				
Glu	Ala	Leu	Lys	Glu	Phe	Phe	Arg	Val	Leu	Lys	Pro	Arg	Gly	Val	Leu
145					150					155					160
Val	Ile	Leu	Glu	Phe	Leu	Lys	Lys	Asp	Asn	Pro	Thr	Trp	Leu	Asp	Lys
			165					170						175	
Ile	Ser	Gly	Phe	Tyr	Thr	Asn	Lys	Val	Leu	Pro	Leu	Val	Gly	Gly	Ala
			180					185					190		
Ile	Ser	Lys	Asn	Tyr	Gly	Ala	Tyr	Ser	Tyr	Leu	Pro	Gln	Ser	Ile	Glu
	195						200					205			
Gly	Phe	Leu	Ser	Leu	Glu	Gly	Leu	Lys	His	Glu	Leu	Arg	Asn	Ala	Gly
	210					215					220				
Phe	Glu	Ile	Leu	Arg	Thr	Glu	Asp	Ser	Ile	Ala	Gln	Ile	Ser	Thr	Thr
225					230					235					240
Met	Leu	Val	Lys	Lys	Asn										
				245											

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 57...1403
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

AAAATTCTGA GATTTTATAT ATTTTATATT TATCGTTAGG TTTTAGGTTT AAAGTT ATG	59
Met	
1	
GGG AGG AAT CAA GGA GCT TAT TTG GAT CCG TCT GAA TCG ATT TTG ATG	107
Gly Arg Asn Gln Gly Ala Tyr Leu Asp Pro Ser Glu Ser Ile Leu Met	
5 10 15	
TTG ATG GTT GCT TTT TTA TTG GTG CTG TTG AAC GCT TTT TTT GTG CTT	155

Leu	Glu	Asn	Lys	Ala	Ser	Phe	Ile	Gln	Ala	Gln	Ala	Lys	Asp	Leu	Lys	
				110					115					120		
GGC	GTT	GAA	AAT	AAC	AGC	GTG	GAT	ATC	CTC	TCT	ATT	GCG	TAT	GGC	TTG	495
Gly	Val	Glu	Asn	Asn	Ser	Val	Asp	Ile	Leu	Ser	Ile	Ala	Tyr	Gly	Leu	
			125					130				135				
CGT	AAT	GTC	GTG	GAA	AGA	CAA	GAG	GCC	TTA	AAA	GAG	TTT	TTT	AGG	GTG	543
Arg	Asn	Val	Val	Glu	Arg	Gln	Glu	Ala	Leu	Lys	Glu	Phe	Phe	Arg	Val	
		140					145					150				
TTA	AAA	CCC	AGG	GGC	GTT	TTA	GTG	ATT	TTA	GAA	TTT	TTA	AAA	AAA	GAC	591
Leu	Lys	Pro	Arg	Gly	Val	Leu	Val	Ile	Leu	Glu	Phe	Leu	Lys	Lys	Asp	
	155					160					165					
AAC	CCC	ACA	TGG	CTG	GAT	AAA	ATC	TCA	GGG	TTT	TAC	ACG	AAT	AAG	GTT	639
Asn	Pro	Thr	Trp	Leu	Asp	Lys	Ile	Ser	Gly	Phe	Tyr	Thr	Asn	Lys	Val	
170					175					180				185		
TTG	CCT	TTA	GTG	GGA	GGG	GCT	ATC	AGT	AAG	AAT	TAT	GGT	GCT	TAT	TCT	687
Leu	Pro	Leu	Val	Gly	Gly	Ala	Ile	Ser	Lys	Asn	Tyr	Gly	Ala	Tyr	Ser	
			190						195				200			
TAT	TTA	CCG	CAA	TCC	ATT	GAG	GGG	TTT	TTG	AGT	TTA	GAG	GGT	TTG	AAG	735
Tyr	Leu	Pro	Gln	Ser	Ile	Glu	Gly	Phe	Leu	Ser	Leu	Glu	Gly	Leu	Lys	
			205				210						215			
CAT	GAA	TTA	AGA	AAC	GCA	GGG	TTT	GAG	ATT	TTA	AGG	ACT	GAA	GAT	TCT	783
His	Glu	Leu	Arg	Asn	Ala	Gly	Phe	Glu	Ile	Leu	Arg	Thr	Glu	Asp	Ser	
		220				225					230					
ATC	GCT	CAA	ATT	TCA	ACG	ACC	ATG	CTT	GTT	AAA	AAA	AAC	TAAAGGAATG	TT		834
Ile	Ala	Gln	Ile	Ser	Thr	Thr	Met	Leu	Val	Lys	Lys	Asn				
	235					240				245						
ATGCAAGATG	AATTATTTGA	AACC														858

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

Met	Lys	Lys	Glu	Lys	His	Leu	Lys	Gln	Glu	Lys	Ile	Ile	Asn	Met	Phe
1				5					10					15	
Asp	Asp	Ile	Ala	Ser	Ser	Tyr	Asp	Gln	Ala	Asn	Arg	Leu	Met	Ser	Phe
			20					25					30		
Gly	Leu	Asp	Val	Lys	Trp	Arg	Glu	Arg	Ala	Cys	Glu	His	Ala	Phe	Leu
	35						40					45			

65		70		75		80									
Leu	Glu	Leu	Leu	Asn	Thr	Phe	Ala	Leu	Ser	Ile	Leu	Leu	Leu	Ser	Lys
			85						90					95	
Phe	Phe	Ala													

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 85...822
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GGCGCCAACG	ATTTTAATGA	TCCTCATTGT	GATTTTAGTG	GTTGTCAAGC	CTTTTAAAG	60										
ACAAGCCATG	AAAAAAGAAA	AGTC	ATG	AAA	AAA	GAA	AAG	CAT	CTC	AAG	CAA	111				
		Met	Lys	Lys	Glu	Lys	His	Leu	Lys	Gln						
		1				5										
GAA	AAA	ATC	ATC	AAC	ATG	TTT	GAT	GAT	ATA	GCC	AGC	TCT	TAC	GAT	CAA	159
Glu	Lys	Ile	Ile	Asn	Met	Phe	Asp	Asp	Ile	Ala	Ser	Ser	Tyr	Asp	Gln	
10				15					20					25		
GCC	AAC	CGC	TTG	ATG	AGT	TTT	GGC	TTA	GAC	GTT	AAA	TGG	CGA	GAA	AGG	207
Ala	Asn	Arg	Leu	Met	Ser	Phe	Gly	Leu	Asp	Val	Lys	Trp	Arg	Glu	Arg	
			30					35						40		
GCT	TGC	GAG	CAT	GCG	TTT	TTA	TTT	TTA	GAA	AAC	AAG	AAA	GCG	TTA	AGG	255
Ala	Cys	Glu	His	Ala	Phe	Leu	Phe	Leu	Glu	Asn	Lys	Lys	Ala	Leu	Arg	
			45					50					55			
CTT	GTG	GAT	GTG	GCA	TGC	GGG	ACG	GGG	GAT	ATG	CTT	GTG	GCT	TGG	CAA	303
Leu	Val	Asp	Val	Ala	Cys	Gly	Thr	Gly	Asp	Met	Leu	Val	Ala	Trp	Gln	
		60					65					70				
AAA	AGC	GCT	CTC	AAT	TGC	GGT	ATA	GAG	TTT	AAG	GAA	TGT	TTG	GGG	ATT	351
Lys	Ser	Ala	Leu	Asn	Cys	Gly	Ile	Glu	Phe	Lys	Glu	Cys	Leu	Gly	Ile	
	75					80				85						
GAC	CCC	TCT	AAT	AAC	ATG	CTT	GAA	TTA	GCC	ATC	AAA	AAA	TGT	GAA	GAG	399
Asp	Pro	Ser	Asn	Asn	Met	Leu	Glu	Leu	Ala	Ile	Lys	Lys	Cys	Glu	Glu	
90				95					100					105		
CTT	GAA	AAC	AAA	GCT	TCT	TTC	ATC	CAA	GCT	CAA	GCC	AAA	GAT	TTA	AAA	447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

CTCCCTGAAG	CG	ATG	CTC	GCA	TGG	ATG	TCT	TGC	TCG	TTG	AAA	AAA	GTA	CCA	51	
	Met	Leu	Ala	Trp	Met	Ser	Cys	Ser	Leu	Lys	Lys	Val	Pro			
	1				5					10						
CTA	GGC	CGT	AAA	TCT	TTC	ATG	GCG	TTT	TTA	AGG	TTA	ATA	TTA	GAT	TCT	99
Leu	Gly	Arg	Lys	Ser	Phe	Met	Ala	Phe	Leu	Arg	Leu	Ile	Leu	Asp	Ser	
	15				20					25						
TCT	AAC	GCC	ACG	ACA	TGC	GCG	TTT	TTA	GAC	GCC	ACG	ACA	AAA	ACT	TCA	147
Ser	Asn	Ala	Thr	Thr	Cys	Ala	Phe	Leu	Asp	Ala	Thr	Thr	Lys	Thr	Ser	
	30				35				40					45		
ATT	TCT	TTG	GGT	AAT	TTT	TCT	AAA	AAC	CGC	AAG	GCT	AGG	GGT	ATC	CCG	195
Ile	Ser	Leu	Gly	Asn	Phe	Ser	Lys	Asn	Arg	Lys	Ala	Arg	Gly	Ile	Pro	
			50					55					60			
CTC	GCT	CCA	CTG	ATG	CCT	AAA	ACC	AAT	TTC	ATG	AAT	GTC	CTT	TAT	AAG	243
Leu	Ala	Pro	Leu	Met	Pro	Lys	Thr	Asn	Phe	Met	Asn	Val	Leu	Tyr	Lys	
			65					70					75			
ATT	TGC	GCT	TTA	GAG	CTG	CTC	AAC	ACT	TTT	GCT	TTG	AGT	ATT	TTA	TTG	291
Ile	Cys	Ala	Leu	Glu	Leu	Leu	Asn	Thr	Phe	Ala	Leu	Ser	Ile	Leu	Leu	
		80					85					90				
CTT	TCT	AAA	TTT	TTC	GCT	TGAATGATT	GATTAAGCGC	GCCATTTTCT	AG							341
Leu	Ser	Lys	Phe	Phe	Ala											
			95													

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

Met	Leu	Ala	Trp	Met	Ser	Cys	Ser	Leu	Lys	Lys	Val	Pro	Leu	Gly	Arg
1				5				10					15		
Lys	Ser	Phe	Met	Ala	Phe	Leu	Arg	Leu	Ile	Leu	Asp	Ser	Ser	Asn	Ala
			20					25					30		
Thr	Thr	Cys	Ala	Phe	Leu	Asp	Ala	Thr	Thr	Lys	Thr	Ser	Ile	Ser	Leu
		35					40					45			
Gly	Asn	Phe	Ser	Lys	Asn	Arg	Lys	Ala	Arg	Gly	Ile	Pro	Leu	Ala	Pro
	50					55				60					
Leu	Met	Pro	Lys	Thr	Asn	Phe	Met	Asn	Val	Leu	Tyr	Lys	Ile	Cys	Ala

Asn

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

```

Met Lys Leu Val Leu Gly Ile Ser Gly Ala Ser Gly Ile Pro Leu Ala
 1           5           10           15
Leu Arg Phe Leu Glu Lys Leu Pro Lys Glu Ile Glu Val Phe Val Val
          20           25           30
Ala Ser Lys Asn Ala His Val Val Ala Leu Glu Glu Ser Asn Ile Asn
          35           40           45
Leu Lys Asn Ala Met Lys Asp Leu Arg Pro Ser Gly Thr Phe Phe Asn
          50           55           60
Glu Gln Asp Ile His Ala Ser Ile Ala Ser Gly Ser Tyr Gly Ile His
65           70           75           80
Lys Met Ala Ile Ile Pro Ala Ser Met Asp Met Val Ala Lys Ile Ala
          85           90           95
His Gly Phe Gly Gly Asp Leu Ile Ser Arg Ser Ala Ser Val Met Leu
          100          105          110
Lys Glu Lys Arg Pro Leu Leu Ile Ala Pro Arg Glu Met Pro Leu Ser
          115          120          125
Ala Ile Met Leu Glu Asn Leu Leu Lys Leu Ser His Ser Asn Ala Ile
          130          135          140
Ile Ala Pro Pro Met Met Thr Tyr Tyr Thr Gln Ser Lys Thr Leu Glu
145          150          155          160
Ala Met Gln Asp Phe Leu Val Gly Lys Trp Phe Asp Ser Leu Gly Ile
          165          170          175
Glu Asn Asp Leu Tyr Pro Arg Trp Gly Met Asn
          180          185

```

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...309
- (D) OTHER INFORMATION:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GCAAATCTTA TAAAGGACAT TC ATG AAA TTG GTT TTA GGC ATC AGT GGA GCG	52
Met Lys Leu Val Leu Gly Ile Ser Gly Ala	
1 5 10	
AGC GGG ATA CCC CTA GCC TTG CGG TTT TTA GAA AAA TTA CCC AAA GAA	100
Ser Gly Ile Pro Leu Ala Leu Arg Phe Leu Glu Lys Leu Pro Lys Glu	
15 20 25	
ATT GAA GTT TTT GTC GTG GCG TCT AAA AAC GCG CAT GTC GTG GCG TTA	148
Ile Glu Val Phe Val Val Ala Ser Lys Asn Ala His Val Val Ala Leu	
30 35 40	
GAA GAA TCT AAT ATT AAC CTT AAA AAC GCC ATG AAA GAT TTA CGG CCT	196
Glu Glu Ser Asn Ile Asn Leu Lys Asn Ala Met Lys Asp Leu Arg Pro	
45 50 55	
AGT GGT ACT TTT TTC AAC GAG CAA GAC ATC CAT GCG AGC ATC GCT TCA	244
Ser Gly Thr Phe Phe Asn Glu Gln Asp Ile His Ala Ser Ile Ala Ser	
60 65 70	
GGG AGT TAT GGT ATC CAT AAA ATG GCG ATC ATT CCA GCG AGC ATG GAC	292
Gly Ser Tyr Gly Ile His Lys Met Ala Ile Ile Pro Ala Ser Met Asp	
75 80 85 90	
ATG GTG GCT AAA ATC GCG CAT GGC TTT GGG GGG GAT TTG ATT TCT AGG	340
Met Val Ala Lys Ile Ala His Gly Phe Gly Gly Asp Leu Ile Ser Arg	
95 100 105	
AGT GCG TCT GTG ATG CTT AAA GAA AAG CGC CCC TTA CTC ATT GCC CCT	388
Ser Ala Ser Val Met Leu Lys Glu Lys Arg Pro Leu Leu Ile Ala Pro	
110 115 120	
AGA GAA ATG CCT TTA AGC GCT ATC ATG TTA GAA AAT TTG CTC AAA CTC	436
Arg Glu Met Pro Leu Ser Ala Ile Met Leu Glu Asn Leu Leu Lys Leu	
125 130 135	
TCC CAT TCT AAT GCA ATC ATT GCG CCG CCG ATG ATG ACT TAT TAC ACC	484
Ser His Ser Asn Ala Ile Ile Ala Pro Pro Met Met Thr Tyr Tyr Thr	
140 145 150	
CAG AGC AAG ACT TTA GAA GCG ATG CAA GAT TTT TTA GTG GGG AAG TGG	532
Gln Ser Lys Thr Leu Glu Ala Met Gln Asp Phe Leu Val Gly Lys Trp	
155 160 165 170	
TTT GAC AGC TTA GGG ATA GAA AAT GAC TTA TAC CCA CGA TGG GGA ATG	580
Phe Asp Ser Leu Gly Ile Glu Asn Asp Leu Tyr Pro Arg Trp Gly Met	
175 180 185	
AAC TGATGCAAAA AATCGGCATT TACCCGGGCA CTTTGA	620

Phe Ile Lys Cys Ala Val
190

AATTGCTTG

644

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

Met	Tyr	Val	Val	Leu	Glu	Gly	Val	Asp	Gly	Ala	Gly	Lys	Ser	Thr	Gln
1				5					10					15	
Val	Glu	Leu	Leu	Lys	Asp	Arg	Phe	Lys	Asn	Ala	Leu	Phe	Thr	Lys	Glu
			20					25					30		
Pro	Gly	Gly	Thr	Arg	Met	Gly	Glu	Ser	Leu	Arg	Arg	Ile	Ala	Leu	Asn
		35				40						45			
Glu	Asn	Ile	Ser	Glu	Leu	Ala	Arg	Ala	Phe	Leu	Phe	Leu	Ser	Asp	Arg
	50					55					60				
Ala	Glu	His	Thr	Glu	Ser	Val	Ile	Lys	Pro	Ala	Leu	Lys	Glu	Lys	Lys
65					70					75					80
Leu	Ile	Ile	Ser	Asp	Arg	Ser	Leu	Ile	Ser	Gly	Met	Ala	Tyr	Ser	Gln
			85					90						95	
Phe	Ser	Ser	Leu	Glu	Leu	Asn	Leu	Leu	Ala	Thr	Gln	Ser	Val	Leu	Pro
			100					105					110		
Ala	Lys	Ile	Ile	Leu	Leu	Leu	Ile	Asp	Lys	Glu	Gly	Leu	Lys	Gln	Arg
		115					120					125			
Leu	Ser	Leu	Lys	Ser	Leu	Asp	Lys	Ile	Glu	Asn	Gln	Gly	Ile	Glu	Lys
		130				135					140				
Leu	Leu	His	Ile	Gln	Gln	Lys	Leu	Lys	Thr	His	Ala	Tyr	Ala	Leu	Gln
145					150					155					160
Glu	Lys	Phe	Gly	Cys	Glu	Val	Leu	Glu	Leu	Asp	Ala	Lys	Glu	Ser	Val
			165					170						175	
Lys	Asn	Leu	His	Glu	Lys	Ile	Ala	Ala	Phe	Ile	Lys	Cys	Ala	Val	
		180						185						190	

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 23...583

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

ATCCTTTGAT TTCAAAGGCT TAAA ATG TAT GTG GTG TTA GAA GGC GTT GAT	51
Met Tyr Val Val Leu Glu Gly Val Asp	
1 5	
GGC GCG GGC AAA AGC ACT CAA GTA GAA TTA TTA AAA GAC CGG TTT AAA	99
Gly Ala Gly Lys Ser Thr Gln Val Glu Leu Leu Lys Asp Arg Phe Lys	
10 15 20 25	
AAC GCC CTT TTT ACC AAA GAG CCA GGG GGG ACG AGA ATG GGC GAG AGT	147
Asn Ala Leu Phe Thr Lys Glu Pro Gly Gly Thr Arg Met Gly Glu Ser	
30 35 40	
TTA AGG CGT ATC GCT TTG AAT GAA AAC ATT AGC GAA TTG GCT AGA GCG	195
Leu Arg Arg Ile Ala Leu Asn Glu Asn Ile Ser Glu Leu Ala Arg Ala	
45 50 55	
TTT TTA TTC TTA AGC GAT AGG GCT GAG CAT ACA GAA AGC GTG ATA AAA	243
Phe Leu Phe Leu Ser Asp Arg Ala Glu His Thr Glu Ser Val Ile Lys	
60 65 70	
CCG GCA TTG AAA GAA AAA AAG CTC ATC ATT AGC GAC AGG AGC TTG ATC	291
Pro Ala Leu Lys Glu Lys Lys Leu Ile Ile Ser Asp Arg Ser Leu Ile	
75 80 85	
TCT GGC ATG GCT TAT AGC CAA TTT TCA AGC TTA GAA TTA AAC CTG CTT	339
Ser Gly Met Ala Tyr Ser Gln Phe Ser Ser Leu Glu Leu Asn Leu Leu	
90 95 100 105	
GCC ACC CAA AGC GTC TTG CCT GCA AAA ATC ATT CTT TTA CTC ATA GAC	387
Ala Thr Gln Ser Val Leu Pro Ala Lys Ile Ile Leu Leu Leu Ile Asp	
110 115 120	
AAA GAG GGC TTA AAA CAG CGC TTA AGC CTT AAA AGT TTA GAT AAA ATA	435
Lys Glu Gly Leu Lys Gln Arg Leu Ser Leu Lys Ser Leu Asp Lys Ile	
125 130 135	
GAA AAC CAA GGC ATA GAA AAA TTA CTT CAT ATC CAG CAA AAG CTC AAA	483
Glu Asn Gln Gly Ile Glu Lys Leu Leu His Ile Gln Gln Lys Leu Lys	
140 145 150	
ACC CAC GCT TAT GCG TTA CAA GAA AAA TTT GGG TGC GAA GTT TTG GAA	531
Thr His Ala Tyr Ala Leu Gln Glu Lys Phe Gly Cys Glu Val Leu Glu	
155 160 165	
TTA GAC GCT AAA GAA AGC GTT AAA AAC TTG CAC GAA AAA ATC GCC GCT	579
Leu Asp Ala Lys Glu Ser Val Lys Asn Leu His Glu Lys Ile Ala Ala	
170 175 180 185	
TTT ATA AAA TGC GCT GTT TAACCTGTTT GAAGCTTTCT TTTAAGCCTC TTTGCCCA	635


```

      355              360              365
Pro Tyr Val Ala Thr Leu Leu Ala Arg Leu Ser Lys Val Asn Lys Asp
      370              375              380
Ser Phe Val Trp Asp Phe Ala Thr Gly Ser Ala Gly Leu Leu Val Ala
385              390              395              400
Ser Met Asn Leu Met Ile Glu Asp Ala Lys Lys Arg Ile Thr Ser Pro
      405              410              415
Glu Glu Leu Glu Gln Lys Ile Ala His Ile Lys Ala Lys Gln Leu Leu
      420              425              430
Gly Ile Glu Ile Leu Ser Asp Ile His Thr Leu Ala Val Leu Asn Met
      435              440              445
Ile Leu Met Gly Asp Gly Ser Ser Gln Ile Leu Asn Gln Asp Gly Leu
      450              455              460
Ser Gly Phe Asp Gly Lys Val Asn Asn Glu Ala Phe Lys Ala Asn Ala
465              470              475              480
Phe Val Leu Asn Pro Pro Tyr Ser Ala Ser Gly Asn Gly Met Val Phe
      485              490              495
Val Glu Gln Ala Leu Glu Lys Met Gln Ser Gly Tyr Ala Ser Val Ile
      500              505              510
Ile Gln Ser Ser Ala Gly Ser Gly Lys Ala Lys Glu Tyr Asn Val Arg
      515              520              525
Ile Leu Glu Lys His Thr Leu Leu Ala Ser Ile Lys Met Pro Leu Asp
      530              535              540
Leu Phe Ile Gly Lys Ser Ser Val Gln Thr His Ile Tyr Val Phe Arg
545              550              555              560
Val Asn Glu Lys His Asp Ala Lys Gln Arg Val Lys Phe Ile Asn Phe
      565              570              575
Ser Asn Asp Gly Tyr Ala Arg Ala Asn Arg Lys Lys Ala Lys Ala Ser
      580              585              590
His Asn Leu Lys Asp Thr His Asn Ala Lys Glu Arg Tyr Asn Glu Val
      595              600              605
Val Asp Leu Val His Ile Gly Gln Ser Cys Leu Lys Phe Leu Ser Glu
      610              615              620
Asp Asp Tyr Tyr Glu Asn Thr Ile Asp Pro Lys Asn Gly Ser Asp Trp
625              630              635              640
Asn Gln Asn Lys Pro Thr Asp Thr Lys Pro Glu Leu Glu Asp Phe Lys
      645              650              655
Arg Thr Ile Ala Asp Tyr Leu Ser Tyr Glu Val Ser Leu Ile Leu Lys
      660              665              670
Asn Gln Met Pro Pro Lys Arg
      675

```

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...597

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

```

Met Asn Lys Val Gln Ser Ile Asp Pro Leu Ile Ala Asp Lys Phe Asn
 1           5           10           15
Asn Glu Leu Arg Ser Tyr Asn Leu Glu Tyr Lys Leu Glu Gln Glu Ser
      20           25           30
Leu Asn Lys Glu Ile Asp Glu Ala Leu Lys Asn Tyr Ala Ser Lys Asn
      35           40           45
Gly Gly Leu Gly Gly Asn Arg Pro Asp Val Lys Leu Leu Leu Asn Thr
      50           55           60
Gln Asp Pro Asn Arg Arg Val Pro Ile Leu Ile Glu Tyr Lys Gly Leu
      65           70           75           80
Lys Asp Lys Leu Ile Lys Leu Asp Lys Asn Lys Leu Val Glu Asn Phe
      85           90           95
Lys Asn His Glu Pro His Tyr Lys Asn Ile Arg Glu Tyr Ala Leu Asn
      100          105          110
Gly Ala Leu His Tyr Ala Asn Ala Ile Leu His His Thr Ser Tyr Thr
      115          120          125
Glu Cys Ile Ala Ile Gly Ile Thr Gly Tyr Lys Asp Asn Lys Gly Gly
      130          135          140
Ile Cys Ser Gln Ile Ala Val Tyr Tyr Val Asn Lys Ser Asn Leu Gly
      145          150          155          160
Met Gly Ile Asp Val Ser Lys Gly Glu Gln Gly Tyr Ser Asp Leu Ser
      165          170          175
Phe Leu Ser Arg Lys His Phe Asn Asp Phe Ile Lys Arg Val Asp Thr
      180          185          190
Leu Ser Leu Ser Asp Glu Asp Leu Glu Arg Ile Arg Glu Lys Lys Asn
      195          200          205
Gln Glu Ile Glu Asp Cys Leu Met Arg Leu Asn Asn Asn Ile Tyr Asn
      210          215          220
Lys Glu Lys Asn Phe Leu Ser Glu His Asn Arg Val Tyr Leu Val Ile
      225          230          235          240
Ala Ser Ile Ile Ala Asn Leu Gly Ile Pro Asn Leu Val Thr Pro Leu
      245          250          255
Asn Lys Glu Asp Leu Lys Ser Ser Asp Glu Val His Gln Arg Asp Gly
      260          265          270
Asp Ile Met Leu Arg Lys Ile Gln Ser Phe Leu Glu Asn Lys Asp Leu
      275          280          285
Ser Pro Glu Lys Arg Gln Ser Ile Ile Ser Ser Leu Glu Thr Leu Leu
      290          295          300
Arg Asn Glu Asn Asn Asn Lys Ala Thr Asn Gly Glu Ser Cys Leu Lys
      305          310          315          320
Arg Cys Phe Ser Glu Ile Val Asp Ser Leu Gly Ile Tyr Tyr Lys Ile
      325          330          335
Gly Leu Ser Thr Asp Phe Thr Gly Lys Leu Phe Asn Glu Met Tyr Arg
      340          345          350
Trp Leu Gly Phe Thr Lys Asp Gln Leu Asn Asp Val Val Leu Thr Pro

```

AAC GAA GCG TTT AAG GCT AAT GCC TTT GTT TTA AAC CCG CCT TAT TCC	1494
Asn Glu Ala Phe Lys Ala Asn Ala Phe Val Leu Asn Pro Pro Tyr Ser	
475 480 485	
GCT AGC GGT AAT GGC ATG GTG TTT GTG GAG CAG GCT TTA GAA AAA ATG	1542
Ala Ser Gly Asn Gly Met Val Phe Val Glu Gln Ala Leu Glu Lys Met	
490 495 500	
CAA AGC GGT TAT GCG AGC GTG ATC ATC CAA TCA AGC GCC GGC AGT GGT	1590
Gln Ser Gly Tyr Ala Ser Val Ile Ile Gln Ser Ser Ala Gly Ser Gly	
505 510 515 520	
AAA GCC AAA GAA TAC AAT GTA AGG ATT TTG GAA AAA CAC ACG CTT TTA	1638
Lys Ala Lys Glu Tyr Asn Val Arg Ile Leu Glu Lys His Thr Leu Leu	
525 530 535	
GCG AGC ATT AAA ATG CCT TTA GAT TTA TTC ATC GGT AAA AGC AGC GTT	1686
Ala Ser Ile Lys Met Pro Leu Asp Leu Phe Ile Gly Lys Ser Ser Val	
540 545 550	
CAA ACC CAT ATC TAT GTT TTT AGG GTC AAT GAA AAG CAT GAC GCT AAG	1734
Gln Thr His Ile Tyr Val Phe Arg Val Asn Glu Lys His Asp Ala Lys	
555 560 565	
CAA AGG GTG AAA TTT ATT AAT TTC AGT AAC GAC GGC TAC GCT AGA GCG	1782
Gln Arg Val Lys Phe Ile Asn Phe Ser Asn Asp Gly Tyr Ala Arg Ala	
570 575 580	
AAT CGC AAA AAA GCC AAA GCC AGC CAC AAT TTA AAA GAC ACG CAT AAC	1830
Asn Arg Lys Lys Ala Lys Ala Ser His Asn Leu Lys Asp Thr His Asn	
585 590 595 600	
GCC AAA GAG CGC TAC AAC GAA GTC GTG GAT TTA GTC CAT ATT GGC CAA	1878
Ala Lys Glu Arg Tyr Asn Glu Val Val Asp Leu Val His Ile Gly Gln	
605 610 615	
TCA TGT TTG AAA TTT CTA AGC GAA GAT GAC TAT TAT GAA AAC ACC ATA	1926
Ser Cys Leu Lys Phe Leu Ser Glu Asp Asp Tyr Tyr Glu Asn Thr Ile	
620 625 630	
GAT CCC AAA AAC GGG AGC GAT TGG AAC CAA AAC AAA CCC ACT GAC ACC	1974
Asp Pro Lys Asn Gly Ser Asp Trp Asn Gln Asn Lys Pro Thr Asp Thr	
635 640 645	
AAA CCC GAA TTA GAG GAT TTT AAA AGA ACG ATA GCC GAT TAC CTT TCT	2022
Lys Pro Glu Leu Glu Asp Phe Lys Arg Thr Ile Ala Asp Tyr Leu Ser	
650 655 660	
TAT GAA GTA AGC TTG ATT TTA AAA AAC CAA ATG CCC CCA AAG CGA TAGGC	2072
Tyr Glu Val Ser Leu Ile Leu Lys Asn Gln Met Pro Pro Lys Arg	
665 670 675	
CCCCCTTAATA GCCAACTCAA CGCTATTAAG TGGGGCGAG	2111

(2) INFORMATION FOR SEQ ID NO:1096:

ATC CCT AAT TTG GTA ACC CCC CTA AAC AAA GAA GAT CTA AAA TCC AGC	822
Ile Pro Asn Leu Val Thr Pro Leu Asn Lys Glu Asp Leu Lys Ser Ser	
250 255 260	
GAT GAG GTC CAT CAA AGA GAT GGC GAC ATC ATG CTC AGA AAA ATC CAA	870
Asp Glu Val His Gln Arg Asp Gly Asp Ile Met Leu Arg Lys Ile Gln	
265 270 275 280	
TCC TTT TTA GAG AAT AAG GAT TTG TCT CCA GAG AAA AGG CAA AGC ATT	918
Ser Phe Leu Glu Asn Lys Asp Leu Ser Pro Glu Lys Arg Gln Ser Ile	
285 290 295	
ATT TCT TCA TTA GAG ACT TTA TTA AGA AAC GAA AAC AAC AAC AAA GCC	966
Ile Ser Ser Leu Glu Thr Leu Leu Arg Asn Glu Asn Asn Asn Lys Ala	
300 305 310	
ACT AAT GGC GAA AGC TGT TTG AAG CGT TGT TTT AGT GAG ATT GTG GAT	1014
Thr Asn Gly Glu Ser Cys Leu Lys Arg Cys Phe Ser Glu Ile Val Asp	
315 320 325	
AGT TTG GGC ATT TAT TAT AAA ATC GGT CTT AGC ACG GAT TTT ACC GGT	1062
Ser Leu Gly Ile Tyr Tyr Lys Ile Gly Leu Ser Thr Asp Phe Thr Gly	
330 335 340	
AAA TTG TTC AAT GAA ATG TAT CGC TGG CTG GGT TTC ACG AAA GAC CAA	1110
Lys Leu Phe Asn Glu Met Tyr Arg Trp Leu Gly Phe Thr Lys Asp Gln	
345 350 355 360	
TTA AAC GAT GTG GTG CTC ACA CCC CCT TAT GTC GCC ACG CTT TTA GCT	1158
Leu Asn Asp Val Val Leu Thr Pro Pro Tyr Val Ala Thr Leu Leu Ala	
365 370 375	
AGA CTT TCT AAA GTC AAT AAG GAT AGT TTC GTG TGG GAT TTT GCC ACC	1206
Arg Leu Ser Lys Val Asn Lys Asp Ser Phe Val Trp Asp Phe Ala Thr	
380 385 390	
GGA AGC GCT GGG CTA TTA GTC GCA AGC ATG AAT TTG ATG ATA GAA GAC	1254
Gly Ser Ala Gly Leu Leu Val Ala Ser Met Asn Leu Met Ile Glu Asp	
395 400 405	
GCT AAA AAG CGT ATC ACT AGT CCA GAG GAA TTA GAG CAA AAA ATC GCC	1302
Ala Lys Lys Arg Ile Thr Ser Pro Glu Glu Leu Glu Gln Lys Ile Ala	
410 415 420	
CAC ATT AAA GCC AAG CAA CTT TTA GGG ATA GAA ATC TTA TCG GAT ATC	1350
His Ile Lys Ala Lys Gln Leu Leu Gly Ile Glu Ile Leu Ser Asp Ile	
425 430 435 440	
CAT ACT TTA GCG GTG TTA AAC ATG ATT TTA ATG GGC GAT GGG AGC AGT	1398
His Thr Leu Ala Val Leu Asn Met Ile Leu Met Gly Asp Gly Ser Ser	
445 450 455	
CAA ATC TTA AAC CAA GAC GGC TTG AGC GGT TTT GAT GGC AAA GTC AAT	1446
Gln Ile Leu Asn Gln Asp Gly Leu Ser Gly Phe Asp Gly Lys Val Asn	
460 465 470	

Glu Tyr Lys Leu Glu Gln Glu Ser Leu Asn Lys Glu Ile Asp Glu Ala	
25 30 35 40	
TTA AAA AAT TAC GCT TCT AAA AAT GGG GGT TTA GGG GGT AAC CGC CCT	198
Leu Lys Asn Tyr Ala Ser Lys Asn Gly Gly Leu Gly Gly Asn Arg Pro	
45 50 55	
GAT GTG AAA CTT TTA TTA AAC ACA CAA GAC CCC AAC AGA AGA GTC CCT	246
Asp Val Lys Leu Leu Leu Asn Thr Gln Asp Pro Asn Arg Arg Val Pro	
60 65 70	
ATT TTA ATA GAA TAC AAA GGG CTA AAA GAT AAG CTC ATT AAA TTA GAC	294
Ile Leu Ile Glu Tyr Lys Gly Leu Lys Asp Lys Leu Ile Lys Leu Asp	
75 80 85	
AAA AAC AAA CTG GTA GAA AAC TTT AAA AAC CAT GAG CCT CAT TAT AAA	342
Lys Asn Lys Leu Val Glu Asn Phe Lys Asn His Glu Pro His Tyr Lys	
90 95 100	
AAC ATT AGA GAA TAC GCC CTA AAT GGG GCT TTG CAT TAC GCT AAT GCG	390
Asn Ile Arg Glu Tyr Ala Leu Asn Gly Ala Leu His Tyr Ala Asn Ala	
105 110 115 120	
ATT TTA CAC CAC ACG AGC TAC ACT GAA TGC ATC GCC ATA GGC ATT ACA	438
Ile Leu His His Thr Ser Tyr Thr Glu Cys Ile Ala Ile Gly Ile Thr	
125 130 135	
GGC TAT AAA GAC AAT AAG GGC GGC ATA TGC TCT CAA ATC GCT GTC TAT	486
Gly Tyr Lys Asp Asn Lys Gly Gly Ile Cys Ser Gln Ile Ala Val Tyr	
140 145 150	
TAT GTG AAT AAA AGC AAT CTA GGC ATG GGG ATA GAT GTT TCA AAA GGC	534
Tyr Val Asn Lys Ser Asn Leu Gly Met Gly Ile Asp Val Ser Lys Gly	
155 160 165	
GAG CAA GGT TAT AGC GAT CTC TCC TTT TTA AGC CGT AAG CAT TTT AAC	582
Glu Gln Gly Tyr Ser Asp Leu Ser Phe Leu Ser Arg Lys His Phe Asn	
170 175 180	
GAC TTT ATT AAA CGA GTA GAC ACC CTT TCT TTA AGC GAT GAA GAT TTA	630
Asp Phe Ile Lys Arg Val Asp Thr Leu Ser Leu Ser Asp Glu Asp Leu	
185 190 195 200	
GAG CGC ATT AGA GAA AAG AAA AAC CAA GAA ATA GAA GAC TGC TTA ATG	678
Glu Arg Ile Arg Glu Lys Lys Asn Gln Glu Ile Glu Asp Cys Leu Met	
205 210 215	
CGG CTC AAC AAC AAT ATT TAC AAC AAA GAA AAG AAT TTT TTA AGC GAA	726
Arg Leu Asn Asn Asn Ile Tyr Asn Lys Glu Lys Asn Phe Leu Ser Glu	
220 225 230	
CAC AAT CGG GTA TAT TTA GTG ATT GCG AGC ATT ATC GCT AAT TTA GGC	774
His Asn Arg Val Tyr Leu Val Ile Ala Ser Ile Ile Ala Asn Leu Gly	
235 240 245	

```

Glu Tyr Leu Phe Ile Val Phe Cys Ala Pro Val Gly Ala Tyr Phe Lys
145                      150                      155                      160
Gly Gly Ile Glu Lys Gly Gly Ala Arg Phe Ile Thr Thr Ile Phe Asp
                      165                      170                      175
Arg Ala Ala Pro Lys Gly Thr Gly Gly Val Lys Val Gly Gly Asn Tyr
                      180                      185                      190
Ala Ala Ser Leu Leu Ala His Lys Met Ala Thr Glu Gln Gly Tyr Asp
                      195                      200                      205
Asp Cys Ile Tyr Leu Asp Pro Thr Thr His Thr Lys Ile Glu Glu Val
                      210                      215                      220
Gly Ala Ala Asn Phe Phe Gly Ile Thr His Asp Asp Ala Phe Ile Thr
225                      230                      235                      240
Pro His Ser Pro Ser Ile Leu Pro Ser Ile Thr Lys Lys Ser Leu Met
                      245                      250                      255
Val Leu Ala Lys Glu Tyr Leu Asn Leu Lys Val Glu Glu Arg Glu Ile
                      260                      265                      270
Leu Met Asp Glu Leu Asp Ala Phe Lys Glu Ala Gly Ala Cys Gly Thr
                      275                      280                      285
Ala Ala Ile Ile Thr Pro Ile Lys Glu Ile Val His Asn Asn Lys Ser
                      290                      295                      300
Tyr Phe Phe Glu Ala Pro Gly His Ile Thr Lys Arg Leu Tyr Asp Leu
305                      310                      315                      320
Leu Leu Ser Ile Gln Gln Gly Glu Gln Glu Ala Pro Lys Asp Trp Ile
                      325                      330                      335
Phe Glu Val Gly
                      340

```

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...2067
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

```

GTTATAATTT TATTTTTTTAA AAGGATACCC ATG AAT AAA GTT CAA TCT ATT GAT      54
                               Met Asn Lys Val Gln Ser Ile Asp
                               1                      5

CCT TTA ATC GCT GAT AAG TTC AAC AAC GAG TTA AGA AGT TAT AAC CTA      102
Pro Leu Ile Ala Asp Lys Phe Asn Asn Glu Leu Arg Ser Tyr Asn Leu
10                      15                      20

GAA TAC AAA CTA GAG CAA GAA AGC CTG AAT AAA GAA ATT GAT GAA GCT      150

```

```

Ile Thr Lys Lys Ser Leu Met Val Leu Ala Lys Glu Tyr Leu Asn Leu
250                      255                      260                      265

AAA GTA GAA GAG AGG GAA ATC CTA ATG GAT GAG TTG GAT GCG TTT AAA      870
Lys Val Glu Glu Arg Glu Ile Leu Met Asp Glu Leu Asp Ala Phe Lys
                      270                      275                      280

GAA GCT GGA GCG TGC GGG ACA GCT GCG ATC ATT ACG CCC ATT AAA GAA      918
Glu Ala Gly Ala Cys Gly Thr Ala Ala Ile Ile Thr Pro Ile Lys Glu
                      285                      290                      295

ATC GTG CAC AAC AAC AAG TCT TAT TTT TTT GAA GCG CCG GGC CAT ATT      966
Ile Val His Asn Asn Lys Ser Tyr Phe Phe Glu Ala Pro Gly His Ile
                      300                      305                      310

ACT AAA CGA CTC TAT GAT TTG CTT TTA TCC ATC CAA CAA GGC GAA CAA      1014
Thr Lys Arg Leu Tyr Asp Leu Leu Leu Ser Ile Gln Gln Gly Glu Gln
                      315                      320                      325

GAA GCC CCC AAA GAT TGG ATT TTT GAA GTT GGC TAAAGGTTA AAATTTATAG      1067
Glu Ala Pro Lys Asp Trp Ile Phe Glu Val Gly
330                      335                      340

CTGTATGCCG CATAAAATAA GGGCG                                          1092

```

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

```

Met Ala Asn Leu Glu Asn Leu Asp Trp Lys Asn Leu Gly Phe Ser Tyr
 1                      5                      10                      15
Ile Lys Thr Asp Phe Arg Phe Ile Ala Thr Tyr Lys Asn Gly Ser Trp
                20                      25                      30
Ser Gln Gly Gly Leu Val Ser Glu Asn Met Leu Gln Leu Ser Glu Gly
    35                      40                      45
Ser Pro Val Leu His Tyr Gly Gln Ala Cys Phe Glu Gly Leu Lys Ala
    50                      55                      60
Tyr Arg Ser Gln Lys Gly Lys Ala Leu Leu Phe Arg Pro Leu Glu Asn
    65                      70                      75                      80
Ala Lys Arg Leu Gln Thr Ser Cys Glu Arg Leu Leu Met Pro Lys Val
                85                      90                      95
Ser Glu Glu Leu Phe Leu Arg Ala Cys Ala Glu Val Val Lys Ala Asn
                100                      105                      110
Gln Lys Trp Leu Ala Pro Tyr Lys Ser Gly Ala Ser Leu Tyr Leu Arg
    115                      120                      125
Pro Phe Val Ile Gly Val Gly Asp Asn Leu Gly Val Lys Pro Ala Asn
    130                      135                      140

```

	30	35	40	
ATG TTA CAA CTC AGC GAA GGC TCG CCG GTC TTG CAC TAC GGG CAG GCT				198
Met Leu Gln Leu Ser Glu Gly Ser Pro Val Leu His Tyr Gly Gln Ala				
	45	50	55	
TGT TTT GAA GGC TTG AAG GCT TAC CGC TCT CAA AAG GGG AAA GCT TTA				246
Cys Phe Glu Gly Leu Lys Ala Tyr Arg Ser Gln Lys Gly Lys Ala Leu				
	60	65	70	
CTC TTT CGC CCT TTA GAA AAC GCC AAA CGC TTG CAA ACT TCA TGC GAA				294
Leu Phe Arg Pro Leu Glu Asn Ala Lys Arg Leu Gln Thr Ser Cys Glu				
	75	80	85	
AGA CTG CTC ATG CCC AAA GTG AGC GAA GAG CTG TTT TTA AGG GCA TGC				342
Arg Leu Leu Met Pro Lys Val Ser Glu Glu Leu Phe Leu Arg Ala Cys				
	90	95	100	105
GCT GAA GTG GTG AAA GCG AAT CAA AAA TGG CTC GCT CCT TAT AAA AGC				390
Ala Glu Val Val Lys Ala Asn Gln Lys Trp Leu Ala Pro Tyr Lys Ser				
	110	115	120	
GGG GCG AGT TTG TAT TTG CGC CCT TTT GTC ATA GGC GTA GGG GAT AAT				438
Gly Ala Ser Leu Tyr Leu Arg Pro Phe Val Ile Gly Val Gly Asp Asn				
	125	130	135	
TTG GGG GTG AAG CCG GCT AAT GAA TAC CTT TTT ATC GTG TTT TGT GCG				486
Leu Gly Val Lys Pro Ala Asn Glu Tyr Leu Phe Ile Val Phe Cys Ala				
	140	145	150	
CCT GTG GGG GCG TAT TTT AAG GGG GGT ATA GAA AAA GGG GGG GCT AGG				534
Pro Val Gly Ala Tyr Phe Lys Gly Gly Ile Glu Lys Gly Gly Ala Arg				
	155	160	165	
TTT ATC ACT ACG ATT TTT GAT AGG GCC GCG CCT AAA GGC ACC GGT GGG				582
Phe Ile Thr Thr Ile Phe Asp Arg Ala Ala Pro Lys Gly Thr Gly Gly				
	170	175	180	185
GTG AAA GTG GGA GGG AAT TAC GCT GCA AGC CTG TTA GCC CAT AAA ATG				630
Val Lys Val Gly Gly Asn Tyr Ala Ala Ser Leu Leu Ala His Lys Met				
	190	195	200	
GCC ACA GAG CAA GGC TAT GAT GAT TGC ATT TAT TTA GAC CCT ACT ACG				678
Ala Thr Glu Gln Gly Tyr Asp Asp Cys Ile Tyr Leu Asp Pro Thr Thr				
	205	210	215	
CAC ACT AAA ATT GAA GAA GTG GGG GCG GCG AAT TTT TTT GGC ATC ACG				726
His Thr Lys Ile Glu Glu Val Gly Ala Ala Asn Phe Phe Gly Ile Thr				
	220	225	230	
CAT GAT GAT GCC TTT ATC ACC CCG CAT TCG CCA AGC ATT CTG CCA AGC				774
His Asp Asp Ala Phe Ile Thr Pro His Ser Pro Ser Ile Leu Pro Ser				
	235	240	245	
ATT ACC-AAA AAA AGC TTG ATG GTT TTG GCT AAA GAA TAT TTG AAC CTC				822

(2) INFORMATION FOR SEO ID NO:1093:

(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 28...1047
(D) OTHER INFORMATION:

TGAAACTATC	CATTTAAAGG	TGTGAAA	ATG	GCA	AAT	TTA	GAA	AAT	TTA	GAC	TGG	54				
			Met	Ala	Asn	Leu	Glu	Asn	Leu	Asp	Trp					
			1				5									
AAA	AAT	TTA	GGC	TTT	AGC	TAC	ATT	AAA	ACG	GAT	TTT	CGC	TTC	ATC	GCC	102
Lys	Asn	Leu	Gly	Phe	Ser	Tyr	Ile	Lys	Thr	Asp	Phe	Arg	Phe	Ile	Ala	
10					15				20					25		
ACT	TAT	AAA	AAC	GGC	TCT	TGG	TCG	CAA	GGC	GGA	TTG	GTG	AGC	GAA	AAC	150
Thr	Tyr	Lys	Asn	Gly	Ser	Trp	Ser	Gln	Gly	Gly	Leu	Val	Ser	Glu	Asn	

TAT AGC ATG GGA TCT TTA GTG GGC GCG GAC ACC AAT TTT TTC ATC TCG	450
Tyr Ser Met Gly Ser Leu Val Gly Ala Asp Thr Asn Phe Phe Ile Ser	
105 110 115	
CAA TAC AAA AGC ACT AAC GCC ACT TCT TAT GGC GAA GTC ATT GAA AAT	498
Gln Tyr Lys Ser Thr Asn Ala Thr Ser Tyr Gly Glu Val Ile Glu Asn	
120 125 130 135	
TTT GAA GAA GAG CCT TTA GAA AAT CGC CTA GAA ATC TAT GCA CCA AAT	546
Phe Glu Glu Glu Pro Leu Glu Asn Arg Leu Glu Ile Tyr Ala Pro Asn	
140 145 150	
CAT GTT TTT TGC AGC ACC AAA GCC GTT TAT CAA GCT TAT AAG CCT GAA	594
His Val Phe Cys Ser Thr Lys Ala Val Tyr Gln Ala Tyr Lys Pro Glu	
155 160 165	
ACT TGT TTT TCT CAA GCT AAA GAA TGG CTT AAA AAG CCG AGT TTG GAA	642
Thr Cys Phe Ser Gln Ala Lys Glu Trp Leu Lys Lys Pro Ser Leu Glu	
170 175 180	
TGC CTA AAA ACT TAT GAT AGA AAC GGA TTA AAC GAC CTT TTA AAG CCG	690
Cys Leu Lys Thr Tyr Asp Arg Asn Gly Leu Asn Asp Leu Leu Lys Pro	
185 190 195	
GCT TTA CTC ACT AAC CAA GCC TTA AAA GAT ATA GAA AGC GAA CTA GGC	738
Ala Leu Leu Thr Asn Gln Ala Leu Lys Asp Ile Glu Ser Glu Leu Gly	
200 205 210 215	
AAG GAG TGG TTT TTT AGC GGG AGC GGG AGC GCG TTT TTT AGG CTA AAG	786
Lys Glu Trp Phe Phe Ser Gly Ser Gly Ser Ala Phe Phe Arg Leu Lys	
220 225 230	
CCT ATG CAA AAA GGG GGC GAA TGAAACTCAT TGCCAGCAAC AAAAAAGCCT ATTT	841
Pro Met Gln Lys Gly Gly Glu	
235	
TGACTA	847

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

Met Cys Leu Val Lys Asp Lys Leu Lys Asp Ile Ile Ser Val Lys Ser
1 5 10 15
Ala Leu Ser Phe Ser Leu Lys Gly Asp Phe Asp Cys Pro Leu Glu Glu
20 25 30
Asn Ser Leu Phe Lys Ala Leu Gln Ile Leu Lys Asn Phe Leu Lys Ser

290		295		300
Leu Lys Phe Gly Glu Ser Phe Thr Ala His Tyr Lys Cys Gln Asn Leu				
305		310		315
Ile Glu Val Gly Val Lys Thr Asp Lys Gly Ser Trp Thr Phe Asn Phe				
	325		330	335
Asn Arg				

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 94...807
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

GCCTTGACGC ATGTTTTTGA AGTTTATCCT AAAGTCAATA TTTTTTTAAA AATCCTTCAC	60
AAAGAAGGGG CTTACCACAA GCTTATTTCT CGC ATG TGT TTG GTC AAA GAC AAG	114
Met Cys Leu Val Lys Asp Lys	
1 5	
CTC AAA GAC ATT ATC AGC GTC AAA AGC GCG CTT TCT TTT TCG TTA AAA	162
Leu Lys Asp Ile Ile Ser Val Lys Ser Ala Leu Ser Phe Ser Leu Lys	
10 15 20	
GGG GAT TTT GAC TGC CCT TTA GAA GAA AAC TCG CTC TTT AAA GCC CTC	210
Gly Asp Phe Asp Cys Pro Leu Glu Glu Asn Ser Leu Phe Lys Ala Leu	
25 30 35	
CAA ATT TTA AAG AAT TTT TTA AAA TCA AAA AAT TTC TCT CAT TCT GTC	258
Gln Ile Leu Lys Asn Phe Leu Lys Ser Lys Asn Phe Ser His Ser Val	
40 45 50 55	
ATC AAA TCC CTA GAC ACC CTA GCG ATT GAA GTG GAA AAA AAC ATC CCC	306
Ile Lys Ser Leu Asp Thr Leu Ala Ile Glu Val Glu Lys Asn Ile Pro	
60 65 70	
ACT CAA GCC GGA TTA GGC GGT GGG AGC ACT GAT GCT GGG GGG CTA TTG	354
Thr Gln Ala Gly Leu Gly Gly Gly Ser Thr Asp Ala Gly Gly Leu Leu	
75 80 85	
TAT CAT TTA AAT CAG ATT TTT GAC TGG CGT TTG AGT TTA GAA GAG CTT	402
Tyr His Leu Asn Gln Ile Phe Asp Trp Arg Leu Ser Leu Glu Glu Leu	
90 95 100	

ACC GAT AAA GGC TCC TGG ACT TTC AAC TTT AAC AGA TAAATCAGGC AAATAT 1066
 Thr Asp Lys Gly Ser Trp Thr Phe Asn Phe Asn Arg
 330 335

GGACAATAGC ACAGACAGAG CAAAAATCCT TATAGAAGAG CTAAAAAT 1114

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

Met	Phe	Phe	Lys	Thr	Tyr	Gln	Lys	Leu	Leu	Gly	Ala	Ser	Cys	Leu	Thr	1	5	10	15
Leu	Tyr	Leu	Ala	Gly	Cys	Gly	Ser	Asp	Ser	Ser	Glu	Pro	Leu	Val	Gly	20	25	30	
Ile	Glu	Lys	Asn	Ser	Phe	Asn	Ser	Thr	Val	Lys	Ile	Ile	Ser	Lys	Thr	35	40	45	
Asp	Asn	Ile	Glu	Ile	Gln	Asp	Leu	Lys	Leu	Asn	Arg	Gly	Asn	Cys	Glu	50	55	60	
His	Asp	Gln	Asn	Phe	Leu	Val	Lys	Leu	Ile	Gln	Glu	Thr	Ala	Asn	Thr	65	70	75	80
Tyr	Leu	Phe	Ala	Ser	Glu	Lys	Glu	Lys	Ala	Ile	Lys	Asn	His	Gln	Ala	85	90	95	
Lys	Ile	Ala	Arg	Leu	Gln	Lys	Asp	Leu	Glu	Glu	Leu	Thr	Gln	His	Val	100	105	110	
Gln	Gln	Ser	Asn	Asn	Leu	Asp	Lys	Leu	Leu	Glu	Asn	Gly	Gly	Leu	Phe	115	120	125	
Val	Ser	Gly	His	Asp	Tyr	Lys	Tyr	Thr	Lys	Asp	Asp	Asn	Pro	Ile	Tyr	130	135	140	
Val	Val	Lys	Arg	Met	Leu	Asp	Asn	Leu	Asp	Ser	Tyr	Lys	Tyr	Glu	Ser	145	150	155	160
Asp	Asp	Val	Leu	Asp	Val	Pro	Tyr	Glu	Lys	Leu	Leu	Glu	Ile	Ser	Ile	165	170	175	
Ala	Ile	Glu	Asp	Thr	Lys	Asn	Pro	Lys	Asp	Tyr	Pro	Tyr	Ile	Asn	Leu	180	185	190	
Lys	Glu	Leu	Lys	Lys	Leu	Ile	Asp	Ser	Ile	Ile	Asp	Asp	His	Gly	Tyr	195	200	205	
Met	Ala	Asp	Gly	Phe	Leu	Asn	Glu	Tyr	Ser	Asn	Arg	Val	Ser	Lys	Lys	210	215	220	
Gly	Leu	Gln	Ile	Leu	Ala	Lys	Leu	Lys	Ser	Met	Trp	Pro	Ser	Val	Gly	225	230	235	240
Lys	Phe	Tyr	Phe	Ala	Ser	Leu	Lys	Glu	Ala	Ile	Pro	Arg	His	Ala	Lys	245	250	255	
Glu	Val	Thr	Asp	Lys	Met	Ile	Ser	Ser	Glu	Glu	Lys	Ser	Ile	Lys	Ala	260	265	270	
Asn	Gln	Val	Lys	Leu	Thr	Glu	Ala	Lys	Gln	Asp	Ile	Asp	Lys	Met	Glu	275	280	285	
Lys	Ile	Ile	Lys	Asp	Leu	Glu	Ser	Lys	Lys	Asn	Thr	Leu	Ser	Val	Tyr				

AAA	GAT	TTA	GAA	GAA	CTC	ACA	CAG	CAT	GTG	CAA	CAA	TCC	AAT	AAT	CTT	390
Lys	Asp	Leu	Glu	Glu	Leu	Thr	Gln	His	Val	Gln	Gln	Ser	Asn	Asn	Leu	
		105					110					115				
GAT	AAA	TTG	TTA	GAA	AAT	GGA	GGA	CTA	TTC	GTT	AGT	GGC	CAT	GAT	TAT	438
Asp	Lys	Leu	Leu	Glu	Asn	Gly	Gly	Leu	Phe	Val	Ser	Gly	His	Asp	Tyr	
		120				125					130					
AAA	TAT	ACA	AAA	GAT	GAT	AAC	CCA	ATA	TAT	GTT	GTT	AAG	AGG	ATG	CTT	486
Lys	Tyr	Thr	Lys	Asp	Asp	Asn	Pro	Ile	Tyr	Val	Val	Lys	Arg	Met	Leu	
135					140					145					150	
GAT	AAC	CTT	GAT	AGC	TAT	AAA	TAT	GAA	TCA	GAC	GAC	GTG	CTA	GAC	GTG	534
Asp	Asn	Leu	Asp	Ser	Tyr	Lys	Tyr	Glu	Ser	Asp	Asp	Val	Leu	Asp	Val	
				155				160						165		
CCA	TAT	GAG	AAG	CTA	TTG	GAA	ATA	AGC	ATT	GCT	ATT	GAA	GAC	ACT	AAA	582
Pro	Tyr	Glu	Lys	Leu	Leu	Glu	Ile	Ser	Ile	Ala	Ile	Glu	Asp	Thr	Lys	
		170					175						180			
AAC	CCC	AAA	GAC	TAC	CCT	TAT	ATC	AAC	CTT	AAA	GAA	CTC	AAA	AAA	TTA	630
Asn	Pro	Lys	Asp	Tyr	Pro	Tyr	Ile	Asn	Leu	Lys	Glu	Leu	Lys	Lys	Leu	
		185					190					195				
ATA	GAT	AGT	ATT	ATT	GAT	GAT	CAT	GGT	TAT	ATG	GCC	GAT	GGC	TTT	TTG	678
Ile	Asp	Ser	Ile	Ile	Asp	Asp	His	Gly	Tyr	Met	Ala	Asp	Gly	Phe	Leu	
	200					205					210					
AAT	GAA	TAT	TCT	AAT	AGG	GTA	TCA	AAA	AAA	GGT	CTC	CAA	ATC	CTT	GCT	726
Asn	Glu	Tyr	Ser	Asn	Arg	Val	Ser	Lys	Lys	Gly	Leu	Gln	Ile	Leu	Ala	
215					220					225					230	
AAA	CTA	AAA	TCC	ATG	TGG	CCT	AGC	GTA	GGG	AAA	TTT	TAT	TTC	GCC	TCT	774
Lys	Leu	Lys	Ser	Met	Trp	Pro	Ser	Val	Gly	Lys	Phe	Tyr	Phe	Ala	Ser	
				235				240						245		
TTG	AAA	GAG	GCT	ATC	CCA	AGG	CAT	GCC	AAA	GAA	GTT	ACT	GAC	AAG	ATG	822
Leu	Lys	Glu	Ala	Ile	Pro	Arg	His	Ala	Lys	Glu	Val	Thr	Asp	Lys	Met	
		250					255						260			
ATT	AGC	TCT	GAA	GAA	AAA	TCT	ATC	AAA	GCC	AAT	CAA	GTC	AAA	CTC	ACT	870
Ile	Ser	Ser	Glu	Glu	Lys	Ser	Ile	Lys	Ala	Asn	Gln	Val	Lys	Leu	Thr	
		265					270					275				
GAA	GCG	AAG	CAA	GAT	ATT	GAC	AAA	ATG	GAA	AAA	ATC	ATT	AAA	GAT	TTA	918
Glu	Ala	Lys	Gln	Asp	Ile	Asp	Lys	Met	Glu	Lys	Ile	Ile	Lys	Asp	Leu	
	280					285					290					
GAA	AGC	AAG	AAA	AAC	ACC	TTA	TCA	GTG	TAT	TTA	AAA	TTT	GGA	GAA	AGT	966
Glu	Ser	Lys	Lys	Asn	Thr	Leu	Ser	Val	Tyr	Leu	Lys	Phe	Gly	Glu	Ser	
295					300					305					310	
TTC	ACA	GCG	CAT	TAT	AAG	TGT	CAA	AAT	CTC	ATA	GAA	GTT	GGA	GTC	AAA	1014
Phe	Thr	Ala	His	Tyr	Lys	Cys	Gln	Asn	Leu	Ile	Glu	Val	Gly	Val	Lys	
				315					320					325		

```

Thr Ile Lys Gln Ala Gln Asp Arg Leu Met Glu Leu Ser Lys Val Lys
                245                      250                      255
Lys Ala Tyr Trp Leu Glu Lys Ser Pro Met Glu Arg Phe Ile Glu Lys
                260                      265                      270
Ala Thr Gln Ser Ala Thr Asn Ile Ile Thr Gln Ala Phe Gly Tyr Gln
                275                      280                      285
Leu Leu Met Arg
                290

```

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...1050
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

```

CGAGCTATCA CAACAAATCA ATTTGTAGGA ACAAGC ATG TTT TTT AAA ACT TAT      54
                               Met Phe Phe Lys Thr Tyr
                               1                      5

CAA AAA TTA TTG GGT GCG AGC TGT TTG ACG TTG TAT TTA GCG GGC TGT      102
Gln Lys Leu Leu Gly Ala Ser Cys Leu Thr Leu Tyr Leu Ala Gly Cys
                10                      15                      20

GGG AGT GAT AGT AGC GAG CCA TTG GTG GGA ATT GAA AAA AAT AGC TTC      150
Gly Ser Asp Ser Ser Glu Pro Leu Val Gly Ile Glu Lys Asn Ser Phe
                25                      30                      35

AAT TCT ACC GTG AAA ATC ATT TCT AAA ACC GAC AAC ATA GAA ATC CAA      198
Asn Ser Thr Val Lys Ile Ile Ser Lys Thr Asp Asn Ile Glu Ile Gln
                40                      45                      50

GAC TTG AAG CTC AAT CGT GGC AAT TGT GAG CAT GAT CAA AAT TTC TTG      246
Asp Leu Lys Leu Asn Arg Gly Asn Cys Glu His Asp Gln Asn Phe Leu
                55                      60                      65                      70

GTA AAG TTA ATC CAA GAA ACA GCC AAT ACA TAC CTG TTT GCA TCA GAA      294
Val Lys Leu Ile Gln Glu Thr Ala Asn Thr Tyr Leu Phe Ala Ser Glu
                75                      80                      85

AAA GAA AAA GCG ATC AAA AAC CAC CAA GCA AAA ATC GCA AGA CTT CAA      342
Lys Glu Lys Ala Ile Lys Asn His Gln Ala Lys Ile Ala Arg Leu Gln
                90                      95                      100

```

Lys Lys Ala Tyr Trp Leu Glu Lys Ser Pro Met Glu Arg Phe Ile Glu
 260 265 270

AAA GCC ACG CAA TCA GCC ACA AAC ATC ATC ACA CAA GCC TTT GGC TAT 924
 Lys Ala Thr Gln Ser Ala Thr Asn Ile Ile Thr Gln Ala Phe Gly Tyr
 275 280 285

CAA TTA TTA ATG AGA TAAAGATGTT AGAATTTATT TTAAAAATTC AAGCTAGAGA C 980
 Gln Leu Leu Met Arg
 290

TCTAAAGGCT T 991

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

Met Trp Ser Phe Ile Gln Lys Ile Phe Lys Ala Leu Ile Ile Ala Pro
 1 5 10 15
 Leu Asp Phe Ile Thr Lys Tyr Phe Lys Ser Phe Val Leu Leu Ile
 20 25 30
 Val Leu Val Phe Phe Ser Ala Lys Glu Ser Ala Pro Ser Ala Pro Pro
 35 40 45
 Asn Leu Ala Lys Leu Tyr Leu Asn Gly Ala Ile Phe Ser Thr Glu Asp
 50 55 60
 Phe Asp Lys Glu Val Asp Lys Ile Leu Lys Thr Pro Ser Ile Lys Gly
 65 70 75 80
 Val Leu Leu Leu Ile Asp Ser Pro Gly Gly Ala Val Ser Ala Ser Val
 85 90 95
 Glu Leu Ser Glu Lys Ile Ala Asp Leu Lys Gln Lys Met Pro Val Leu
 100 105 110
 Ala Tyr Ala Arg Gly Val Met Ala Ser Gly Ser Tyr Tyr Ala Gly Met
 115 120 125
 Gln Ala Ser Glu Val Tyr Ala Ser Lys Ala Ser Leu Ile Gly Ser Ile
 130 135 140
 Gly Val Ile Phe Ser Gly Ala Asn Val Glu Asn Leu Leu Asn Lys Val
 145 150 155 160
 Gly Val Ala Thr Gln Gly Val His Ala Gly Glu Tyr Lys Glu Ile Gly
 165 170 175
 Thr Phe Thr Arg Ala Trp Lys Pro Asn Glu Lys Asp Phe Leu Gln Asn
 180 185 190
 Leu Val Asn Glu Gln Tyr Gln Met Phe Val Asn Asp Val Ala Lys Ala
 195 200 205
 Arg Lys Leu Asp Ala Lys Asp Tyr Lys Asp Phe Ala Glu Gly Lys Val
 210 215 220
 Phe Ser Ala Gln Lys Ala Leu Lys Leu Lys Leu Ile Asp Lys Ile Ser
 225 230 235 240

35						40						45						
CCT	AAT	CTC	GCT	AAA	CTC	TAT	TTA	AAT	GGG	GCG	ATT	TTT	AGC	ACC	GAG	252		
Pro	Asn	Leu	Ala	Lys	Leu	Tyr	Leu	Asn	Gly	Ala	Ile	Phe	Ser	Thr	Glu			
		50					55					60						
GAT	TTT	GAC	AAA	GAA	GTG	GAT	AAA	ATC	CTA	AAA	ACC	CCT	AGC	ATT	AAG	300		
Asp	Phe	Asp	Lys	Glu	Val	Asp	Lys	Ile	Leu	Lys	Thr	Pro	Ser	Ile	Lys			
	65					70					75							
GGC	GTT	TTG	CTT	TTG	ATT	GAC	TCT	CCT	GGT	GGG	GCG	GTG	TCA	GCG	AGC	348		
Gly	Val	Leu	Leu	Leu	Ile	Asp	Ser	Pro	Gly	Gly	Ala	Val	Ser	Ala	Ser			
80					85					90					95			
GTG	GAA	TTG	AGC	GAA	AAA	ATC	GCT	GAT	TTG	AAG	CAA	AAA	ATG	CCC	GTT	396		
Val	Glu	Leu	Ser	Glu	Lys	Ile	Ala	Asp	Leu	Lys	Gln	Lys	Met	Pro	Val			
				100					105					110				
TTA	GCG	TAT	GCT	AGG	GGG	GTT	ATG	GCG	AGC	GGG	AGC	TAT	TAT	GCG	GGC	444		
Leu	Ala	Tyr	Ala	Arg	Gly	Val	Met	Ala	Ser	Gly	Ser	Tyr	Tyr	Ala	Gly			
			115					120					125					
ATG	CAA	GCG	AGC	GAA	GTT	TAT	GCC	TCT	AAA	GCG	AGT	TTG	ATA	GGA	TCC	492		
Met	Gln	Ala	Ser	Glu	Val	Tyr	Ala	Ser	Lys	Ala	Ser	Leu	Ile	Gly	Ser			
		130					135					140						
ATT	GGG	GTG	ATT	TTT	TCA	GGT	GCG	AAT	GTG	GAA	AAT	TTG	CTC	AAT	AAA	540		
Ile	Gly	Val	Ile	Phe	Ser	Gly	Ala	Asn	Val	Glu	Asn	Leu	Leu	Asn	Lys			
	145					150					155							
GTC	GGC	GTA	GCC	ACT	CAA	GGC	GTG	CAT	GCG	GGC	GAA	TAC	AAA	GAA	ATA	588		
Val	Gly	Val	Ala	Thr	Gln	Gly	Val	His	Ala	Gly	Glu	Tyr	Lys	Glu	Ile			
160					165					170					175			
GGC	ACT	TTC	ACC	AGA	GCG	TGG	AAA	CCC	AAC	GAA	AAA	GAT	TTT	TTG	CAA	636		
Gly	Thr	Phe	Thr	Arg	Ala	Trp	Lys	Pro	Asn	Glu	Lys	Asp	Phe	Leu	Gln			
				180					185					190				
AAT	TTA	GTC	AAT	GAG	CAA	TAC	CAA	ATG	TTT	GTG	AAT	GAT	GTC	GCA	AAA	684		
Asn	Leu	Val	Asn	Glu	Gln	Tyr	Gln	Met	Phe	Val	Asn	Asp	Val	Ala	Lys			
			195					200					205					
GCT	AGG	AAA	TTA	GAC	GCT	AAG	GAT	TAT	AAG	GAT	TTT	GCT	GAA	GGG	AAG	732		
Ala	Arg	Lys	Leu	Asp	Ala	Lys	Asp	Tyr	Lys	Asp	Phe	Ala	Glu	Gly	Lys			
		210					215					220						
GTC	TTT	AGC	GCT	CAA	AAG	GCT	CTG	AAA	TTA	AAA	CTC	ATT	GAT	AAA	ATC	780		
Val	Phe	Ser	Ala	Gln	Lys	Ala	Leu	Lys	Leu	Lys	Leu	Ile	Asp	Lys	Ile			
	225					230					235							
AGC	ACG	ATT	AAG	CAA	GCG	CAA	GAT	CGC	TTA	ATG	GAA	TTG	AGT	AAG	GTT	828		
Ser	Thr	Ile	Lys	Gln	Ala	Gln	Asp	Arg	Leu	Met	Glu	Leu	Ser	Lys</				


```

Leu Ser Leu Lys Ile Gln Lys Glu Ala Cys Pro Ile Asn Thr Ala Pro
145                      150                      155                      160
Thr Thr Ser Thr Thr Leu Thr Leu Ala Leu Gly Asp Val Leu Met Ala
                      165                      170                      175
Cys Leu Met Arg Ala Lys Asn Phe Ser Gln Glu Asp Phe Ala Ser Phe
                      180                      185                      190
His Pro Gly Gly Leu Leu Gly Lys Lys Leu Phe Val Lys Val Lys Asp
                      195                      200                      205
Leu Leu Gln Thr Thr Asn Leu Pro Leu Ile Ala Pro Ser Thr Ser Phe
                      210                      215                      220
Lys Asp Ala Leu Ile Glu Met Ser Glu Lys Arg Leu Gly Ser Ala Ile
225                      230                      235                      240
Leu Val Asn Glu Ala Asn Glu Leu Val Gly Val Leu Ser Asp Gly Asp
                      245                      250                      255
Val Arg Arg Ala Leu Leu Lys Gly Val Ser Leu Lys Ser Glu Val Arg
                      260                      265                      270
His Phe Ala Thr Leu Lys Pro Lys Ser Phe Lys Asn Leu Asp Ala Leu
                      275                      280                      285
Leu Leu Glu Ala Leu Glu Phe Leu Glu Arg His Lys Ile Gln Leu Leu
                      290                      295                      300
Val Cys Val Asp Asp His Asn Lys Val Leu Gly Val Leu His Leu His
305                      310                      315                      320
Gln Leu Leu Glu Leu Gly Leu Lys Ala
                      325

```

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 64...939
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

```

TCCTTAAAC ATTTGAAGTA TAATACACTC TTATGGTCAA ATATTAAGTT TAGGAAAAGC      60
TGC ATG TGG AGT TTC ATT CAA AAA ATC TTT AAG GCT TTA ATC ATC GCA      108
    Met Trp Ser Phe Ile Gln Lys Ile Phe Lys Ala Leu Ile Ile Ala
      1              5              10              15

CCT TTA GAT TTT ATC ACG AAG TAT TTC AAG TCG TTT GTG CTG TTA CTC      156
Pro Leu Asp Phe Ile Thr Lys Tyr Phe Lys Ser Phe Val Leu Leu Leu
      20              25              30

ATT GTA TTA GTC TTT TTT AGC GCT AAA GAA AGC GCG CCA AGC GCC CCG      204
Ile Val Leu Val Phe Phe Ser Ala Lys Glu Ser Ala Pro Ser Ala Pro

```

```

TTA GTC AAT GAA GCT AAC GAG CTT GTG GGG GTG TTA AGC GAT GGC GAT      768
Leu Val Asn Glu Ala Asn Glu Leu Val Gly Val Leu Ser Asp Gly Asp
                245                250                255

GTC CGT AGG GCG TTA TTA AAA GGG GTG AGT TTA AAG AGC GAA GTG AGG      816
Val Arg Arg Ala Leu Leu Lys Gly Val Ser Leu Lys Ser Glu Val Arg
                260                265                270

CAT TTT GCC ACT TTA AAA CCT AAA AGC TTT AAG AAT TTA GAC GCT CTT      864
His Phe Ala Thr Leu Lys Pro Lys Ser Phe Lys Asn Leu Asp Ala Leu
                275                280                285

CTT TTA GAA GCG TTG GAA TTT TTA GAG CGC CAT AAG ATC CAG CTT TTA      912
Leu Leu Glu Ala Leu Glu Phe Leu Glu Arg His Lys Ile Gln Leu Leu
                290                295                300

GTG TGC GTA GAT GAT CAT AAT AAG GTT TTA GGG GTC TTG CAC TTG CAC      960
Val Cys Val Asp Asp His Asn Lys Val Leu Gly Val Leu His Leu His
305                310                315                320

CAA CTT TTA GAA TTA GGG CTT AAA GCA TGA                                990
Gln Leu Leu Glu Leu Gly Leu Lys Ala
                325

```

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

```

Met Pro Ile Leu Phe Asp Cys Asn Ala Ile Ala Ser Gln Val Leu Lys
 1          5          10          15
Asp Glu Ala Ser Ala Leu Leu Glu Ser Val Gly Gln Phe Gln Lys Pro
          20          25          30
Asn Asp Leu Glu Ala Ile Val Lys Leu Ile Leu Lys Ser Gln Glu Asn
          35          40          45
Gly Gly Lys Leu Val Ile Val Gly Val Gly Lys Ser Ala Leu Val Ala
          50          55          60
Gln Lys Ile Val Ala Ser Met Leu Ser Thr Gly Asn Arg Ser Ala Phe
          65          70          75          80
Leu His Pro Thr Glu Ala Met His Gly Asp Leu Gly Met Val Glu Lys
          85          90          95
Asn Asp Val Val Leu Met Ile Ser Tyr Gly Gly Glu Ser Leu Glu Leu
          100         105         110
Leu Asn Leu Val Ser His Leu Lys Arg Leu Ser His Lys Ile Ile Thr
          115         120         125
Phe Thr Lys Ser Pro Asn Ser Ser Leu Ser Lys Leu Gly Asp Tyr Tyr
          130         135         140

```

GAT GAA GCG AGC GCG CTT TTA GAA AGC GTT GGA CAA TTC CAA AAA CCC	96
Asp Glu Ala Ser Ala Leu Leu Glu Ser Val Gly Gln Phe Gln Lys Pro	
20 25 30	
AAC GAT TTA GAA GCG ATT GTC AAA CTC ATT TTA AAA AGC CAA GAA AAT	144
Asn Asp Leu Glu Ala Ile Val Lys Leu Ile Leu Lys Ser Gln Glu Asn	
35 40 45	
GGG GGT AAG CTT GTG ATA GTG GGT GTG GGT AAG AGC GCT TTA GTG GCG	192
Gly Gly Lys Leu Val Ile Val Gly Val Gly Lys Ser Ala Leu Val Ala	
50 55 60	
CAA AAA ATC GTT GCT TCC ATG CTA AGC ACC GGT AAC AGG AGC GCG TTT	240
Gln Lys Ile Val Ala Ser Met Leu Ser Thr Gly Asn Arg Ser Ala Phe	
65 70 75 80	
TTA CAC CCC ACA GAA GCC ATG CAT GGG GAT TTG GGC ATG GTG GAA AAA	288
Leu His Pro Thr Glu Ala Met His Gly Asp Leu Gly Met Val Glu Lys	
85 90 95	
AAC GAT GTG GTT TTA ATG ATT AGC TAT GGG GGC GAG TCT TTA GAA TTA	336
Asn Asp Val Val Leu Met Ile Ser Tyr Gly Gly Glu Ser Leu Glu Leu	
100 105 110	
TTG AAT CTG GTG AGC CAT TTA AAA CGC TTG AGC CAT AAA ATC ATC ACT	384
Leu Asn Leu Val Ser His Leu Lys Arg Leu Ser His Lys Ile Ile Thr	
115 120 125	
TTC ACT AAA AGC CCT AAT AGC TCG CTC TCT AAA CTC GGC GAT TAT TAT	432
Phe Thr Lys Ser Pro Asn Ser Ser Leu Ser Lys Leu Gly Asp Tyr Tyr	
130 135 140	
TTG AGC TTG AAA ATT CAA AAA GAA GCT TGC CCG ATT AAC ACC GCT CCA	480
Leu Ser Leu Lys Ile Gln Lys Glu Ala Cys Pro Ile Asn Thr Ala Pro	
145 150 155 160	
ACG ACT TCT ACC ACC CTA ACT CTA GCG TTA GGC GAT GTT TTA ATG GCA	528
Thr Thr Ser Thr Thr Leu Thr Leu Ala Leu Gly Asp Val Leu Met Ala	
165 170 175	
TGC TTG ATG CGA GCG AAA AAC TTT AGC CAA GAA GAT TTT GCC TCC TTT	576
Cys Leu Met Arg Ala Lys Asn Phe Ser Gln Glu Asp Phe Ala Ser Phe	
180 185 190	
CAT CCG GGC GGG CTT TTA GGC AAA AAA CTT TTT GTC AAG GTT AAA GAT	624
His Pro Gly Gly Leu Leu Gly Lys Lys Leu Phe Val Lys Val Lys Asp	
195 200 205	
TTA CTG CAA ACC ACG AAC CTC CCC CTA ATC GCT CCT AGC ACA AGT TTT	672
Leu Leu Gln Thr Thr Asn Leu Pro Leu Ile Ala Pro Ser Thr Ser Phe	
210 215 220	
AAA GAC GCG CTC ATA GAA ATG AGT GAA AAA CGC TTA GGC AGC GCG ATT	720
Lys Asp Ala Leu Ile Glu Met Ser Glu Lys Arg Leu Gly Ser Ala Ile	
225 230 235 240	

```

Tyr Thr Val Cys Val Ser Cys Gln Ile Gly Cys Gln Val Gly Cys Ser
    115                      120                      125
Phe Cys Phe Thr Gln Lys Gly Gly Phe Val Arg Asn Leu Lys Ala Ser
    130                      135                      140
Glu Ile Ile Gln Gln Ala Leu Leu Ile Lys Glu Asp Asn Asn Leu Pro
    145                      150                      155                      160
Leu Glu Lys Ala Leu Asn Ile Val Phe Met Gly Met Gly Glu Pro Leu
    165                      170                      175
Asn Asn Leu Asp Glu Val Cys Lys Ala Ile Glu Ile Phe Asn Thr Gly
    180                      185                      190
Met Gln Ile Ser Pro Lys Arg Ile Thr Ile Ser Thr Ser Gly Val Ala
    195                      200                      205
Asp Lys Ile Pro Ile Leu Ala Gly Lys Asn Leu Gly Val Gln Leu Ala
    210                      215                      220
Ile Ser Leu His Ala Val Asp Asp Lys Thr Arg Ser Ser Leu Met Pro
    225                      230                      235                      240
Leu Asn Lys Lys Tyr Asn Ile Glu Cys Val Leu Asn Glu Val Arg Lys
    245                      250                      255
Trp Pro Leu Glu Gln Arg Lys Arg Val Met Phe Glu Tyr Leu Leu Ile
    260                      265                      270
Lys Asp Leu Asn Asp Ser Leu Asp Cys Ala Lys Lys Leu Leu Lys Leu
    275                      280                      285
Leu Asn Gly Ile Lys Ser Lys Val Asn Leu Ile Leu Phe Asn Pro His
    290                      295                      300
Glu Gly Ser Lys Phe Glu Arg Pro Ser Leu Glu Asn Ala Arg Met Phe
    305                      310                      315                      320
Ala Asp Phe Leu Asn Ser Lys Gly Leu Leu Cys Thr Ile Arg Glu Ser
    325                      330                      335
Lys Ala Leu Asp Ile Glu Ala Ala Cys Gly Gln Leu Arg Glu Lys Lys
    340                      345                      350
Leu Ser Gln Gln Ile
    355

```

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...987
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

```

ATG CCC ATT CTT TTT GAT TGT AAC GCT ATT GCT TCA CAA GTT TTA AAA
Met Pro Ile Leu Phe Asp Cys Asn Ala Ile Ala Ser Gln Val Leu Lys
  1      --          5              10              15

```

48

```

Leu Asn Glu Val Arg Lys Trp Pro Leu Glu Gln Arg Lys Arg Val Met
                255                      260                      265

TTT GAA TAC CTT TTG ATC AAA GAT TTG AAC GAT AGC CTA GAC TGC GCT      869
Phe Glu Tyr Leu Leu Ile Lys Asp Leu Asn Asp Ser Leu Asp Cys Ala
                270                      275                      280

AAA AAA CTT TTA AAA CTT TTA AAC GGC ATT AAA TCC AAA GTG AAT TTG      917
Lys Lys Leu Leu Lys Leu Leu Asn Gly Ile Lys Ser Lys Val Asn Leu
                285                      290                      295

ATC TTA TTC AAC CCG CAT GAA GGC TCT AAG TTT GAA CGC CCT AGC TTA      965
Ile Leu Phe Asn Pro His Glu Gly Ser Lys Phe Glu Arg Pro Ser Leu
                300                      305                      310

GAG AAC GCT AGA ATG TTT GCG GAT TTT TTA AAC TCT AAA GGC TTA TTA      1013
Glu Asn Ala Arg Met Phe Ala Asp Phe Leu Asn Ser Lys Gly Leu Leu
                315                      320                      325                      330

TGC ACC ATT AGA GAG TCT AAA GCC TTG GAT ATT GAA GCG GCT TGC GGG      1061
Cys Thr Ile Arg Glu Ser Lys Ala Leu Asp Ile Glu Ala Ala Cys Gly
                335                      340                      345

CAG TTG AGG GAG AAA AAA CTC TCT CAG CAA ATT TGAAACTTT TTTGTGGTGT      1114
Gln Leu Arg Glu Lys Lys Leu Ser Gln Ile
                350                      355

TTGTCTTTTT TCTAATGGGG GGTGTTGG      1142

```

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

```

Met Lys Ala Ser Ile Tyr Asp Phe Thr Leu Lys Glu Leu Ser Gln Leu
 1           5           10           15
Leu Lys Pro Ser Phe Arg Ala Lys Gln Leu Tyr Leu Trp Leu Tyr Ala
 20           25           30
Lys Tyr Lys Thr Ser Phe Lys Asp Met Gln Asn Asn Phe Ser Lys Asp
 35           40           45
Phe Ile Ala Tyr Leu Glu Arg Glu Phe Ala Leu Arg Thr Ile Glu Ile
 50           55           60
Thr His Val Arg Glu Ser Val Asp Gly Ser Lys Lys Tyr Leu Phe Lys
 65           70           75           80
Ser Leu Arg Asp Asn His Thr Phe Glu Ala Val Leu Leu Lys Met Lys
 85           90           95
Asp Lys Lys Ile Asp Ala Glu Thr Asn Ala Ile Leu Glu Arg Glu Lys
100          105          110

```

-1581-

TTG CTT TAAACTTGCT ATGGACGATT AGAAATCG
 Leu Leu
 55

232

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

Met	Ser	Leu	Gly	Ala	Val	Ile	Lys	Leu	Ile	Phe	Cys	Tyr	Lys	Leu	Glu
1				5					10					15	
Gly	Val	Ile	Leu	Asp	Leu	Lys	Arg	Ile	Asn	Phe	Lys	Ser	Tyr	Tyr	Pro
			20				25						30		
Asn	Asn	Lys	Asn	Ala	Leu	Phe	Ile	Asn	Asn	Lys	Lys	Ile	His	Tyr	Leu
		35					40						45		
Val	Pro	Gln	Arg	Phe	Ile	Leu	Leu								
	50						55								

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...1094
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

CTTTTAGAAT TAGGGCTTAA AGC ATG AAA GCT AGT ATT TAT GAT TTC ACT CTA	53
Met Lys Ala Ser Ile Tyr Asp Phe Thr Leu	
1 5 10	
AAG GAA TTG AGC CAG CTT TTA AAA CCA AGC TTT AGG GCT AAA CAG CTT	101
Lys Glu Leu Ser Gln Leu Leu Lys Pro Ser Phe Arg Ala Lys Gln Leu	
15 20 25	
TAT TTG TGG CTC TAT GCG AAG TAT AAA ACA AGC TTT AAG GAC ATG CAA	149
Tyr Leu Trp Leu Tyr Ala Lys Tyr Lys Thr Ser Phe Lys Asp Met Gln	

580					585					590					
Phe	Pro	Phe	Val	Ser	Pro	Phe	Gln	Phe	Ile	Leu	Asp	Ala	Arg	Tyr	Asn
595					600					605					
Trp	Arg	Lys	Thr	Thr	Ile	Gly	Ile	Ser	Ser	Tyr	Phe	Tyr	Ser	Arg	Ala
610					615					620					
Tyr	Ser	Gly	Ile	Ser	Asn	Ser	Ala	Ala	Gly	Gly	Tyr	Tyr	Gly	Met	Gln
625					630					635					
Tyr	Tyr	Ser	Gly	Gly	Asn	Asn	Tyr	Glu	Ser	Val	Leu	Asn	Ser	Gly	Tyr
645					650					655					
Gln	Cys	Glu	Ala	Trp	Cys	Met	Thr	Gln	His	Glu	Gly	Leu	Leu	Pro	Trp
660					665					670					
Tyr	Trp	Val	Trp	Asn	Ile	Gln	Val	Ser	Gln	Ile	Phe	Trp	Glu	Asn	Gly
675					680					685					
Arg	His	Arg	Val	Thr	Gly	Ser	Leu	Gln	Ile	Asn	Asn	Ile	Phe	Asn	Met
690					695					700					
Lys	Tyr	Tyr	Phe	Thr	Gly	Ile	Gly	Ser	Ser	Pro	Ala	Gly	Leu	Gln	Pro
705					710					715					
Ala	Pro	Gly	Arg	Ser	Val	Thr	Ala	Tyr	Leu	Asn	Tyr	Thr	Phe		
725					730										

(2) INFORMATION FOR SEO ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 37...204
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

CATTGGAGAT	TGTGCCATTC	TTTGATTTTA	TCTAAA	ATG	TCT	TTA	GGG	GCA	GTG		54					
				Met	Ser	Leu	Gly	Ala	Val							
				1				5								
ATT	AAG	CTT	ATT	TTT	TGT	TAT	AAA	TTA	GAG	GGG	GTA	ATA	TTA	GAT	TTA	102
Ile	Lys	Leu	Ile	Phe	Cys	Tyr	Lys	Leu	Glu	Gly	Val	Ile	Leu	Asp	Leu	
			10					15					20			
AAG	CGC	ATC	AAT	TTC	AAA	TCC	TAT	TAT	CCC	AAT	AAT	AAA	AAT	GCA	TTA	150
Lys	Arg	Ile	Asn	Phe	Lys	Ser	Tyr	Tyr	Pro	Asn	Asn	Lys	Asn	Ala	Leu	
			25					30				35				
TTT	ATC	AAC	AAT	AAA	AAA	ATC	CAT	TAT	CTA	GTG	CCT	CAA	AGG	TTC	ATA	198
Phe	Ile	Asn	Asn	Lys	Lys	Ile	His	Tyr	Leu	Val	Pro	Gln	Arg	Phe	Ile	
			40			45				50						


```

Asn Trp Val Arg Gly Gln Gly Phe Arg Asp Asn Ser Pro Ser Asn Ile
145          150          155          160
Ser Asn Tyr Trp Leu Asp Gly Val Tyr Asp Ile Asn Glu Asn Asn Gly
          165          170          175
Ile Lys Ala Tyr Tyr Gln Tyr Tyr Asp Phe Ala Ile Ala Gln Pro Gly
          180          185          190
Ser Leu Ser Glu Gln Asp Tyr Lys Ile Asn Arg Phe Ala Asn Leu Arg
          195          200          205
Pro Leu Asn Gln Lys Gly Gly Arg Ser Gln Arg Phe Gly Ala Val Tyr
          210          215          220
Glu Asn Arg Phe Gly Asp Leu Asp Lys Val Gly Gly Thr Phe Ser Phe
225          230          235          240
Thr Tyr Tyr Gly Gln Leu Met Thr Arg Asp Phe Gln Val Ser Ser Ser
          245          250          255
Tyr Asn Ser Ala Asn Met Val Thr Cys Phe Ser Glu Ala Ala Cys Arg
          260          265          270
Ala Ala Gly Leu Pro Ala Gly Tyr Asn Leu Ala Val Pro Tyr Tyr Ala
          275          280          285
Thr Asn Tyr Asn Gly Trp Ala Glu Val Glu Asn Pro Val Arg Ser Ile
          290          295          300
Asn Asn Ala Phe Glu Pro Lys Val Asn Leu Ile Val Asn Thr Gly Lys
305          310          315          320
Val Lys Gln Thr Phe Ile Met Gly Leu Arg Phe Met Thr Thr Thr Phe
          325          330          335
Leu Gln Arg Gln Tyr Leu Asn Thr Asn Glu Cys Ala Thr Lys Thr Ser
          340          345          350
Gly Glu Gly Ala Gly Phe Leu Cys Glu Gly Ala Asn Val Met Ser Gly
          355          360          365
Trp Lys Pro His Ile Lys His Gly Val Tyr Arg Asn Trp Asn Asn Trp
          370          375          380
Arg Asn Asn Tyr Thr Ala Val Tyr Leu Ser Asp Arg Ile Glu Ala Trp
385          390          395          400
Asp Gly Arg Phe Phe Ile Val Pro Gly Leu Arg Tyr Ala Phe Val Gln
          405          410          415
Tyr Asn Asn Glu Asn Ala Ser Asn Trp Met Gln Ile Pro Glu Lys Asp
          420          425          430
Leu Arg Lys Ile Lys His Met Asn Asn Trp Met Pro Ser Thr Asn Ile
          435          440          445
Gly Phe Ile Pro Val Gln Gly Asp His Asn Val Leu Thr Tyr Phe Asn
          450          455          460
Tyr Gln Arg Ser Phe Val Pro Pro Gln Leu Asp Val Leu Ser Tyr Gly
465          470          475          480
Gly Ala Glu Tyr Phe Thr Gln His Phe Asp Thr Val Glu Ala Gly Ala
          485          490          495
Arg Tyr Thr Tyr Lys Asp Lys Phe Ser Phe Asn Ala Asp Tyr Phe Arg
          500          505          510
Ile Trp Ala Arg Asp Phe Ala Thr Gly Gln Tyr Ser Val Tyr Thr Ser
          515          520          525
Gly Pro Met Lys Gly Asn Val Arg Pro Ile Asn Gly Tyr Ser Gln Gly
          530          535          540
Val Glu Leu Glu Leu Tyr Tyr Arg Pro Ile Arg Gly Leu Gln Phe His
545          550          555          560
Ala Ala Phe Asn Tyr Ile Asp Thr Arg Val Thr Ser His Gly Pro Leu
          565          570          575
Thr Asp Leu Asn Gly Asp Val Leu Lys Gly Thr Ser Tyr Asn Lys His

```

```

GTT CTT AAT AGC GGT TAT CAA TGC GAA GCT TGG TGT ATG ACC CAA CAT      2079
Val Leu Asn Ser Gly Tyr Gln Cys Glu Ala Trp Cys Met Thr Gln His
                      655                      660                      665

GAA GGG CTC TTG CCT TGG TAT TGG GTG TGG AAT ATC CAA GTG AGC CAA      2127
Glu Gly Leu Leu Pro Trp Tyr Trp Val Trp Asn Ile Gln Val Ser Gln
                      670                      675                      680

ATT TTC TGG GAA AAC GGG AGA CAC AGA GTT ACA GGA AGC TTG CAA ATC      2175
Ile Phe Trp Glu Asn Gly Arg His Arg Val Thr Gly Ser Leu Gln Ile
                      685                      690                      695

AAT AAT ATC TTC AAC ATG AAG TAT TAT TTT ACA GGG ATT GGC TCT AGC      2223
Asn Asn Ile Phe Asn Met Lys Tyr Tyr Phe Thr Gly Ile Gly Ser Ser
                      700                      705                      710

CCT GCA GGC TTG CAA CCT GCG CCT GGA AGA TCG GTT ACA GCG TAT TTG      2271
Pro Ala Gly Leu Gln Pro Ala Pro Gly Arg Ser Val Thr Ala Tyr Leu
715                      720                      725                      730

AAC TAC ACT TTC TAAAGGCTTT AAAAAGGAGG GGGTTATTGC GCGATGATGA GCCG      2327
Asn Tyr Thr Phe

```

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

```

Met Pro Thr Ile Gln Ile Arg Gly Phe Gly Ala Gly Gly Ser Gly His
 1           5           10           15
Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val Tyr Met Ala
          20          25          30
Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr Phe Gln Ala
          35          40          45
Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val Gln Tyr Gly
          50          55          60
Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys Pro Ile Pro
          65          70          75          80
Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Ile Thr Tyr Trp Ala Lys
          85          90          95
Ala Arg Asn Ala Gly Phe Ala Ala Pro Pro Asp Lys Thr Gly Asp Pro
          100         105         110
Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn Thr Tyr Val
          115         120         125
Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln Ala Gln Ala
          130         135         140

```

CAA ATC CCT GAG AAG GAT TTA AGA AAA ATC AAG CAC ATG AAC AAT TGG	1407
Gln Ile Pro Glu Lys Asp Leu Arg Lys Ile Lys His Met Asn Asn Trp	
430 435 440	
ATG CCC TCA ACC AAC ATT GGC TTT ATC CCC GTG CAA GGC GAT CAC AAT	1455
Met Pro Ser Thr Asn Ile Gly Phe Ile Pro Val Gln Gly Asp His Asn	
445 450 455	
GTG CTT ACC TAC TTT AAC TAC CAA CGC TCT TTC GTC CCG CCT CAA TTA	1503
Val Leu Thr Tyr Phe Asn Tyr Gln Arg Ser Phe Val Pro Pro Gln Leu	
460 465 470	
GAC GTT TTG AGC TAT GGA GGA GCG GAG TAT TTT ACC CAG CAC TTT GAC	1551
Asp Val Leu Ser Tyr Gly Gly Ala Glu Tyr Phe Thr Gln His Phe Asp	
475 480 485 490	
ACG GTG GAA GCA GGA GCG CGC TAC ACC TAT AAG GAT AAA TTC AGC TTC	1599
Thr Val Glu Ala Gly Ala Arg Tyr Thr Tyr Lys Asp Lys Phe Ser Phe	
495 500 505	
AAT GCG GAC TAC TTC AGG ATT TGG GCG CGC GAT TTT GCC ACC GGG CAG	1647
Asn Ala Asp Tyr Phe Arg Ile Trp Ala Arg Asp Phe Ala Thr Gly Gln	
510 515 520	
TAT TCA GTC TAT ACA AGC GGT CCC ATG AAG GGT AAT GTG CGC CCC ATT	1695
Tyr Ser Val Tyr Thr Ser Gly Pro Met Lys Gly Asn Val Arg Pro Ile	
525 530 535	
AAT GGC TAT TCT CAA GGC GTG GAG CTG GAA TTG TAT TAC AGG CCT ATT	1743
Asn Gly Tyr Ser Gln Gly Val Glu Leu Glu Leu Tyr Tyr Arg Pro Ile	
540 545 550	
AGA GGG TTG CAA TTC CAT GCC GCT TTC AAC TAC ATT GAC ACT CGT GTA	1791
Arg Gly Leu Gln Phe His Ala Ala Phe Asn Tyr Ile Asp Thr Arg Val	
555 560 565 570	
ACC AGC CAT GGC CCT TTA ACC GAC TTG AAC GGG GAT GTG CTA AAA GGG	1839
Thr Ser His Gly Pro Leu Thr Asp Leu Asn Gly Asp Val Leu Lys Gly	
575 580 585	
ACT AGC TAT AAC AAG CAT TTC CCT TTT GTA AGC CCT TTC CAA TTC ATT	1887
Thr Ser Tyr Asn Lys His Phe Pro Phe Val Ser Pro Phe Gln Phe Ile	
590 595 600	
CTT GAC GCT CGT TAC AAT TGG CGT AAA ACC ACC ATC GGT ATT TCT AGC	1935
Leu Asp Ala Arg Tyr Asn Trp Arg Lys Thr Thr Ile Gly Ile Ser Ser	
605 610 615	
TAT TTT TAC AGC CGT GCT TAT AGC GGG ATT AGC AAC AGT GCA GCA GGA	1983
Tyr Phe Tyr Ser Arg Ala Tyr Ser Gly Ile Ser Asn Ser Ala Ala Gly	
620 625 630	
GGC TAT TAT GGG ATG CAA TAT TAT AGT GGG GGG AAC AAC TAT GAA AGC	2031
Gly Tyr Tyr Gly Met Gln Tyr Tyr Ser Gly Gly Asn Asn Tyr Glu Ser	
635 640 645 650	

CGC TTC GCT AAT TTG CGC CCC TTA AAC CAA AAA GGC GGG CGT TCA CAA	735
Arg Phe Ala Asn Leu Arg Pro Leu Asn Gln Lys Gly Gly Arg Ser Gln	
205 210 215	
CGC TTT GGG GCT GTG TAT GAA AAC CGC TTC GGG GAT TTA GAC AAA GTG	783
Arg Phe Gly Ala Val Tyr Glu Asn Arg Phe Gly Asp Leu Asp Lys Val	
220 225 230	
GGC GGG ACT TTT AGC TTC ACT TAC TAT GGG CAG TTG ATG ACT AGG GAT	831
Gly Gly Thr Phe Ser Phe Thr Tyr Tyr Gly Gln Leu Met Thr Arg Asp	
235 240 245 250	
TTT CAA GTG AGC TCT AGC TAC AAT AGC GCT AAC ATG GTT ACT TGT TTT	879
Phe Gln Val Ser Ser Ser Tyr Asn Ser Ala Asn Met Val Thr Cys Phe	
255 260 265	
AGC GAA GCG GCA TGC AGG GCG GCA GGA CTT CCG GCA GGG TAT AAC TTG	927
Ser Glu Ala Ala Cys Arg Ala Ala Gly Leu Pro Ala Gly Tyr Asn Leu	
270 275 280	
GCT GTG CCT TAT TAT GCC ACT AAC TAC AAT GGC TGG GCA GAA GTA GAA	975
Ala Val Pro Tyr Tyr Ala Thr Asn Tyr Asn Gly Trp Ala Glu Val Glu	
285 290 295	
AAC CCT GTG CGC TCC ATT AAC AAC GCT TTT GAG CCT AAA GTG AAT TTG	1023
Asn Pro Val Arg Ser Ile Asn Asn Ala Phe Glu Pro Lys Val Asn Leu	
300 305 310	
ATC GTC AAT ACC GGG AAA GTC AAG CAA ACC TTT ATC ATG GGC TTG CGT	1071
Ile Val Asn Thr Gly Lys Val Lys Gln Thr Phe Ile Met Gly Leu Arg	
315 320 325 330	
TTC ATG ACC ACC ACT TTT TTA CAG CGC CAA TAC TTA AAC ACC AAT GAA	1119
Phe Met Thr Thr Thr Phe Leu Gln Arg Gln Tyr Leu Asn Thr Asn Glu	
335 340 345	
TGC GCC ACC AAA ACG AGC GGT GAG GGG GCA GGA TTC TTG TGT GAG GGC	1167
Cys Ala Thr Lys Thr Ser Gly Glu Gly Ala Gly Phe Leu Cys Glu Gly	
350 355 360	
GCT AAT GTG ATG AGC GGT TGG AAA CCT CAC ATC AAG CAT GGC GTT TAT	1215
Ala Asn Val Met Ser Gly Trp Lys Pro His Ile Lys His Gly Val Tyr	
365 370 375	
AGA AAC TGG AAT AAC TGG CGT AAC AAT TAC ACA GCG GTT TAT TTG AGC	1263
Arg Asn Trp Asn Asn Trp Arg Asn Asn Tyr Thr Ala Val Tyr Leu Ser	
380 385 390	
GAT CGC ATT GAA GCT TGG GAT GGG CGC TTT TTC ATC GTG CCT GGT TTG	1311
Asp Arg Ile Glu Ala Trp Asp Gly Arg Phe Phe Ile Val Pro Gly Leu	
395 400 405 410	
CGC TAC GCT TTT GTG CAA TAC AAC AAC GAA AAT GCG TCT AAC TGG ATG	1359
Arg Tyr Ala Phe Val Gln Tyr Asn Asn Glu Asn Ala Ser Asn Trp Met	
415 420 425	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

CAACAAGCTA ACCAAAGCAT TGAAGAAGCT TTACAGAATG TCCCGGGTCT GCAAATTAGG	60
AATGCGACAG GTGTAGGGGC T ATG CCT ACT ATC CAA ATC CGT GGC TTT GGA	111
Met Pro Thr Ile Gln Ile Arg Gly Phe Gly	
1 5 10	
GCT GGG GGT TCA GGG CAT AGC GAT GCG ACG CTG ATG TTA GTC AAT GGT	159
Ala Gly Gly Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly	
15 20 25	
ATT CCT GTT TAT ATG GCC CCC TAC GCT CAC ATT GAG CTA GAC ATT TTC	207
Ile Pro Val Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe	
30 35 40	
CCC GTT ACC TTT CAA GCC ATT GAT CGC ATT GAT GTG ATC AAG GGT GGA	255
Pro Val Thr Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly	
45 50 55	
GGC AGC GTG CAA TAC GGG CCT AAC ACT TAT GGG GGT ATT GTC AAT ATC	303
Gly Ser Val Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile	
60 65 70	
ATC ACT AAG CCT ATC CCT AAT CAA TGG GAA AAC CAA GCG GCT GAA AGG	351
Ile Thr Lys Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg	
75 80 85 90	
ATC ACT TAT TGG GCT AAG GCT AGA AAC GCT GGG TTT GCC GCT CCT CCT	399
Ile Thr Tyr Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Pro	
95 100 105	
GAT AAA ACC GGC GAT CCT TCT TTC ATC AAG TCT TTA GGC AAC AAC CTC	447
Asp Lys Thr Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu	
110 115 120	
CTC TAT AAC ACT TAT GTG AGG AGT GGA GGG ATG ATC AAT AAG CAT GTG	495
Leu Tyr Asn Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val	
125 130 135	
GGT ATC CAA GCG CAA GCT AAC TGG GTT AGA GGA CAA GGC TTT AGG GAC	543
Gly Ile Gln Ala Gln Ala Asn Trp Val Arg Gly Gln Gly Phe Arg Asp	
140 145 150	
AAT AGC CCC TCT AAC ATT TCA AAC TAT TGG CTA GAT GGA GTC TAT GAC	591
Asn Ser Pro Ser Asn Ile Ser Asn Tyr Trp Leu Asp Gly Val Tyr Asp	
155 160 165 170	
ATC AAT GAA AAC AAT GGG ATT AAA GCC TAT TAC CAA TAC TAC GAT TTT	639
Ile Asn Glu Asn Asn Gly Ile Lys Ala Tyr Tyr Gln Tyr Tyr Asp Phe	
175 180 185	
GCT ATC GCT CAA CCA GGA TCA CTC AGC GAG CAA GAT TAC AAA ATA AAC	687
Ala Ile Ala Gln Pro Gly Ser Leu Ser Glu Gln Asp Tyr Lys Ile Asn	
190 195 200	

155

160

165

AAAAATTCAA ACTCTAAGGA TCTATCTTTT CGTTAG

572

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

```

Met Ser Glu Pro Leu Glu Thr Leu Asp Lys Asp Lys Gln Ala Met Ser
 1           5           10           15
Glu Ala Ile Lys Lys Asp Ile Glu Lys Asp Lys Glu Asn Leu Ala Arg
 20           25           30
Val Lys Ala Asp Lys Lys Val Lys Ala Asp Glu Ser Glu Lys Gly Tyr
 35           40           45
Glu Lys Asp Asp Asp Lys Lys Ala Glu Asn Leu Asp Lys Glu Ile Ala
 50           55           60
Lys Asp Lys Lys Ala Ser Pro Asn Asp Asn Glu Leu Tyr Glu Glu Asp Asp
 65           70           75           80
Arg Val Lys Arg Asp Lys Glu Arg Asp Asp Ala Leu Arg Asp Lys Glu
 85           90           95
Lys Ala Lys Asp Asp Ala Cys Met Val Arg Ala Asp Asp Asp Thr Ile
 100          105          110
Glu Asp Asp Glu Glu Tyr Gly Asp Asp Asp Lys Leu Arg Asp Glu Ile
 115          120          125
Leu Gly Val Met Glu Glu Leu Cys Asp Thr Leu Asn Asp Asn Leu Asn
 130          135          140
Phe Lys Lys Val Val Cys Met Gly Gly Lys Val Ser Ile Ala Phe Lys
 145          150          155          160
Phe Leu Ile Phe Cys Ser
          165

```

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 82...2283
- (D) OTHER INFORMATION:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 27...524

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

AAAAGGCTTT TTAAAAGGAC ACACCA ATG AGC GAA CCA TTA GAA ACA TTA GAC	53
Met Ser Glu Pro Leu Glu Thr Leu Asp	
1 5	
AAG GAT AAA CAA GCT ATG AGT GAA GCA ATT AAA AAA GAT ATT GAA AAA	101
Lys Asp Lys Gln Ala Met Ser Glu Ala Ile Lys Lys Asp Ile Glu Lys	
10 15 20 25	
GAC AAA GAA AAC CTC GCA CGA GTC AAA GCA GAC AAA AAA GTC AAA GCC	149
Asp Lys Glu Asn Leu Ala Arg Val Lys Ala Asp Lys Lys Val Lys Ala	
30 35 40	
GAT GAA AGT GAA AAA GGC TAC GAA AAA GAC GAT GAC AAA AAA GCC GAG	197
Asp Glu Ser Glu Lys Gly Tyr Glu Lys Asp Asp Asp Lys Lys Ala Glu	
45 50 55	
AAT CTT GAC AAA GAA ATC GCT AAA GAC AAA GCT AGC CCT AAC GAT AAT	245
Asn Leu Asp Lys Glu Ile Ala Lys Asp Lys Ala Ser Pro Asn Asp Asn	
60 65 70	
GAG CTT TAT GAA GAG GAC GAT AGA GTT AAA CGA GAC AAA GAA AGA GAC	293
Glu Leu Tyr Glu Glu Asp Asp Arg Val Lys Arg Asp Lys Glu Arg Asp	
75 80 85	
GAT GCC TTG CGT GAT AAA GAA AAA GCC AAA GAT GAC GCA TGC ATG GTA	341
Asp Ala Leu Arg Asp Lys Glu Lys Ala Lys Asp Asp Ala Cys Met Val	
90 95 100 105	
AGA GCG GAC GAT GAC ACC ATA GAG GAC GAT GAG GAA TAT GGT GAT GAT	389
Arg Ala Asp Asp Asp Thr Ile Glu Asp Asp Glu Glu Tyr Gly Asp Asp	
110 115 120	
GAT AAG TTA AGA GAC GAA ATA CTC GGT GTT ATG GAG GAG TTA TGC GAT	437
Asp Lys Leu Arg Asp Glu Ile Leu Gly Val Met Glu Glu Leu Cys Asp	
125 130 135	
ACC CTT AAT GAT AAC CTT AAC TTC AAA AAA GTC GTC TGT ATG GGC GGT	485
Thr Leu Asn Asp Asn Leu Asn Phe Lys Lys Val Val Cys Met Gly Gly	
140 145 150	
AAG GTT TCA ATT GCG TTC AAA TTT CTA ATT TTT TGC TCT TAATCTTTTA GA	536
Lys Val Ser Ile Ala Phe Lys Phe Leu Ile Phe Cys Ser	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

```

AGCTCACATT TTAGAAAAAT ATTTAAAGGG AGA ATG ATG CAA AAT AGC GTT AAA      54
                               Met Met Gln Asn Ser Val Lys
                               1           5

AAA TTA GAA TAT GAA GAG CGT TTC AAT GAC GCT CTT TTG AAA TTA CAA      102
Lys Leu Glu Tyr Glu Glu Arg Phe Asn Asp Ala Leu Leu Lys Leu Gln
    10           15           20

GCA TGC CAA GAA GAA AAG CAG GTA ACG AGT TGT TTG AAA TGC GAG CAG      150
Ala Cys Gln Glu Glu Lys Gln Val Thr Ser Cys Leu Lys Cys Glu Gln
    25           30           35

GTT TTG AAT TGC AAG ATC CGC AAC AGC TAT GTG GAT GCG GCT TAT GAG      198
Val Leu Asn Cys Lys Ile Arg Asn Ser Tyr Val Asp Ala Ala Tyr Glu
    40           45           50           55

AGC ATG AGT TTA GGC GAA CGG GGC GGG TTT GAT TTC AAT TAAATGGGAT TA      249
Ser Met Ser Leu Gly Glu Arg Gly Gly Phe Asp Phe Asn
           60           65

AAATGGCTAG TAATACTACC TT      271

```

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

```

Met Met Gln Asn Ser Val Lys Lys Leu Glu Tyr Glu Glu Arg Phe Asn
 1           5           10           15
Asp Ala Leu Leu Lys Leu Gln Ala Cys Gln Glu Glu Lys Gln Val Thr
    20           25           30
Ser Cys Leu Lys Cys Glu Gln Val Leu Asn Cys Lys Ile Arg Asn Ser
    35           40           45
Tyr Val Asp Ala Ala Tyr Glu Ser Met Ser Leu Gly Glu Arg Gly Gly
    50           55           60
Phe Asp Phe Asn
65

```

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

CCC AGC AAC CAG CAA ACA ACC ATA AGA GAT TAT CTT AAA CCC GGA TCT	159
Pro Ser Asn Gln Gln Thr Thr Ile Arg Asp Tyr Leu Lys Pro Gly Ser	
15 20 25	
ATT GTT GTG TTT GCC ATA ATT GTA ATA ATA ATT TCA TCT CAT TTC TCC	207
Ile Val Val Phe Ala Ile Ile Val Ile Ile Ile Ser Ser His Phe Ser	
30 35 40 45	
AAC GCC TAT AAA ACC CTT ATC GCT TCT AAT AAA AAA CCA GTT TTA AGC	255
Asn Ala Tyr Lys Thr Leu Ile Ala Ser Asn Lys Lys Pro Val Leu Ser	
50 55 60	
CAT TTA GAA ATT TGATTCTTA AACCTTTTTA TCAAAAATAC CGGTGTT	304
His Leu Glu Ile	
65	

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

Met Asp Tyr Arg Leu Phe His Met Asp Ser Met Asp Leu Pro Ser Asn	
1 5 10 15	
Gln Gln Thr Thr Ile Arg Asp Tyr Leu Lys Pro Gly Ser Ile Val Val	
20 25 30	
Phe Ala Ile Ile Val Ile Ile Ile Ser Ser His Phe Ser Asn Ala Tyr	
35 40 45	
Lys Thr Leu Ile Ala Ser Asn Lys Lys Pro Val Leu Ser His Leu Glu	
50 55 60	
Ile	
65	

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...237
- (D) OTHER INFORMATION:

```

      35              40              45
Glu Cys Val Gly Phe Glu Lys Ile Leu Glu Cys Asp Val Ile Phe Leu
      50              55              60
Ala Ile Pro Val Glu Gly Ile Ile Gly Cys Leu Lys Lys Met Thr Ser
      65              70              75              80
Ile Lys Lys Ser Ala Thr Ile Ile Asp Leu Gly Gly Ala Lys Ala Gln
      85              90              95
Ile Ile Arg Asn Ile Pro Lys Ser Ile Arg Lys Asn Phe Ile Ala Ala
      100             105             110
His Pro Met Cys Gly Thr Glu Phe Tyr Gly Pro Lys Ala Ser Val Lys
      115             120             125
Gly Leu Tyr Glu Asn Ala Leu Val Ile Leu Cys Asp Leu Glu Asp Ser
      130             135             140
Gly Thr Glu Gln Val Glu Ile Ala Lys Glu Ile Phe Leu Gly Val Lys
      145             150             155             160
Ala Arg Leu Ile Lys Met Lys Ser Asn Glu His Asp Thr His Val Ala
      165             170             175
Tyr Ile Ser His Leu Pro His Val Leu Ser Tyr Ala Leu Ala Asn Ser
      180             185             190
Val Leu Lys Gln Asn Asp Pro Glu Met Ile Leu Ser Leu Ala Gly Gly
      195             200             205
Gly Phe Arg Asp Met Ser Arg Leu Ser Lys Ser Ser Pro Leu Met Trp
      210             215             220
Lys Asp Ile Phe Lys Gln Asn Arg Asp Asn Val Leu Glu Ala Ile Lys
      225             230             235             240
Lys Cys Glu Lys Glu Ile Val Gln Ala Lys Ala Trp Ile Glu Asn Asn
      245             250             255
Asp Tyr Glu Ser Leu Ala Glu Trp Met Ala Gln Ala Asn Lys Leu Gln
      260             265             270
Glu Phe Met
      275

```

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...267
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

```

AATAATTTAA AATTTTTTAT ATTGTTGTTT TTAGGGGTGC GAGGAGCGAA ATGGGGTATT      60
TGGATTGTTT TT ATG GAT TAT AGG CTG TTT CAT ATG GAT AGC ATG GAT TTA      111
      Met Asp Tyr Arg Leu Phe His Met Asp Ser Met Asp Leu
          1              5              10

```

GTG ATA TTG TGC GAT TTA GAA GAT TCA GGG ACT GAG CAA GTA GAG ATC	486
Val Ile Leu Cys Asp Leu Glu Asp Ser Gly Thr Glu Gln Val Glu Ile	
140 145 150	
GCT AAA GAA ATC TTT TTA GGC GTT AAA GCG CGC TTG ATT AAA ATG AAA	534
Ala Lys Glu Ile Phe Leu Gly Val Lys Ala Arg Leu Ile Lys Met Lys	
155 160 165	
TCC AAT GAG CAT GAC ACC CAT GTG GCT TAT ATC AGC CAT TTA CCC CAT	582
Ser Asn Glu His Asp Thr His Val Ala Tyr Ile Ser His Leu Pro His	
170 175 180	
GTT TTG AGC TAT GCG TTA GCC AAT AGC GTT TTA AAG CAA AAC GAC CCA	630
Val Leu Ser Tyr Ala Leu Ala Asn Ser Val Leu Lys Gln Asn Asp Pro	
185 190 195	
GAG ATG ATT TTA TCT TTA GCG GGT GGG GGT TTT AGG GAT ATG AGC CGT	678
Glu Met Ile Leu Ser Leu Ala Gly Gly Gly Phe Arg Asp Met Ser Arg	
200 205 210 215	
CTG TCC AAA AGC TCG CCT TTA ATG TGG AAA GAT ATT TTC AAA CAA AAC	726
Leu Ser Lys Ser Ser Pro Leu Met Trp Lys Asp Ile Phe Lys Gln Asn	
220 225 230	
CGA GAC AAT GTC TTA GAA GCG ATT AAA AAA TGC GAA AAA GAA ATC GTG	774
Arg Asp Asn Val Leu Glu Ala Ile Lys Lys Cys Glu Lys Glu Ile Val	
235 240 245	
CAA GCT AAG GCG TGG ATA GAA AAT AAC GAT TAT GAA AGC CTT GCA GAA	822
Gln Ala Lys Ala Trp Ile Glu Asn Asn Asp Tyr Glu Ser Leu Ala Glu	
250 255 260	
TGG ATG GCG CAA GCG AAC AAA CTC CAG GAG TTC ATG TAAAGTAAAA TGATGT	874
Trp Met Ala Gln Ala Asn Lys Leu Gln Glu Phe Met	
265 270 275	
AAAATAATTT AAAATTTTTT ATATTGTTGT TTTTAGG	911

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

Met Lys Ala Gly Ile Ile Gly Leu Gly Leu Met Gly Gly Ser Leu Gly	
1 5 10 15	
Leu Ala Leu Gln Glu Trp Gly Arg Phe Lys Ser Val Ile Gly Tyr Asp	
20 25 30	
His Asn Ala Leu His Ala Lys Leu Ala Leu Thr Leu Gly Leu Val Asp	

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...858
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

```

AGTGTTAGAA AAAACTTTGC TTTGAAATTT GGC ATG AAA GCA GGC ATT ATT GGT      54
                Met Lys Ala Gly Ile Ile Gly
                        1                      5

TTA GGG CTT ATG GGG GGG AGT TTA GGG CTA GCC TTG CAA GAA TGG GGG      102
Leu Gly Leu Met Gly Gly Ser Leu Gly Leu Ala Leu Gln Glu Trp Gly
        10                      15                      20

CGT TTT AAA AGC GTT ATA GGC TAT GAT CAT AAC GCT TTG CAT GCT AAA      150
Arg Phe Lys Ser Val Ile Gly Tyr Asp His Asn Ala Leu His Ala Lys
        25                      30                      35

TTG GCT TTG ACT TTG GGG CTT GTA GAT GAA TGC GTG GGA TTT GAA AAG      198
Leu Ala Leu Thr Leu Gly Leu Val Asp Glu Cys Val Gly Phe Glu Lys
        40                      45                      50                      55

ATT TTA GAA TGC GAT GTG ATT TTT TTG GCC ATT CCG GTT GAG GGC ATC      246
Ile Leu Glu Cys Asp Val Ile Phe Leu Ala Ile Pro Val Glu Gly Ile
                60                      65                      70

ATT GGA TGT CTG AAA AAA ATG ACC TCT ATC AAA AAA AGC GCG ACC ATT      294
Ile Gly Cys Leu Lys Lys Met Thr Ser Ile Lys Lys Ser Ala Thr Ile
                75                      80                      85

ATT GAT TTA GGG GGC GCT AAA GCG CAA ATC ATT CGC AAT ATC CCT AAA      342
Ile Asp Leu Gly Gly Ala Lys Ala Gln Ile Ile Arg Asn Ile Pro Lys
        90                      95                      100

AGC ATT CGT AAG AAT TTC ATC GCT GCG CAC CCC ATG TGC GGG ACA GAG      390
Ser Ile Arg Lys Asn Phe Ile Ala Ala His Pro Met Cys Gly Thr Glu
        105                      110                      115

TTT TAT GGC CCT AAA GCG AGC GTT AAG GGG CTG TAT GAA AAC GCT CTA      438
Phe Tyr Gly Pro Lys Ala Ser Val Lys Gly Leu Tyr Glu Asn Ala Leu
        120                      125                      130                      135

```

1		5		10		15
Asp	Pro	Lys	Lys	Arg	Arg	Ile
		20		25		30
Val	Cys	Val	Cys	Glu	Tyr	Cys
		35		40		45
Lys	Tyr	Asp	Asn	Ser	Leu	Leu
		50		55		60
Met	Glu	Ser	Ser	Ala	Tyr	Glu
		65		70		75
Ala	Pro	Lys	Glu	Leu	Lys	Ala
		85		90		95
Glu	Gln	Ala	Lys	Lys	Val	Phe
		100		105		110
Arg	Leu	Ser	Phe	Lys	Glu	Lys
		115		120		125
Asn	Val	Glu	Leu	Glu	His	Leu
		130		135		140
Ile	Leu	Leu	Ile	Gly	Pro	Thr
		145		150		155
Thr	Leu	Ala	Lys	His	Leu	Asp
		165		170		175
Ser	Leu	Thr	Glu	Ala	Gly	Tyr
		180		185		190
Thr	Arg	Leu	Leu	Gln	Ala	Ser
		195		200		205
Gly	Ile	Val	Phe	Ile	Asp	Glu
		210		215		220
Asn	Arg	Ser	Ile	Thr	Arg	Asp
		225		230		235
Leu	Leu	Lys	Ile	Val	Glu	Gly
		245		250		255
Gly	Arg	Lys	His	Pro	Glu	Gly
		260		265		270
Ile	Leu	Phe	Ile	Cys	Ala	Gly
		275		280		285
Lys	Lys	Arg	Thr	Thr	Gln	Asn
		290		295		300
Ser	Lys	Lys	Glu	Gln	Glu	Ala
		305		310		315
Leu	Val	Thr	Tyr	Gly	Leu	Ile
		325		330		335
Leu	Ser	Thr	Leu	Asp	Ser	Ile
		340		345		350
Gln	Lys	Pro	Lys	Asn	Ala	Leu
		355		360		365
Met	Asp	Glu	Val	Asp	Leu	Ile
		370		375		380
Ala	Gln	Leu	Ala	Leu	Glu	Arg
		385		390		395
Ile	Ile	Glu	Asp	Phe	Cys	Leu
		405		410		415
Lys	Gly	Ser	Glu	Val	Arg	Ile
		420		425		430
Glu	Pro	Leu	Ile	Ile	Ala	Lys
		435		440		445

ATC ATT AAA AAA CGC ACC ACG CAG AAT GTG TTG GGT TTC ACT CAA GAA	972
Ile Ile Lys Lys Arg Thr Thr Gln Asn Val Leu Gly Phe Thr Gln Glu	
290 295 300	
AAG ATG AGC AAA AAA GAG CAA GAA GCG ATC TTG CAT TTA GTC CAA ACC	1020
Lys Met Ser Lys Lys Glu Gln Glu Ala Ile Leu His Leu Val Gln Thr	
305 310 315	
CAT GAC CTG GTT ACT TAT GGG CTT ATC CCT GAG CTT ATT GGC CGT TTG	1068
His Asp Leu Val Thr Tyr Gly Leu Ile Pro Glu Leu Ile Gly Arg Leu	
320 325 330	
CCG GTT TTA AGC ACG CTA GAT AGC ATC AGT TTA GAA GCG ATG GTG GAT	1116
Pro Val Leu Ser Thr Leu Asp Ser Ile Ser Leu Glu Ala Met Val Asp	
335 340 345 350	
ATT TTA CAA AAA CCT AAA AAC GCT CTT ATC AAG CAA TAC CAG CAG CTT	1164
Ile Leu Gln Lys Pro Lys Asn Ala Leu Ile Lys Gln Tyr Gln Gln Leu	
355 360 365	
TTC AAA ATG GAT GAG GTG GAT TTG ATC TTT GAA GAA GAA GCC ATT AAA	1212
Phe Lys Met Asp Glu Val Asp Leu Ile Phe Glu Glu Glu Ala Ile Lys	
370 375 380	
GAA ATC GCT CAA CTC GCA TTA GAA AGA AAA ACC GGG GCT AGG GGC TTA	1260
Glu Ile Ala Gln Leu Ala Leu Glu Arg Lys Thr Gly Ala Arg Gly Leu	
385 390 395	
AGG GCG ATC ATT GAA GAT TTT TGT TTG GAT ATT ATG TTT GAT TTA CCC	1308
Arg Ala Ile Ile Glu Asp Phe Cys Leu Asp Ile Met Phe Asp Leu Pro	
400 405 410	
AAG CTT AAA GGA TCG GAA GTG CGT ATC ACT AAA GAT TGT GTT TTA AAA	1356
Lys Leu Lys Gly Ser Glu Val Arg Ile Thr Lys Asp Cys Val Leu Lys	
415 420 425 430	
CAG GCT GAA CCT TTG ATC ATT GCT AAA ACG CAT TCT AAA ATT CTT CCT T	1405
Gln Ala Glu Pro Leu Ile Ile Ala Lys Thr His Ser Lys Ile Leu Pro	
435 440 445	
AAGGAACACG CTTATAAATT TAACGATAAA GGATTAGAAA GGG	1448

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

Met Asn Glu Thr Leu Tyr Cys Ser Phe Cys Lys Lys Pro Glu Ser Arg

Arg	Arg	Met	Glu	Ser	Ser	Ala	Tyr	Glu	Glu	Glu	Phe	Leu	Leu	Ser	Tyr	
		65					70					75				
ATT	CCA	GCC	CCT	AAA	GAG	CTT	AAG	GCG	GTT	TTA	GAC	AAT	TAT	GTG	ATA	348
Ile	Pro	Ala	Pro	Lys	Glu	Leu	Lys	Ala	Val	Leu	Asp	Asn	Tyr	Val	Ile	
	80					85					90					
GGG	CAA	GAG	CAG	GCT	AAA	AAG	GTT	TTT	TCC	GTA	GCC	GTG	TAT	AAC	CAT	396
Gly	Gln	Glu	Gln	Ala	Lys	Lys	Val	Phe	Ser	Val	Ala	Val	Tyr	Asn	His	
95					100					105					110	
TAC	AAA	CGC	TTA	TCT	TTT	AAA	GAA	AAA	CTC	AAA	AAA	CAA	GAC	AAC	CAA	444
Tyr	Lys	Arg	Leu	Ser	Phe	Lys	Glu	Lys	Leu	Lys	Lys	Gln	Asp	Asn	Gln	
				115					120					125		
GAC	AGC	AAT	GTG	GAG	TTA	GAG	CAT	TTA	GAA	GAA	GTG	GAG	TTG	AGC	AAG	492
Asp	Ser	Asn	Val	Glu	Leu	Glu	His	Leu	Glu	Glu	Val	Glu	Leu	Ser	Lys	
			130					135					140			
TCT	AAT	ATT	TTA	CTA	ATC	GGC	CCT	ACA	GGA	TCA	GGC	AAA	ACT	TTA	ATG	540
Ser	Asn	Ile	Leu	Leu	Ile	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Met	
	145						150					155				
GCG	CAA	ACT	CTG	GCC	AAG	CAT	TTG	GAT	ATT	CCT	ATC	GCC	ATT	AGC	GAT	588
Ala	Gln	Thr	Leu	Ala	Lys	His	Leu	Asp	Ile	Pro	Ile	Ala	Ile	Ser	Asp	
	160					165					170					
GCG	ACT	AGC	TTG	ACT	GAA	GCG	GGC	TAT	GTG	GGC	GAA	GAC	GTG	GAA	AAT	636
Ala	Thr	Ser	Leu	Thr	Glu	Ala	Gly	Tyr	Val	Gly	Glu	Asp	Val	Glu	Asn	
175					180					185					190	
ATT	CTC	ACA	AGA	TTG	TTG	CAA	GCG	AGC	GAC	TGG	AAT	GTC	CAA	AAA	GCC	684
Ile	Leu	Thr	Arg	Leu	Leu	Gln	Ala	Ser	Asp	Trp	Asn	Val	Gln	Lys	Ala	
				195					200					205		
CAA	AAA	GGC	ATT	GTG	TTT	ATT	GAT	GAG	ATT	GAT	AAA	ATC	AGC	CGT	TTG	732
Gln	Lys	Gly	Ile	Val	Phe	Ile	Asp	Glu	Ile	Asp	Lys	Ile	Ser	Arg	Leu	
			210					215					220			
TCA	GAA	AAC	CGC	TCT	ATC	ACT	AGA	GAT	GTT	TCT	GGC	GAG	GGC	GTT	CAG	780
Ser	Glu	Asn	Arg	Ser	Ile	Thr	Arg	Asp	Val	Ser	Gly	Glu	Gly	Val	Gln	
		225					230					235				
CAA	GCG	TTG	TTG	AAA	ATC	GTT	GAA	GGT	TCT	TTA	GTG	AAT	ATC	CCC	CCC	828
Gln	Ala	Leu	Leu	Lys	Ile	Val	Glu	Gly	Ser	Leu	Val	Asn	Ile	Pro	Pro	
	240					245					250					
AAA	GGC	GGC	AGA	AAG	CAC	CCT	GAG	GGC	AAT	TTC	ATT	CAA	ATT	GAC	ACG	876
Lys	Gly	Gly	Arg	Lys	His	Pro	Glu	Gly	Asn	Phe	Ile	Gln	Ile	Asp	Thr	
255					260					265					270	
AGC	GAT	ATT	TTA	TTC	ATT	TGT	GCT	GGA	GCG	TTT	GAT	GGG	TTA	GCT	GAA	924
Ser	Asp	Ile	Leu	Phe	Ile	Cys	Ala	Gly	Ala	Phe	Asp	Gly	Leu	Ala	Glu	
				275					280					285		

```

65          70          75          80
Tyr Glu Ser Ala Glu Arg Ile Lys His Ala Gln Ser Lys Gly Ile Leu
      85          90          95
Lys Asn Asn Lys Arg Trp Phe Pro Asn Pro Lys Gly Lys Leu Cys Leu
      100         105         110
Asp Val Trp Glu Ile Thr Ser Gln Arg His Val Glu Lys Glu Lys Gly
      115         120         125
Lys Ile Leu Lys Pro Lys His Pro Ser Ile Lys Pro Lys Ala Leu Ile
      130         135         140
Glu Arg Met Ile Lys Ala Ser Ser His Lys Asn Asp Leu Ile Leu Asp
145         150         155         160
Leu Phe Ser Gly Ser Gly Met Thr Ser Leu Val Ala Lys Ser Leu Glu
      165         170         175
Arg Asn Phe Ile Gly Cys Glu Ser His Ala Glu Tyr Val His Gly Ser
      180         185         190
Leu Glu Met Phe Arg Tyr Asn Glu Cys Glu
      195         200

```

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...1404
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

```

AGAGTTCTAG GGGCGTGGCG TATAAGTCAA GCGAATATTC TAGCGAAGAA AAACAAGAGG      60
AATAAC ATG AAC GAA ACG CTT TAT TGC AGT TTT TGC AAA AAA CCA GAA      108
  Met Asn Glu Thr Leu Tyr Cys Ser Phe Cys Lys Lys Pro Glu
    1             5             10

TCA AGA GAT CCC AAA AAA CGC CGC ATT ATT TTT GCG AGC AAT CTC AAT      156
Ser Arg Asp Pro Lys Lys Arg Arg Ile Ile Phe Ala Ser Asn Leu Asn
15             20             25             30

AAA GAT GTG TGC GTG TGC GAA TAT TGT ATA GAT GTG ATG CAT GGG GAA      204
Lys Asp Val Cys Val Cys Glu Tyr Cys Ile Asp Val Met His Gly Glu
      35             40             45

TTG CAC AAA TAC GAC AAT TCT TTA TTG GCG CTC AAA AGA GAC CGA TTG      252
Leu His Lys Tyr Asp Asn Ser Leu Leu Ala Leu Lys Arg Asp Arg Leu
      50             55             60

AGA AGA ATG GAA TCT AGC GCT TAT GAA GAA GAG TTT TTA CTC TCT TAC      300

```


TAT GAA TCC GCT GAA CGC ATC AAA CAT GCT CAA AGT AAG GGG ATT TTA	347
Tyr Glu Ser Ala Glu Arg Ile Lys His Ala Gln Ser Lys Gly Ile Leu	
85 90 95	
AAA AAT AAC AAA CGC TGG TTC CCT AAC CCT AAG GGC AAA TTA TGC CTT	395
Lys Asn Asn Lys Arg Trp Phe Pro Asn Pro Lys Gly Lys Leu Cys Leu	
100 105 110	
GAT GTG TGG GAA ATC ACT TCA CAA AGG CAT GTT GAA AAA GAG AAG GGT	443
Asp Val Trp Glu Ile Thr Ser Gln Arg His Val Glu Lys Glu Lys Gly	
115 120 125	
AAA ATC CTT AAG CCC AAA CAC CCC AGC ATC AAA CCT AAA GCG CTC ATT	491
Lys Ile Leu Lys Pro Lys His Pro Ser Ile Lys Pro Lys Ala Leu Ile	
130 135 140	
GAA CGC ATG ATA AAA GCT AGC TCT CAC AAA AAC GAT TTG ATT TTA GAT	539
Glu Arg Met Ile Lys Ala Ser Ser His Lys Asn Asp Leu Ile Leu Asp	
145 150 155 160	
TTG TTT AGC GGC AGT GGC ATG ACT AGC TTA GTG GCT AAA AGT TTG GAG	587
Leu Phe Ser Gly Ser Gly Met Thr Ser Leu Val Ala Lys Ser Leu Glu	
165 170 175	
CGT AAT TTT ATA GGG TGT GAG AGC CAT GCT GAA TAC GTG CAT GGG AGT	635
Arg Asn Phe Ile Gly Cys Glu Ser His Ala Glu Tyr Val His Gly Ser	
180 185 190	
TTG GAA ATG TTT AGG TAT AAT GAA TGC GAA TAAAAAAGGA TATTTGACAT GCCA	689
Leu Glu Met Phe Arg Tyr Asn Glu Cys Glu	
195 200	
AAATTAGAAA AAAT	703

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

Met Leu Pro Lys Leu Lys Asp Thr Gly Ser Phe Tyr Ile Phe Asn Thr	
1 5 10 15	
Pro Phe Asn Cys Ala Leu Phe Leu Ala Tyr Leu His His Lys Lys Val	
20 25 30	
His Phe Leu Asn Phe Ile Thr Trp Val Lys Lys Asp Gly Phe Ala Asn	
35 40 45	
Ala Lys Lys Arg Tyr Asn His Ala Gln Glu Ser Ile Leu Phe Tyr Ser	
50 55 60	
Met His Lys Lys Asn Tyr Thr Phe Asn Ala Asp Glu Ile Arg Ile Ala	

```

      290              295              300
Tyr Glu Ile Pro Lys Asp Lys Ile Thr Glu Leu Ser Val Arg Tyr Val
305              310              315              320
Arg Phe Asn Ser Gly Val Leu Gly Tyr Gly Ile Gly Leu Gly Leu Val
      325              330              335
Lys Lys Val Cys Glu Lys Tyr Lys Met Arg Leu Glu Ile His Ser Glu
      340              345              350
Pro Ser Leu Lys Gly Ser Phe Tyr Glu Asn Ser Phe Cys Val Gln Phe
      355              360              365
Gln Gly
      370

```

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...665
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

```

GGGATAGTTT TAAAAATGAT GAAGAGTTTT TAACATTTTC TTACGCTTGG ATTGATAAA      59

ATG CTG CCC AAA CTT AAA GAC ACA GGG AGT TTT TAT ATC TTT AAT ACC      107
Met Leu Pro Lys Leu Lys Asp Thr Gly Ser Phe Tyr Ile Phe Asn Thr
  1              5              10              15

CCT TTT AAT TGC GCT TTA TTT TTA GCG TAT TTG CAC CAT AAA AAA GTG      155
Pro Phe Asn Cys Ala Leu Phe Leu Ala Tyr Leu His His Lys Lys Val
      20              25              30

CAT TTT TTA AAT TTT ATC ACT TGG GTT AAA AAA GAT GGG TTT GCC AAC      203
His Phe Leu Asn Phe Ile Thr Trp Val Lys Lys Asp Gly Phe Ala Asn
      35              40              45

GCC AAA AAG CGT TAT AAC CAC GCG CAA GAA AGC ATT TTA TTT TAT AGC      251
Ala Lys Lys Arg Tyr Asn His Ala Gln Glu Ser Ile Leu Phe Tyr Ser
      50              55              60

ATG CAC AAG AAA AAC TAC ACC TTT AAT GCC GAT GAG ATT CGC ATC GCT      299
Met His Lys Lys Asn Tyr Thr Phe Asn Ala Asp Glu Ile Arg Ile Ala
      65              70              75              80

```

TTT TAT GAA AAT TCG TTT TGC GTT CAA TTT CAA GGA TAAAGATGCT TTCAGT 1223
 Phe Tyr Glu Asn Ser Phe Cys Val Gln Phe Gln Gly
 360 365 370

GTATGAAAAA GTGAATGCTC TAG 1246

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

Met	Leu	Val	Ile	Ser	Val	Leu	Ala	Phe	Asn	Tyr	Glu	Lys	Asn	Glu	Lys	1	5	10	15
Ile	Lys	Met	Ile	Arg	Met	Asp	Met	Asp	Lys	Met	Ala	Ser	Lys	Ile	Ala	20	25	30	
Ser	Glu	Val	Ile	Ala	Leu	His	Met	Gln	Thr	His	Gly	Asp	Tyr	Gln	Asn	35	40	45	
Ala	Leu	Asn	Ala	Leu	Ile	Ser	Arg	Tyr	Lys	Asp	Ala	Ser	Ile	Ala	Leu	50	55	60	
Phe	Asp	Ser	Lys	Lys	Arg	Val	Leu	Tyr	Ser	Asn	Ile	Pro	Glu	Ser	Ala	65	70	75	80
Asn	Leu	Ile	Lys	Asn	His	Lys	Glu	Ala	Gly	Phe	Phe	Ser	Phe	Arg	Gly	85	90	95	
Glu	Tyr	Tyr	Leu	Leu	Ser	Asp	Glu	Thr	Phe	Ala	His	Leu	Gly	Val	Ala	100	105	110	
Lys	Met	Leu	Phe	Lys	Asn	Ser	Lys	Pro	Leu	His	Phe	Ser	Ser	Leu	Tyr	115	120	125	
Arg	Asn	Ile	Val	Leu	Val	Phe	Val	Val	Ala	Phe	Leu	Cys	Val	Ile	Gly	130	135	140	
Val	Ser	Val	Phe	Leu	Gly	Arg	Leu	Phe	Leu	Lys	Pro	Ile	Arg	Asn	Glu	145	150	155	160
Ile	Thr	Arg	Ile	Asp	His	Phe	Leu	Lys	Asn	Thr	Thr	His	Glu	Leu	Asn	165	170	175	
Thr	Pro	Met	Ser	Ala	Leu	Val	Leu	Ser	Leu	Lys	Thr	Leu	Glu	Asp	Asn	180	185	190	
Gln	Gln	His	Arg	Arg	Ile	Lys	Ile	Ala	Ile	Gln	Arg	Met	Ser	Phe	Leu	195	200	205	
Tyr	Arg	Ser	Leu	Ser	Tyr	Leu	Val	Met	Gln	Asp	Ile	Glu	Arg	Glu	Ser	210	215	220	
Phe	Val	Leu	Leu	Asp	Leu	Lys	Ala	Leu	Ile	Ile	Lys	Glu	Asn	Thr	Leu	225	230	235	240
Phe	Ser	Glu	Met	Ile	Asp	Tyr	His	Lys	Leu	Glu	Phe	Lys	Ser	Asp	Leu	245	250	255	
Val	Glu	Val	Glu	Leu	Lys	Ala	Lys	Glu	Gln	Asp	Phe	Ile	Ser	Leu	Tyr	260	265	270	
Ser	Asn	Leu	Leu	Met	Asn	Ala	Ile	Lys	Tyr	Ser	Val	Met	Asn	Gly	Tyr	275	280	285	
Ile	His	Ile	Glu	Leu	Thr	His	Ala	Phe	Leu	Lys	Val	Lys	Asn	Leu	Gly				

TTT GTT GTA GCG TTT TTA TGC GTG ATA GGG GTT TCT GTG TTT TTG GGG	547
Phe Val Val Ala Phe Leu Cys Val Ile Gly Val Ser Val Phe Leu Gly	
135 140 145 150	
CGT TTG TTT TTA AAG CCC ATT AGG AAT GAA ATC ACC CGC ATT GAT CAT	595
Arg Leu Phe Leu Lys Pro Ile Arg Asn Glu Ile Thr Arg Ile Asp His	
155 160 165	
TTT TTA AAA AAC ACC ACG CAT GAA TTA AAC ACC CCC ATG AGC GCT TTA	643
Phe Leu Lys Asn Thr Thr His Glu Leu Asn Thr Pro Met Ser Ala Leu	
170 175 180	
GTC TTG TCT TTA AAA ACC TTA GAA GAC AAC CAA CAA CAC CGC CGC ATT	691
Val Leu Ser Leu Lys Thr Leu Glu Asp Asn Gln Gln His Arg Arg Ile	
185 190 195	
AAA ATC GCT ATC CAG CGC ATG AGT TTT TTA TAC CGC TCG CTC TCG TAT	739
Lys Ile Ala Ile Gln Arg Met Ser Phe Leu Tyr Arg Ser Leu Ser Tyr	
200 205 210	
TTA GTG ATG CAA GAT ATT GAG CGC GAA TCT TTT GTG CTT TTA GAT TTA	787
Leu Val Met Gln Asp Ile Glu Arg Glu Ser Phe Val Leu Leu Asp Leu	
215 220 225 230	
AAA GCC CTG ATT ATT AAA GAA AAC ACG CTT TTT AGC GAG ATG ATA GAC	835
Lys Ala Leu Ile Ile Lys Glu Asn Thr Leu Phe Ser Glu Met Ile Asp	
235 240 245	
TAC CAC AAG CTG GAA TTT AAA AGC GAT TTA GTG GAA GTG GAA CTT AAA	883
Tyr His Lys Leu Glu Phe Lys Ser Asp Leu Val Glu Val Glu Leu Lys	
250 255 260	
GCT AAA GAG CAG GAT TTC ATT TCG CTT TAT AGC AAT TTG CTC ATG AAC	931
Ala Lys Glu Gln Asp Phe Ile Ser Leu Tyr Ser Asn Leu Leu Met Asn	
265 270 275	
GCG ATC AAA TAC AGC GTC ATG AAT GGG TAT ATC CAC ATA GAG CTA ACG	979
Ala Ile Lys Tyr Ser Val Met Asn Gly Tyr Ile His Ile Glu Leu Thr	
280 285 290	
CAT GCG TTT TTG AAA GTG AAA AAT TTA GGG TAT GAA ATC CCT AAA GAC	1027
His Ala Phe Leu Lys Val Lys Asn Leu Gly Tyr Glu Ile Pro Lys Asp	
295 300 305 310	
AAG ATC ACA GAA TTA AGC GTT CGT TAT GTG CGT TTC AAT TCT GGC GTG	1075
Lys Ile Thr Glu Leu Ser Val Arg Tyr Val Arg Phe Asn Ser Gly Val	
315 320 325	
TTG GGT TAT GGT ATA GGG TTA GGT TTG GTG AAA AAA GTG TGC GAA AAG	1123
Leu Gly Tyr Gly Ile Gly Leu Gly Leu Val Lys Lys Val Cys Glu Lys	
330 335 340	
TAT AAA ATG CGT TTA GAA ATT CAT AGC GAA CCC TCT TTA AAG GGA TCG	1171
Tyr Lys Met Arg Leu Glu Ile His Ser Glu Pro Ser Leu Lys Gly Ser	
345 350 355	

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...1207
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

```

GAAACGCATA AGGGGGTTGG CTATCGCTTT AACCCACTAT GAAAAAAAAAT CCCTTAAACT      60
CTTTTTAGGG ATTTATTTAG GCTCTTCGTT TGTGTTG ATG CTA GTG ATT AGC GTT      115
                               Met Leu Val Ile Ser Val
                               1             5

TTA GCG TTT AAC TAT GAA AAA AAC GAA AAA ATC AAA ATG ATA CGC ATG      163
Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Met Ile Arg Met
                10             15             20

GAC ATG GAC AAA ATG GCT TCT AAG ATC GCT AGC GAA GTG ATT GCC TTG      211
Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Val Ile Ala Leu
                25             30             35

CAC ATG CAA ACG CAT GGG GAT TAT CAA AAC GCT TTA AAC GCT CTC ATT      259
His Met Gln Thr His Gly Asp Tyr Gln Asn Ala Leu Asn Ala Leu Ile
                40             45             50

TCA CGC TAT AAA GAC GCT TCC ATA GCC CTT TTT GAT AGT AAA AAG CGT      307
Ser Arg Tyr Lys Asp Ala Ser Ile Ala Leu Phe Asp Ser Lys Lys Arg
                55             60             65             70

GTT TTG TAT TCT AAT ATC CCT GAA AGC GCC AAT TTG ATT AAA AAC CAT      355
Val Leu Tyr Ser Asn Ile Pro Glu Ser Ala Asn Leu Ile Lys Asn His
                75             80             85

AAA GAA GCG GGC TTT TTT AGT TTT AGG GGA GAG TAT TAC CTA TTG AGC      403
Lys Glu Ala Gly Phe Phe Ser Phe Arg Gly Glu Tyr Tyr Leu Leu Ser
                90             95             100

GAT GAA ACT TTC GCT CAC TTA GGC GTG GCT AAA ATG CTT TTT AAA AAT      451
Asp Glu Thr Phe Ala His Leu Gly Val Ala Lys Met Leu Phe Lys Asn
                105             110             115

TCT AAA CCC CTT CAT TTT TCT TCT TTG TAT CGT AAC ATT GTT TTA GTG      499
Ser Lys Pro Leu His Phe Ser Ser Leu Tyr Arg Asn Ile Val Leu Val
                120             125             130

```

50	55	60
Asn Phe Ile Arg Gln Lys Met Pro Lys Asp Lys Gln Ile Lys Glu Glu		
65	70	75
Asp Leu Val Ala Ile Phe Ala Ala Ser Pro Ile Asp Asn Ile Glu Ala		80
	85	90
Tyr Val Glu Glu Ile Lys Asn Ala Ser Ile Lys Arg Lys Leu Phe Gly		95
	100	105
Leu Ala Asn Thr Ile Arg Glu Gln Ala Leu Glu Ser Ala Gln Lys Ser		110
	115	120
Ser Asp Ile Leu Gly Ala Val Glu Arg Glu Val Tyr Ala Leu Leu Asn		125
	130	135
Gly Ser Thr Ile Glu Gly Phe Arg Asn Ile Lys Glu Val Leu Glu Ser		140
145	150	155
Ala Met Asp Leu Ile Thr Glu Asn Gln Arg Lys Gly Ser Leu Glu Val		160
	165	170
Thr Gly Ile Pro Thr Gly Phe Val Gln Leu Asp Asn Tyr Thr Ser Gly		175
	180	185
Phe Asn Lys Gly Ser Leu Val Ile Ile Gly Ala Arg Pro Ser Met Gly		190
	195	200
Lys Thr Ser Leu Met Met Asn Met Val Leu Ser Ala Leu Asn Asp Asp		205
	210	215
Arg Gly Val Ala Val Phe Ser Leu Glu Met Ser Ala Glu Gln Leu Ala		220
225	230	235
Leu Arg Ala Leu Ser Asp Leu Thr Ser Ile Asn Met His Asp Leu Glu		240
	245	250
Ser Gly Arg Leu Asp Asp Asp Gln Trp Glu Asn Leu Ala Lys Cys Phe		255
	260	265
Asp His Leu Ser Gln Lys Lys Leu Phe Phe Tyr Asp Lys Ser Tyr Val		270
	275	280
Arg Ile Glu Gln Ile Arg Leu Gln Leu Arg Lys Leu Lys Ser Gln His		285
	290	295
Lys Glu Leu Gly Ile Ala Phe Ile Asp Tyr Leu Gln Leu Met Ser Gly		300
305	310	315
Ser Lys Ala Thr Lys Glu Arg His Glu Gln Ile Ala Glu Ile Ser Arg		320
	325	330
Glu Leu Lys Thr Leu Ala Arg Glu Leu Glu Ile Pro Ile Ile Ala Leu		335
	340	345
Val Gln Leu Asn Arg Ser Leu Glu Asn Arg Asp Asp Lys Arg Pro Ile		350
	355	360
Leu Ser Asp Ile Lys Asp Ser Gly Gly Ile Glu Gln Asp Ala Asp Ile		365
	370	375
Val Leu Phe Leu Tyr Arg Gly Tyr Ile Tyr Gln Met Arg Ala Glu Asp		380
385	390	395
Asn Lys Ile Asp Lys Leu Lys Lys Glu Gly Lys Ile Glu Glu Ala Gln		400
	405	410
Glu Leu Tyr Leu Lys Val Asn Glu Glu Arg Arg Ile His Lys Gln Asn		415
	420	425
Gly Ser Ile Glu Glu Ala Glu Ile Ile Val Ala Lys Asn Arg Asn Gly		430
	435	440
Ala Thr Gly Thr Val Tyr Thr Arg Phe Asn Ala Pro Phe Thr Arg Tyr		445
	450	455
Glu Asp Met Pro Ile Asp Ser His Leu Glu Glu Gly Gln Glu Thr Lys		460
465	470	475
Val Asp Tyr Asp Ile Val Thr Thr		480
	485	

Glu Asn Arg Asp Asp Lys Arg Pro Ile Leu Ser Asp Ile Lys Asp Ser	
360 365 370 375	
GGG GGG ATT GAA CAA GAC GCT GAT ATT GTT TTA TTT TTA TAT AGA GGC	1206
Gly Gly Ile Glu Gln Asp Ala Asp Ile Val Leu Phe Leu Tyr Arg Gly	
380 385 390	
TAT ATC TAT CAA ATG AGG GCT GAA GAC AAC AAA ATA GAC AAA CTC AAA	1254
Tyr Ile Tyr Gln Met Arg Ala Glu Asp Asn Lys Ile Asp Lys Leu Lys	
395 400 405	
AAA GAA GGT AAA ATT GAA GAG GCG CAA GAG TTG TAC TTA AAA GTT AAT	1302
Lys Glu Gly Lys Ile Glu Glu Ala Gln Glu Leu Tyr Leu Lys Val Asn	
410 415 420	
GAA GAA AGG CGT ATC CAC AAG CAA AAT GGC AGC ATT GAA GAG GCT GAA	1350
Glu Glu Arg Arg Ile His Lys Gln Asn Gly Ser Ile Glu Glu Ala Glu	
425 430 435	
ATC ATT GTG GCT AAA AAC AGG AAT GGG GCT ACA GGA ACG GTT TAT ACG	1398
Ile Ile Val Ala Lys Asn Arg Asn Gly Ala Thr Gly Thr Val Tyr Thr	
440 445 450 455	
CGC TTT AAC GCT CCT TTC ACG CGC TAT GAA GAC ATG CCC ATA GAT TCC	1446
Arg Phe Asn Ala Pro Phe Thr Arg Tyr Glu Asp Met Pro Ile Asp Ser	
460 465 470	
CAT TTA GAA GAA GGG CAA GAA ACT AAA GTG GAT TAT GAT ATA GTT ACA	1494
His Leu Glu Glu Gly Gln Glu Thr Lys Val Asp Tyr Asp Ile Val Thr	
475 480 485	
ACT TGAAAGACAA AACTTTTCAG GGGGCGTTTG AACTTCTTA	1536
Thr	

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

Met Asp His Leu Lys His Leu Gln Gln Leu Gln Asn Ile Glu Arg Ile	
1 5 10 15	
Val Leu Ser Gly Ile Val Leu Ala Asn His Lys Ile Glu Glu Val His	
20 25 30	
Ser Val Leu Glu Pro Ser Asp Phe Tyr Tyr Pro Pro Asn Gly Leu Phe	
35 40 45	
Phe Glu Ile Ala Leu Lys Leu His Glu Glu Asp Cys Pro Ile Asp Glu	

140										145					150					
AGG	AAT	ATT	AAA	GAA	GTG	CTT	GAA	AGC	GCA	ATG	GAT	CTC	ATT	ACA	GAA	534				
Arg	Asn	Ile	Lys	Glu	Val	Leu	Glu	Ser	Ala	Met	Asp	Leu	Ile	Thr	Glu					
			155				160						165							
AAC	CAA	AGA	AAG	GGG	AGT	TTG	GAA	GTT	ACT	GGC	ATA	CCG	ACT	GGC	TTT	582				
Asn	Gln	Arg	Lys	Gly	Ser	Leu	Glu	Val	Thr	Gly	Ile	Pro	Thr	Gly	Phe					
			170				175						180							
GTC	CAA	TTG	GAT	AAC	TAT	ACG	AGC	GGT	TTC	AAT	AAG	GGG	AGT	TTA	GTC	630				
Val	Gln	Leu	Asp	Asn	Tyr	Thr	Ser	Gly	Phe	Asn	Lys	Gly	Ser	Leu	Val					
			185				190						195							
ATT	ATA	GGG	GCA	AGG	CCG	TCT	ATG	GGT	AAA	ACT	AGT	TTG	ATG	ATG	AAC	678				
Ile	Ile	Gly	Ala	Arg	Pro	Ser	Met	Gly	Lys	Thr	Ser	Leu	Met	Met	Asn					
200						205						210				215				
ATG	GTC	TTA	AGC	GCG	CTC	AAT	GAC	GAT	AGG	GGG	GTA	GCG	GTT	TTT	AGT	726				
Met	Val	Leu	Ser	Ala	Leu	Asn	Asp	Asp	Arg	Gly	Val	Ala	Val	Phe	Ser					
			220						225						230					
TTA	GAA	ATG	TCC	GCA	GAG	CAA	CTC	GCT	TTA	AGG	GCG	TTA	TCG	GAT	CTC	774				
Leu	Glu	Met	Ser	Ala	Glu	Gln	Leu	Ala	Leu	Arg	Ala	Leu	Ser	Asp	Leu					
			235						240						245					
ACC	TCT	ATT	AAC	ATG	CAT	GAT	TTA	GAA	AGC	GGG	AGG	CTT	GAT	GAT	GAT	822				
Thr	Ser	Ile	Asn	Met	His	Asp	Leu	Glu	Ser	Gly	Arg	Leu	Asp	Asp	Asp					
			250						255						260					
CAA	TGG	GAA	AAT	TTA	GCC	AAA	TGC	TTT	GAT	CAC	CTT	TCG	CAA	AAA	AAA	870				
Gln	Trp	Glu	Asn	Leu	Ala	Lys	Cys	Phe	Asp	His	Leu	Ser	Gln	Lys	Lys					
			265						270						275					
CTC	TTT	TTC	TAC	GAT	AAA	AGT	TAT	GTG	AGG	ATA	GAG	CAA	ATC	CGC	TTG	918				
Leu	Phe	Phe	Tyr	Asp	Lys	Ser	Tyr	Val	Arg	Ile	Glu	Gln	Ile	Arg	Leu					
280						285						290				295				
CAA	CTA	CGA	AAG	CTT	AAA	TCC	CAA	CAC	AAG	GAA	TTG	GGT	ATC	GCT	TTT	966				
Gln	Leu	Arg	Lys	Leu	Lys	Ser	Gln	His	Lys	Glu	Leu	Gly	Ile	Ala	Phe					
			300						305						310					
ATT	GAC	TAT	TTG	CAG	CTC	ATG	TCA	GGG	AGT	AAA	GCC	ACT	AAA	GAG	CGC	1014				
Ile	Asp	Tyr	Leu	Gln	Leu	Met	Ser	Gly	Ser	Lys	Ala	Thr	Lys	Glu	Arg					
			315						320						325					
CAT	GAG	CAA	ATC	GCT	GAA	ATT	TCA	AGG	GAG	CTT	AAA	ACT	TTA	GCC	AGA	1062				
His	Glu	Gln	Ile	Ala	Glu	Ile	Ser	Arg	Glu	Leu	Lys	Thr	Leu	Ala	Arg					
			330						335						340					
GAA	TTA	GAA	ATC	CCT	ATC	ATA	GCG	TTA	GTG	CAA	CTC	AAC	CGC	AGC	CTA	1110				
Glu	Leu	Glu	Ile	Pro	Ile	Ile	Ala	Leu	Val	Gln	Leu	Asn	Arg	Ser	Leu					
			345						350						355					
GAA	AAC	CGA	GAC	GAT	AAA	CGG	CCC	ATT	CTT	TCG	GAT	ATC	AAA	GAC	AGC	1158				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1497
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

TAGAAAAGAT CAAACAATTA TAAAAGGATA AAA ATG GAT CAT TTA AAG CAT TTG	54
Met Asp His Leu Lys His Leu	
1 5	
CAG CAA TTG CAA AAC ATT GAA AGG ATC GTG CTT TCA GGC ATT GTG TTG	102
Gln Gln Leu Gln Asn Ile Glu Arg Ile Val Leu Ser Gly Ile Val Leu	
10 15 20	
GCC AAT CAT AAG ATT GAA GAG GTC CAT AGC GTT TTA GAG CCT AGC GAT	150
Ala Asn His Lys Ile Glu Glu Val His Ser Val Leu Glu Pro Ser Asp	
25 30 35	
TTT TAC TAC CCG CCT AAC GGC TTA TTT TTT GAA ATC GCT TTA AAA CTG	198
Phe Tyr Tyr Pro Pro Asn Gly Leu Phe Phe Glu Ile Ala Leu Lys Leu	
40 45 50 55	
CAT GAA GAA GAT TGC CCC ATT GAT GAG AAT TTT ATC CGC CAA AAA ATG	246
His Glu Glu Asp Cys Pro Ile Asp Glu Asn Phe Ile Arg Gln Lys Met	
60 65 70	
CCT AAA GAC AAG CAG ATC AAA GAA GAA GAT CTA GTC GCT ATT TTT GCG	294
Pro Lys Asp Lys Gln Ile Lys Glu Glu Asp Leu Val Ala Ile Phe Ala	
75 80 85	
GCA AGC CCC ATA GAT AAT ATT GAA GCC TAT GTG GAA GAG ATT AAA AAC	342
Ala Ser Pro Ile Asp Asn Ile Glu Ala Tyr Val Glu Glu Ile Lys Asn	
90 95 100	
GCT TCC ATT AAA CGA AAA CTT TTT GGC TTG GCT AAC ACC ATT AGA GAG	390
Ala Ser Ile Lys Arg Lys Leu Phe Gly Leu Ala Asn Thr Ile Arg Glu	
105 110 115	
CAA GCC CTA GAA AGC GCG CAA AAA TCC AGC GAT ATT TTA GGC GCT GTG	438
Gln Ala Leu Glu Ser Ala Gln Lys Ser Ser Asp Ile Leu Gly Ala Val	
120 125 130 135	
GAG CGA GAA GTC TAT GCG TTA TTG AAT GGC AGC ACC ATA GAA GGC TTT	486
Glu Arg Glu Val Tyr Ala Leu Leu Asn Gly Ser Thr Ile Glu Gly Phe	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

```

Met Asp Phe Leu Lys Glu Asn Leu Asn Thr Ile Ile Glu Gly Asp Cys
 1          5          10          15
Leu Glu Lys Leu Lys Asp Phe Pro Asn Arg Ser Val Asp Phe Ile Phe
          20          25          30
Ala Asp Pro Pro Tyr Phe Met Gln Thr Glu Gly Glu Leu Lys Arg Phe
          35          40          45
Glu Gly Thr Lys Phe Gln Gly Val Glu Asp Tyr Trp Asp Lys Phe Gly
          50          55          60
Ser Phe Lys Glu Tyr Asp Ala Phe Cys Leu Gly Trp Leu Lys Glu Cys
65          70          75          80
Gln Arg Ile Leu Lys Asp Asn Gly Ser Ile Cys Val Ile Gly Ser Phe
          85          90          95
Gln Asn Ile Phe Arg Ile Gly Phe His Leu Gln Asn Leu Gly Phe Trp
          100          105          110
Ile Leu Asn Asp Ile Ile Trp His Lys Ser Asn Pro Val Pro Asn Phe
          115          120          125
Ala Gly Lys Arg Leu Cys Asn Ala His Glu Thr Leu Ile Trp Cys Ala
          130          135          140
Lys His Lys Asn Ser Lys Val Ala Phe Asn Tyr Lys Thr Met Lys Tyr
145          150          155          160
Leu Asn Asn Asp Lys Gln Glu Lys Ser Val Trp Gln Ile Pro Ile Cys
          165          170          175
Met Gly Asn Glu Arg Leu Lys Asp Ala Gln Gly Lys Lys Val His Ser
          180          185          190
Thr Gln Lys Pro Glu Ala Leu Leu Lys Lys Ile Ile Leu Ser Ala Thr
          195          200          205
Lys Pro Lys Asp Ile Ile Leu Asp Pro Phe Phe Gly Thr Gly Thr Thr
          210          215          220
Gly Ala Val Ala Lys Ser Met Asn Arg Tyr Phe Ile Gly Ile Glu Lys
225          230          235          240
Asp Ser Phe Tyr Ile Lys Glu Ala Ala Lys Arg Leu Asn Asn Thr Arg
          245          250          255
Asp Lys Ser Asp Phe Ile Thr Asn Leu Asp Leu Glu Thr Lys Pro Pro
          260          265          270
Lys Ile Pro Met Ser Leu Leu Ile Ser Lys Gln Leu Leu Lys Ile Gly
          275          280          285
Asp Phe Leu Tyr Ser Pro Asn Lys Glu Lys Ile Cys Gln Val Leu Glu
          290          295          300
Asn Gly Gln Val Arg Asp Asn Glu Asn Tyr Glu Thr Ser Ile His Lys
305          310          315          320
Met Ser Ala Lys Tyr Leu Asn Lys Thr Asn His Asn Gly Trp Lys Phe
          325          330          335
Phe Tyr Ala Tyr Tyr Gln Asn Gln Phe Leu Leu Leu Asp Glu Leu Arg
          340          345          350
Tyr Ile Cys Gln Lys Asp Ser
          355

```

(2) INFORMATION FOR SEQ ID NO:1063:

Trp	Gln	Ile	Pro	Ile	Cys	Met	Gly	Asn	Glu	Arg	Leu	Lys	Asp	Ala	Gln		
				175					180					185			
GGT	AAA	AAA	GTG	CAT	TCC	ACG	CAA	AAA	CCA	GAA	GCG	CTT	TTA	AAA	AAA	627	
Gly	Lys	Lys	Val	His	Ser	Thr	Gln	Lys	Pro	Glu	Ala	Leu	Leu	Lys	Lys		
			190					195					200				
ATC	ATT	TTA	AGC	GCG	ACT	AAA	CCT	AAA	GAT	ATT	ATT	TTA	GAT	CCC	TTT	675	
Ile	Ile	Leu	Ser	Ala	Thr	Lys	Pro	Lys	Asp	Ile	Ile	Leu	Asp	Pro	Phe		
		205					210					215					
TTT	GGC	ACA	GGC	ACA	ACA	GGG	GCT	GTG	GCT	AAA	TCC	ATG	AAC	AGG	TAT	723	
Phe	Gly	Thr	Gly	Thr	Thr	Gly	Ala	Val	Ala	Lys	Ser	Met	Asn	Arg	Tyr		
	220					225				230							
TTT	ATT	GGT	ATT	GAA	AAA	GAT	TCT	TTT	TAT	ATT	AAA	GAA	GCG	GCA	AAA	771	
Phe	Ile	Gly	Ile	Glu	Lys	Asp	Ser	Phe	Tyr	Ile	Lys	Glu	Ala	Ala	Lys		
235					240				245						250		
CGC	CTG	AAT	AAC	ACT	AGG	GAT	AAA	AGC	GAT	TTT	ATC	ACT	AAT	TTA	GAT	819	
Arg	Leu	Asn	Asn	Thr	Arg	Asp	Lys	Ser	Asp	Phe	Ile	Thr	Asn	Leu	Asp		
				255					260					265			
TTA	GAA	ACT	AAA	CCC	CCA	AAA	ATA	CCT	ATG	AGT	CTT	TTA	ATT	TCT	AAA	867	
Leu	Glu	Thr	Lys	Pro	Pro	Lys	Ile	Pro	Met	Ser	Leu	Leu	Ile	Ser	Lys		
			270					275					280				
CAA	TTA	TTA	AAA	ATC	GGG	GAT	TTT	TTA	TAC	TCA	CCT	AAC	AAA	GAA	AAA	915	
Gln	Leu	Leu	Lys	Ile	Gly	Asp	Phe	Leu	Tyr	Ser	Pro	Asn	Lys	Glu	Lys		
		285					290					295					
ATT	TGT	CAA	GTT	TTA	GAA	AAC	GGA	CAA	GTG	AGG	GAT	AAT	GAA	AAC	TAT	963	
Ile	Cys	Gln	Val	Leu	Glu	Asn	Gly	Gln	Val	Arg	Asp	Asn	Glu	Asn	Tyr		
	300					305					310						
GAA	ACT	TCT	ATT	CAT	AAG	ATG	AGC	GCT	AAA	TAT	TTG	AAT	AAA	ACC	AAC	1011	
Glu	Thr	Ser	Ile	His	Lys	Met	Ser	Ala	Lys	Tyr	Leu	Asn	Lys	Thr	Asn		
315					320				325					330			
CAT	AAT	GGC	TGG	AAA	TTT	TTT	TAT	GCG	TAT	TAC	CAA	AAT	CAA	TTT	TTA	1059	
His	Asn	Gly	Trp	Lys	Phe	Phe	Tyr	Ala	Tyr	Tyr	Gln	Asn	Gln	Phe	Leu		
				335				340						345			
TTG	CTA	GAT	GAA	TTG	CGT	TAT	ATC	TGC	CAA	AAG	GAC	TCT	TAATGGACTA	TC	1110		
Leu	Leu	Asp	Glu	Leu	Arg	Tyr	Ile	Cys	Gln	Lys	Asp	Ser					
			350				355										
AAACCTTTAA	CGAGATTTTT	AATCGTTTTG	TCTTTGGAAC													1150	

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 22...1098
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

GATATAAAAG GTTAGTTAAT C ATG GAT TTT TTA AAA GAA AAC TTA AAC ACT	51
Met Asp Phe Leu Lys Glu Asn Leu Asn Thr	
1 5 10	
ATC ATA GAG GGG GAT TGT TTA GAA AAA TTG AAA GAC TTT CCT AAC AGA	99
Ile Ile Glu Gly Asp Cys Leu Glu Lys Leu Lys Asp Phe Pro Asn Arg	
15 20 25	
AGC GTT GAT TTT ATC TTT GCT GAC CCC CCA TAT TTT ATG CAA ACA GAG	147
Ser Val Asp Phe Ile Phe Ala Asp Pro Pro Tyr Phe Met Gln Thr Glu	
30 35 40	
GGG GAA TTG AAG CGT TTT GAA GGC ACA AAA TTT CAA GGC GTT GAG GAT	195
Gly Glu Leu Lys Arg Phe Glu Gly Thr Lys Phe Gln Gly Val Glu Asp	
45 50 55	
TAT TGG GAT AAA TTT GGC TCT TTT AAG GAA TAC GAT GCC TTT TGT TTG	243
Tyr Trp Asp Lys Phe Gly Ser Phe Lys Glu Tyr Asp Ala Phe Cys Leu	
60 65 70	
GGT TGG TTG AAA GAA TGC CAA AGG ATT TTA AAA GAT AAT GGC AGT ATT	291
Gly Trp Leu Lys Glu Cys Gln Arg Ile Leu Lys Asp Asn Gly Ser Ile	
75 80 85 90	
TGT GTG ATA GGG AGT TTT CAA AAT ATT TTT AGA ATT GGT TTT CAT TTG	339
Cys Val Ile Gly Ser Phe Gln Asn Ile Phe Arg Ile Gly Phe His Leu	
95 100 105	
CAA AAT TTA GGG TTT TGG ATA CTC AAT GAT ATT ATT TGG CAC AAG AGT	387
Gln Asn Leu Gly Phe Trp Ile Leu Asn Asp Ile Ile Trp His Lys Ser	
110 115 120	
AAT CCG GTG CCT AAT TTT GCT GGC AAG AGA TTA TGC AAC GCC CAT GAG	435
Asn Pro Val Pro Asn Phe Ala Gly Lys Arg Leu Cys Asn Ala His Glu	
125 130 135	
ACG CTT ATT TGG TGT GCT AAA CAC AAA AAC AGC AAA GTT GCC TTT AAT	483
Thr Leu Ile Trp Cys Ala Lys His Lys Asn Ser Lys Val Ala Phe Asn	
140 145 150	
TAT AAA ACA ATG AAG TAC CTC AAT AAC GAC AAA CAA GAA AAA TCG GTT	531
Tyr Lys Thr Met Lys Tyr Leu Asn Asn Asp Lys Gln Glu Lys Ser Val	
155 160 165 170	
TGG CAA ATC CCT ATT TGC ATG GGT AAC GAA AGA CTA AAA GAT GCG CAA	579

BNSDOCID: <WO 9843478A1 I >

```

ACC GCA CGC TAC TAT TTG CCG AGC GGG CGT ACC ATT CAA GCT AAG GGG      1110
Thr Ala Arg Tyr Tyr Leu Pro Ser Gly Arg Thr Ile Gln Ala Lys Gly
    345                      350                      355

ATC ACG CCT GAT ATT GTG ATT TAT CCG GGT AAA GTG CCA GAA AAT GAA      1158
Ile Thr Pro Asp Ile Val Ile Tyr Pro Gly Lys Val Pro Glu Asn Glu
    360                      365                      370                      375

AAC AAA TTC AGC TTG AAA GAA GCG GAT CTA AAA CAC CAT TTA GAG CAA      1206
Asn Lys Phe Ser Leu Lys Glu Ala Asp Leu Lys His His Leu Glu Gln
                380                      385                      390

GAG CTT AAA AAG ATT GAT GAT AAA ACC CCC AAT TCC AAA GAG GCG GAT      1254
Glu Leu Lys Lys Ile Asp Asp Lys Thr Pro Asn Ser Lys Glu Ala Asp
                395                      400                      405

AAA GAC AAG AAA AAC GAA GAG GAA AAA GAG ATT ACT CCT AAA ATG ATC      1302
Lys Asp Lys Lys Asn Glu Glu Glu Lys Glu Ile Thr Pro Lys Met Ile
    410                      415                      420

AAC GAT GAT ATT CAG CTA AAA ACC GCT ATT GAC AGC TTG AAA ACC TGG      1350
Asn Asp Asp Ile Gln Leu Lys Thr Ala Ile Asp Ser Leu Lys Thr Trp
    425                      430                      435

TCT ATC GTT GAT GAG AAA ATG GAT GAA AAA GCG CCT AAG AAG AAA TAAAA      1400
Ser Ile Val Asp Glu Lys Met Asp Glu Lys Ala Pro Lys Lys Lys
    440                      445                      450

ACTCATGGGG TTTTATTG AAAAATCGTT AATGAGTTTT TTCGCTCATC CAATC      1455

```

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

```

Met Thr Lys Arg Leu Phe Lys Gly Leu Leu Ala Val Ser Leu Ala Val
 1          5          10          15
Ser Leu His Gly Gly Glu Val Lys Glu Lys Lys Pro Val Lys Pro Val
    20          25          30
Lys Glu Asp Pro Gln Glu Leu Ala Ala Lys Arg Val Glu Ala Phe Ser
    35          40          45
Arg Phe Ser Asn Val Val Ser Glu Ile Glu Lys Lys Tyr Val Asp Lys
    50          55          60
Ile Ser Ile Ser Glu Ile Met Thr Lys Ala Ile Glu Gly Leu Leu Ser
    65          70          75          80
Asn Leu Asp Ala His Ser Ala Tyr Leu Asn Glu Lys Lys Phe Lys Glu
    85          90          95
Phe Gln Ala Gln Thr Glu Gly Glu Phe Gly Gly Leu Gly Ile Thr Val

```

ACC GTT ATT GCC CCT TTA GAA GGC ACT CCA GCT TAC AAG GCT GGG GTT	438
Thr Val Ile Ala Pro Leu Glu Gly Thr Pro Ala Tyr Lys Ala Gly Val	
120 125 130 135	
AAG TCA GGC GAT AAC ATT TTA AAA ATC AAT AAC GAA AGC ACG CTG AGC	486
Lys Ser Gly Asp Asn Ile Leu Lys Ile Asn Asn Glu Ser Thr Leu Ser	
140 145 150	
ATG AGC ATT GAT GAT GCG ATC AAC CTC ATG CGC GGC AAG CCA AAA ACC	534
Met Ser Ile Asp Asp Ala Ile Asn Leu Met Arg Gly Lys Pro Lys Thr	
155 160 165	
CCT ATT CAG ATC ACC GTT GTA AGA AAA AAC GAG CCA AAA CCT TTA GTG	582
Pro Ile Gln Ile Thr Val Val Arg Lys Asn Glu Pro Lys Pro Leu Val	
170 175 180	
TTT AAC ATC ATT AGA GAC ATC ATT AAA CTC CCC TCT GTC TAT GTG AAA	630
Phe Asn Ile Ile Arg Asp Ile Ile Lys Leu Pro Ser Val Tyr Val Lys	
185 190 195	
AAG ATT AAA GAA ACC CCT TAT CTG TAT GTG AGA GTG AGT GGT TTT GAC	678
Lys Ile Lys Glu Thr Pro Tyr Leu Tyr Val Arg Val Ser Gly Phe Asp	
200 205 210 215	
AAG AAT GTT ACC AAA TCG GTT TTA GAA GGC TTA AAA GCT AAC CCT AAG	726
Lys Asn Val Thr Lys Ser Val Leu Glu Gly Leu Lys Ala Asn Pro Lys	
220 225 230	
GCT AAG GGG ATC GTG TTG GAT TTA AGG GGC AAT CCT GGA GGG CTA TTA	774
Ala Lys Gly Ile Val Leu Asp Leu Arg Gly Asn Pro Gly Gly Leu Leu	
235 240 245	
AAC CAA GCG GTG GGC TTG TCT AAC CTC TTC ATT AAA GAG GGG GTT TTA	822
Asn Gln Ala Val Gly Leu Ser Asn Leu Phe Ile Lys Glu Gly Val Leu	
250 255 260	
GTC TCT CAA AAA GGC AAA AAT AAA GAA GAA AAT TTA GAA TAC AAG GCT	870
Val Ser Gln Lys Gly Lys Asn Lys Glu Glu Asn Leu Glu Tyr Lys Ala	
265 270 275	
AAC GGC AGA GCC CCT TAT ACC AAT TTG CCT ATT GCG GTG TTA GTC AAT	918
Asn Gly Arg Ala Pro Tyr Thr Asn Leu Pro Ile Ala Val Leu Val Asn	
280 285 290 295	
GGC GGT TCA GCG AGC GCG AGC GAG ATC GTC GCA GGG GCA CTG CAA GAT	966
Gly Gly Ser Ala Ser Ala Ser Glu Ile Val Ala Gly Ala Leu Gln Asp	
300 305 310	
CAC AAA CGG GCC GTG ATT ATC GGT GAA AAA ACC TTT GGT AAG GGA AGC	1014
His Lys Arg Ala Val Ile Ile Gly Glu Lys Thr Phe Gly Lys Gly Ser	
315 320 325	
GTG CAG ATG CTG CTC CCT GTC AAT AAA GAC GAA GCC ATT AAA ATC ACA	1062
Val Gln Met Leu Leu Pro Val Asn Lys Asp Glu Ala Ile Lys Ile Thr	
330 335 340	

Tyr Lys Ile Leu Thr Pro His Glu Gln Ile Gly Trp Val Lys Lys Asp
 370 375 380
 Glu Val Lys
 385

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1395
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

TTCTAATCTC AAAAATGGGT GGTGTTATTA ACA ATG ACA AAA CGA CTT TTT AAA	54
Met Thr Lys Arg Leu Phe Lys	
1 5	
GGG TTG TTA GCG GTT TCT CTT GCT GTG AGT TTG CAT GGT GGT GAA GTT	102
Gly Leu Leu Ala Val Ser Leu Ala Val Ser Leu His Gly Gly Glu Val	
10 15 20	
AAG GAA AAA AAG CCG GTT AAG CCG GTT AAA GAA GAT CCG CAA GAA TTA	150
Lys Glu Lys Lys Pro Val Lys Pro Val Lys Glu Asp Pro Gln Glu Leu	
25 30 35	
GCG GCT AAA AGG GTG GAA GCG TTC AGT CGT TTC TCT AAT GTG GTT TCA	198
Ala Ala Lys Arg Val Glu Ala Phe Ser Arg Phe Ser Asn Val Val Ser	
40 45 50 55	
GAA ATT GAA AAA AAA TAT GTG GAT AAA ATC AGC ATT TCT GAG ATC ATG	246
Glu Ile Glu Lys Lys Tyr Val Asp Lys Ile Ser Ile Ser Glu Ile Met	
60 65 70	
ACT AAA GCG ATT GAA GGC TTG CTC TCT AAT TTG GAC GCG CAT TCA GCG	294
Thr Lys Ala Ile Glu Gly Leu Leu Ser Asn Leu Asp Ala His Ser Ala	
75 80 85	
TAT TTG AAT GAA AAG AAG TTT AAG GAA TTT CAA GCC CAA ACC GAG GGC	342
Tyr Leu Asn Glu Lys Lys Phe Lys Glu Phe Gln Ala Gln Thr Glu Gly	
90 95 100	
GAA TTT GGG GGG CTT GGG ATC ACG GTG GGC ATG CGC GAT GGC GTT TTA	390
Glu Phe Gly Gly Leu Gly Ile Thr Val Gly Met Arg Asp Gly Val Leu	
105 110 115	

- (A) LENGTH: 387 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

```

Met Gly Phe Leu Phe Glu Lys Ser Leu Met Ser Phe Phe Ala His Pro
 1           5           10           15
Ile Lys Ile Leu Lys Ile Ile Ser Leu Ile Leu Ser Phe Leu Val Ser
          20           25           30
Phe Leu Val Ala Glu Asn Ala His Glu Pro Glu Glu Ile Lys Ala Lys
          35           40           45
Val Ala Tyr Val Lys Ile Pro Gln Leu Glu Asp Leu Glu Asn Asn Pro
          50           55           60
Val Tyr Ile Gly Gln Ile Ile Gly Val Thr Tyr Asp Leu Leu Leu Phe
65           70           75           80
Asp Ala Glu Phe Leu Glu Ala Lys Ile Lys Asp Gly Leu Asp Lys Thr
          85           90           95
Gln Ile Glu Leu Leu Asn Lys Met Pro Lys Trp Lys Lys Val Glu Lys
          100          105          110
Glu Leu Phe Arg Ala Thr Tyr Tyr Lys Ile Lys Gly Ile Lys Ala
          115          120          125
Ile Ile Pro Ser Leu Glu Val Ser Ala Phe Ser Asn Lys Asp Lys Tyr
          130          135          140
Ile Asp His Ser Ile Ala Pro Lys Val Thr Leu Gln Val Thr Asp Leu
145          150          155          160
Ser Lys Asn Pro Arg Tyr Ala Asn Val Met Ala Lys Asp Leu Gln Val
          165          170          175
Leu Gln Tyr Lys Thr Lys Asp Tyr Asp Asp Lys Asn Asn Ile Leu Val
          180          185          190
Met Glu Ile Ala Phe Lys Glu Ala Thr Trp Glu Asp Phe His Ile Lys
          195          200          205
Glu Ala Ile Lys Gln Gly Phe Asp Asn Ala Ser Leu Asn Gln Ile Lys
          210          215          220
Ala Lys Glu Gly Ser Val Phe Tyr Tyr Cys Val Leu Pro Lys Thr Ile
225          230          235          240
Gln Asn Leu Ser Phe Asp Tyr Phe Ser Leu Ser Asn Lys Gln Phe Lys
          245          250          255
Thr Leu Ser Phe Ser Thr Ile Pro Thr Gln Asp Thr Thr Gly Ile Gln
          260          265          270
Ser Asp Leu Ile Pro Lys Asn Asn Phe Leu Val Phe Ser Asn Val Ala
          275          280          285
Leu Leu Ala Leu Cys Val Phe Phe Leu Val Leu Phe Phe Ile Phe Gly
          290          295          300
Arg Lys Leu Ile Phe Leu Gly Leu Gly Ile Leu Cys Leu Gly Phe Val
305          310          315          320
Leu Tyr His Leu Leu Phe Thr Gln Lys Ser Ala Leu Leu Leu Ala His
          325          330          335
Lys Lys Ile Arg Ile Leu Pro Thr Gln Asn Ser Thr Ile Leu Gly Leu
          340          345          350
Ser Lys Asn Glu Met Pro Ile Lys Ile Leu Gly Ser His Asp Asp Tyr
          355          360          365

```

190	195	200	
GAT TTT CAC ATC AAA GAA GCG ATC AAG CAA GGG TTT GAT AAC GCC TCT			675
Asp Phe His Ile Lys Glu Ala Ile Lys Gln Gly Phe Asp Asn Ala Ser			
205	210	215	
TTA AAC CAG ATC AAG GCT AAA GAA GGG AGC GTT TTT TAT TAT TGC GTG			723
Leu Asn Gln Ile Lys Ala Lys Glu Gly Ser Val Phe Tyr Tyr Cys Val			
220	225	230	235
TTG CCT AAG ACT ATT CAA AAC CTT TCT TTT GAT TAT TTC TCG CTT TCA			771
Leu Pro Lys Thr Ile Gln Asn Leu Ser Phe Asp Tyr Phe Ser Leu Ser			
240	245	250	
AAT AAG CAA TTT AAA ACC TTA TCT TTT TCA ACC ATT CCC ACT CAA GAC			819
Asn Lys Gln Phe Lys Thr Leu Ser Phe Ser Thr Ile Pro Thr Gln Asp			
255	260	265	
ACT ACC GGT ATT CAA AGC GAT CTC ATC CCT AAA AAC AAT TTT TTA GTC			867
Thr Thr Gly Ile Gln Ser Asp Leu Ile Pro Lys Asn Asn Phe Leu Val			
270	275	280	
TTT TCT AAT GTG GCG TTG CTC GCT TTG TGC GTG TTT TTC TTG GTG CTG			915
Phe Ser Asn Val Ala Leu Leu Ala Leu Cys Val Phe Phe Leu Val Leu			
285	290	295	
TTT TTC ATT TTT GGG CGC AAA CTC ATT TTT TTA GGG CTT GGG ATT TTG			963
Phe Phe Ile Phe Gly Arg Lys Leu Ile Phe Leu Gly Leu Gly Ile Leu			
300	305	310	315
TGC TTA GGG TTT GTT TTG TAT CAC CTT TTA TTC ACG CAA AAA TCA GCC			1011
Cys Leu Gly Phe Val Leu Tyr His Leu Leu Phe Thr Gln Lys Ser Ala			
320	325	330	
CTA TTG CTC GCT CAT AAA AAA ATC CGC ATT CTG CCC ACG CAA AAT TCC			1059
Leu Leu Leu Ala His Lys Lys Ile Arg Ile Leu Pro Thr Gln Asn Ser			
335	340	345	
ACC ATT TTA GGG CTT TCT AAA AAT GAA ATG CCG ATT AAA ATC TTA GGC			1107
Thr Ile Leu Gly Leu Ser Lys Asn Glu Met Pro Ile Lys Ile Leu Gly			
350	355	360	
TCG CAT GAT GAT TAT TAT AAA ATC CTA ACG CCG CAT GAA CAA ATA GGA			1155
Ser His Asp Asp Tyr Tyr Lys Ile Leu Thr Pro His Glu Gln Ile Gly			
365	370	375	
TGG GTC AAA AAA GAT GAA GTC AAA TAAAAAGTCC AATCGTTTAA GAGCGATTAA			1209
Trp Val Lys Lys Asp Glu Val Lys			
380	385		
TAGAGCTTTA GTGATCGCTA TAGGACTAGC TGT			1242

(2) INFORMATION FOR SEQ ID NO:1058:

(i) --SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

AAGAAGAAAT	AAAAACTC	ATG	GGG	TTT	TTA	TTT	GAA	AAA	TCG	TTA	ATG	AGT	51
		Met	Gly	Phe	Leu	Phe	Glu	Lys	Ser	Leu	Met	Ser	
		1				5					10		
TTT	TTC	GCT	CAT	CCA	ATC	AAA	ATC	CTT	AAA	ATC	ATC	AGT	99
Phe	Phe	Ala	His	Pro	Ile	Lys	Ile	Leu	Lys	Ile	Ile	Ser	
		15					20					25	
AGT	TTT	TTG	GTA	AGC	TTT	TTG	GTT	GCT	GAA	AAC	GCT	CAT	147
Ser	Phe	Leu	Val	Ser	Phe	Leu	Val	Ala	Glu	Asn	Ala	His	
		30					35				40		
GAA	ATC	AAG	GCT	AAA	GTG	GCT	TAT	GTG	AAA	ATC	CCC	CAA	195
Glu	Ile	Lys	Ala	Lys	Val	Ala	Tyr	Val	Lys	Ile	Pro	Gln	
	45					50					55		
TTG	GAA	AAC	AAC	CCG	GTT	TAT	ATC	GGT	CAA	ATT	ATA	GGC	243
Leu	Glu	Asn	Asn	Pro	Val	Tyr	Ile	Gly	Gln	Ile	Ile	Gly	
60					65				70			75	
GAT	TTA	TTG	CTG	TTT	GAC	GCT	GAG	TTT	TTG	GAA	GCC	AAA	291
Asp	Leu	Leu	Leu	Phe	Asp	Ala	Glu	Phe	Leu	Glu	Ala	Lys	
				80					85			90	
GGG	TTG	GAT	AAA	ACC	CAA	ATT	GAG	CTT	TTA	AAC	AAG	ATG	339
Gly	Leu	Asp	Lys	Thr	Gln	Ile	Glu	Leu	Leu	Asn	Lys	Met	
			95					100				105	
AAA	AAG	GTG	GAA	AAA	GAG	CTT	TTC	AGA	GCG	ACT	TAT	TAT	387
Lys	Lys	Val	Glu	Lys	Glu	Leu	Phe	Arg	Ala	Thr	Tyr	Tyr	
		110					115				120		
AAG	GCG	ATA	AAA	GCG	ATT	ATT	CCG	TCC	TTA	GAA	GTG	AGC	435
Lys	Gly	Ile	Lys	Ala	Ile	Ile	Pro	Ser	Leu	Glu	Val	Ser	
	125					130				135			
AAT	AAA	GAC	AAA	TAC	ATA	GAT	CAT	TCC	ATA	GCC	CCA	AAA	483
Asn	Lys	Asp	Lys	Tyr	Ile	Asp	His	Ser	Ile	Ala	Pro	Lys	
140					145					150		155	
CAG	GTA	ACG	GAT	TTG	TCC	AAA	AAC	CCT	CGT	TAT	GCG	AAT	531
Gln	Val	Thr	Asp	Leu	Ser	Lys	Asn	Pro	Arg	Tyr	Ala	Asn	
				160					165			170	
AAA	GAT	TTA	CAA	GTC	TTG	CAA	TAC	AAA	ACC	AAA	GAT	TAT	579
Lys	Asp	Leu	Gln	Val	Leu	Gln	Tyr	Lys	Thr	Lys	Asp	Tyr	
		175					180					185	
AAC	AAT	ATT	TTG	GTG	ATG	GAA	ATA	GCG	TTC	AAA	GAA	GCC	627
Asn	Asn	Ile	Leu	Val	Met	Glu	Ile	Ala	Phe	Lys	Glu	Ala	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

```

Met Lys Leu Phe Asp Tyr Ala Pro Leu Ser Leu Ala Trp Arg Glu Phe
 1           5           10           15
Leu Gln Ser Glu Phe Lys Lys Pro Tyr Phe Leu Glu Ile Glu Lys Arg
      20           25           30
Tyr Leu Glu Ala Leu Lys Ile Pro Lys Thr Ile Phe Pro Lys Ser Ser
      35           40           45
Asn Leu Phe Tyr Ala Leu Asn Leu Thr Pro Pro Cys Ala Val Lys Ile
      50           55           60
Ile Leu Leu Gly Gln Asp Pro Tyr His Ser Thr Tyr Leu Glu Asn Asp
65           70           75           80
Gln Glu Leu Pro Val Ala Met Gly Leu Ser Phe Ser Val Glu Lys Asn
      85           90           95
Ala Pro Ile Pro Pro Ser Leu Lys Asn Ile Phe Lys Glu Leu His Ala
      100          105          110
Asn Leu Gly Val Pro Val Pro Cys Cys Gly Asp Leu Ser Ala Trp Ala
      115          120          125
Lys Arg Gly Met Leu Leu Leu Asn Ala Ile Leu Ser Val Glu Lys Asn
      130          135          140
Gln Ala Ala Ser His Gln Tyr Ile Gly Trp Glu Ala Phe Ser Asp Gln
      145          150          155          160
Ile Leu Met Arg Leu Phe Glu Thr Thr Ala Pro Leu Ile Val Val Leu
      165          170          175
Leu Gly Lys Val Ala Gln Lys Lys Ile Ala Leu Ile Pro Lys Asn Lys
      180          185          190
His Ile Ile Ile Thr Ala Pro His Pro Ser Pro Leu Ser Arg Gly Phe
      195          200          205
Leu Gly Ser Gly Val Phe Thr Ser Val Gln Lys Ala Tyr Arg Glu Val
      210          215          220
Tyr Arg Lys Asp Phe Asp Phe Ser Leu
      225          230

```

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1179
- (D) OTHER INFORMATION:

Phe	Leu	Glu	Ile	Glu	Lys	Arg	Tyr	Leu	Glu	Ala	Leu	Lys	Ile	Pro	Lys		
				30					35					40			
ACC	ATT	TTC	CCT	AAA	AGC	TCT	AAT	CTG	TTT	TAT	GCG	CTC	AAT	CTA	ACG		195
Thr	Ile	Phe	Pro	Lys	Ser	Ser	Asn	Leu	Phe	Tyr	Ala	Leu	Asn	Leu	Thr		
			45					50					55				
CCC	CCT	TGT	GCG	GTT	AAA	ATC	ATC	CTT	TTA	GGG	CAA	GAC	CCC	TAC	CAT		243
Pro	Pro	Cys	Ala	Val	Lys	Ile	Ile	Leu	Leu	Gly	Gln	Asp	Pro	Tyr	His		
		60					65					70					
TCC	ACC	TAC	CTA	GAA	AAT	GAT	CAA	GAA	TTG	CCG	GTG	GCG	ATG	GGG	TTG		291
Ser	Thr	Tyr	Leu	Glu	Asn	Asp	Gln	Glu	Leu	Pro	Val	Ala	Met	Gly	Leu		
	75					80					85						
AGC	TTT	AGC	GTG	GAA	AAA	AAC	GCC	CCT	ATT	CCT	CCA	AGT	TTA	AAA	AAT		339
Ser	Phe	Ser	Val	Glu	Lys	Asn	Ala	Pro	Ile	Pro	Pro	Ser	Leu	Lys	Asn		
90					95					100					105		
ATT	TTT	AAA	GAA	TTG	CAT	GCG	AAT	TTA	GGC	GTG	CCT	GTG	CCT	TGT	TGT		387
Ile	Phe	Lys	Glu	Leu	His	Ala	Asn	Leu	Gly	Val	Pro	Val	Pro	Cys	Cys		
				110					115					120			
GGG	GAT	TTG	AGC	GCA	TGG	GCT	AAA	AGG	GGC	ATG	CTC	TTA	TTG	AAC	GCC		435
Gly	Asp	Leu	Ser	Ala	Trp	Ala	Lys	Arg	Gly	Met	Leu	Leu	Leu	Asn	Ala		
			125					130					135				
ATT	TTA	AGC	GTG	GAA	AAA	AAC	CAA	GCC	GCT	TCG	CAC	CAA	TAT	ATT	GGC		483
Ile	Leu	Ser	Val	Glu	Lys	Asn	Gln	Ala	Ala	Ser	His	Gln	Tyr	Ile	Gly		
		140						145					150				
TGG	GAA	GCT	TTT	AGC	GAT	CAA	ATA	CTG	ATG	CGC	CTT	TTT	GAA	ACG	ACC		531
Trp	Glu	Ala	Phe	Ser	Asp	Gln	Ile	Leu	Met	Arg	Leu	Phe	Glu	Thr	Thr		
	155					160					165						
GCC	CCT	TTA	ATC	GTG	GTG	TTA	CTA	GGG	AAA	GTC	GCC	CAA	AAA	AAG	ATC		579
Ala	Pro	Leu	Ile	Val	Val	Leu	Leu	Gly	Lys	Val	Ala	Gln	Lys	Lys	Ile		
170					175					180					185		
GCG	TTA	ATC	CCC	AAA	AAC	AAA	CAC	ATC	ATC	ATC	ACA	GCC	CCT	CAC	CCT		627
Ala	Leu	Ile	Pro	Lys	Asn	Lys	His	Ile	Ile	Ile	Thr	Ala	Pro	His	Pro		
				190					195					200			
AGC	CCA	CTA	TCT	AGG	GGG	TTT	TTA	GGG	AGT	GGG	GTT	TTT	ACA	AGC	GTT		675
Ser	Pro	Leu	Ser	Arg	Gly	Phe	Leu	Gly	Ser	Gly	Val	Phe	Thr	Ser	Val		
			205					210					215				
CAA	AAA	GCT	TAT	AGA	GAG	GTT	TAT	CGC	AAG	GAT	TTT	GAT	TTT	AGT	TTA	T	724
Gln	Lys	Ala	Tyr	Arg	Glu	Val	Tyr	Arg	Lys	Asp	Phe	Asp	Phe	Ser	Leu		
		220					225					230					
GATTGATGCT	TAATGAGACA	GAACCCCTTA	AGAATGCCTT	TATTTAAGAG	CAT												777

(2) INFORMATION FOR SEQ ID NO:1056:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

```

Met Ser Val Ser His Val Ala Leu Ile Leu Arg Lys Leu Phe Tyr His
 1           5           10           15
Arg Gln Gly Val Phe Met Gly Gly Phe Ser Val Gly Met Leu Lys Asp
          20           25           30
Tyr Val Asp Ile Phe Val Phe Ala Val Leu Gly Val Ala Ser Phe Leu
          35           40           45
Ala Leu Trp Phe Ala Ile Glu Arg Val Ile Phe Tyr Ser Lys Val Asp
          50           55           60
Leu Lys Ala Tyr Asp Asp Ile Asp Ala Leu Asn Leu Asp Leu Thr Lys
65           70           75           80
Asn Leu Thr Ile Leu Tyr Val Ile Phe Ser Asn Ala Pro Tyr Val Gly
          85           90           95
Leu Leu Gly Thr Val Leu Gly Ile Met Val Ile Phe Tyr Asp Met Gly
          100          105          110
Val Ser Gly Gly Met Asp Ala Lys Thr Ile Met Val Gly Leu Ser Leu
          115          120          125
Ala Leu Lys Ala Thr Ala Leu Gly Leu Ala Val Ala Ile Pro Thr Leu
          130          135          140
Ile Ala Tyr Asn Ser Leu Leu Arg Lys Ser Asp Val Leu Ser Glu Lys
145          150          155          160
Phe Arg Ile Met Lys Lys
          165

```

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...723
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

```

TCATGAATTA AACCTAGCG AACA ATG AAG CTT TTT GAC TAC GCT CCT TTG      51
          Met Lys Leu Phe Asp Tyr Ala Pro Leu
          1           5

AGT TTG GCT TGG CGG GAG TTT TTG CAA AGC GAA TTT AAA AAG CCT TAT      99
Ser Leu Ala Trp Arg Glu Phe Leu Gln Ser Glu Phe Lys Lys Pro Tyr
10           15           20           25

TTT TTA GAA ATA GAA AAA CGC TAC CTA GAA GCC CTA AAA ATC CCT AAA      147

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

```

GCATGCTCTT AGAGT ATG TCT GTA TCG CAT GTT GCT TTA ATC TTA AGG AAA      51
      Met Ser Val Ser His Val Ala Leu Ile Leu Arg Lys
        1              5              10

TTG TTT TAT CAT AGA CAA GGA GTT TTT ATG GGC GGT TTT TCA GTG GGA      99
Leu Phe Tyr His Arg Gln Gly Val Phe Met Gly Gly Phe Ser Val Gly
      15              20              25

ATG TTG AAA GAT TAT GTG GAC ATA TTT GTT TTT GCG GTG CTT GGC GTG     147
Met Leu Lys Asp Tyr Val Asp Ile Phe Val Phe Ala Val Leu Gly Val
      30              35              40

GCC AGT TTT TTA GCT TTG TGG TTT GCG ATT GAA AGG GTT ATT TTT TAT     195
Ala Ser Phe Leu Ala Leu Trp Phe Ala Ile Glu Arg Val Ile Phe Tyr
      45              50              55              60

TCT AAA GTC GAT TTG AAA GCT TAT GAC GAT ATA GAT GCC CTG AAT TTG     243
Ser Lys Val Asp Leu Lys Ala Tyr Asp Asp Ile Asp Ala Leu Asn Leu
      65              70              75

GAT TTA ACC AAG AAT CTA ACC ATT CTC TAT GTG ATT TTT TCT AAC GCG     291
Asp Leu Thr Lys Asn Leu Thr Ile Leu Tyr Val Ile Phe Ser Asn Ala
      80              85              90

CCT TAT GTG GGC TTA TTA GGG ACG GTT TTA GGG ATT ATG GTG ATT TTC     339
Pro Tyr Val Gly Leu Leu Gly Thr Val Leu Gly Ile Met Val Ile Phe
      95              100              105

TAT GAC ATG GGC GTG AGC GGC GGG ATG GAC GCT AAA ACG ATC ATG GTA     387
Tyr Asp Met Gly Val Ser Gly Gly Met Asp Ala Lys Thr Ile Met Val
      110              115              120

GGT TTG TCT TTG GCT TTA AAA GCG ACC GCT CTA GGG CTT GCT GTG GCG     435
Gly Leu Ser Leu Ala Leu Lys Ala Thr Ala Leu Gly Leu Ala Val Ala
      125              130              135              140

ATT CCC ACT TTG ATC GCT TAT AAT AGC TTG TTG AGA AAA TCC GAT GTT     483
Ile Pro Thr Leu Ile Ala Tyr Asn Ser Leu Leu Arg Lys Ser Asp Val
      145              150              155

TTG AGC GAA AAA TTC AGG ATC ATG AAA AAA TGAAAAGCAT CAGAAGAGGC GAT     536
Leu Ser Glu Lys Phe Arg Ile Met Lys Lys
      160              165

GGGC                                                                    540

```

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

```

Met Ile Phe Tyr Arg Lys Glu Ala Thr Met Asn Ala Leu Lys Lys Leu
 1             5             10             15
Ser Phe Cys Ala Leu Leu Ser Leu Gly Leu Phe Ala Gln Thr Ala His
          20             25             30
Ala Lys His Leu Lys Gly Thr Ile Asn Tyr Pro Asp Trp Leu Glu Ile
          35             40             45
Asn Phe Phe Asp Glu Lys Asn Pro Pro Asn Gln Tyr Val Gly Ser Ala
          50             55             60
Ser Ile Ser Gly Lys Arg Asn Asp Phe Tyr Ala Asn Tyr Ile Pro Tyr
          65             70             75             80
Asp Asp Gln Leu Pro Pro Glu Gln Asn Ala Glu Lys Ile Ala Leu Leu
          85             90             95
Arg Ala Arg Ile Asn Ala Tyr Ser Thr Leu Glu Ser Ile Leu Leu Thr
          100            105            110
Lys Met His Asn Arg Ile Val Lys Val Leu Gln Val Lys Asn Asn Val
          115            120            125
Ile Ser His Leu Phe Gly Leu Val Asp Phe Leu Thr Ser Lys Ser Ile
          130            135            140
Leu Ala Lys Arg Phe Val Asp Thr Thr Asn His Arg Val Tyr Val Met
          145            150            155            160
Val Gln Phe Pro Phe Ile Gln Pro Glu Asp Leu Ile Ala Tyr Phe Lys
          165            170            175
Ala Lys Arg Ile Asp Leu Ser Ser Ala Ser Ala Thr His Leu Ser Ala
          180            185            190
Leu Leu Asn Lys Ala Leu Phe His Leu
          195            200

```

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...513
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

AAGCGTAGGG TGTTTTTA	ATG ATT TTT TAT AGA AAG GAA GCT ACA ATG AAC	51
	Met Ile Phe Tyr Arg Lys Glu Ala Thr Met Asn	
	1 5 10	
GCA TTG AAA AAA TTA AGT TTC TGC GCC TTG TTA TCC CTA GGC CTC TTC	99	
Ala Leu Lys Lys Leu Ser Phe Cys Ala Leu Leu Ser Leu Gly Leu Phe		
	15 20 25	
GCT CAA ACA GCG CAT GCT AAG CAT TTA AAG GGC ACG ATT AAC TAT CCT	147	
Ala Gln Thr Ala His Ala Lys His Leu Lys Gly Thr Ile Asn Tyr Pro		
	30 35 40	
GAT TGG CTT GAA ATC AAT TTT TTT GAC GAA AAA AAC CCG CCC AAT CAA	195	
Asp Trp Leu Glu Ile Asn Phe Phe Asp Glu Lys Asn Pro Pro Asn Gln		
	45 50 55	
TAT GTC GGA TCG GCT TCA ATT TCT GGT AAA AGG AAC GAT TTT TAC GCC	243	
Tyr Val Gly Ser Ala Ser Ile Ser Gly Lys Arg Asn Asp Phe Tyr Ala		
	60 65 70 75	
AAT TAC ATC CCC TAT GAT GAC CAA TTG CCC CCT GAA CAA AAC GCT GAA	291	
Asn Tyr Ile Pro Tyr Asp Asp Gln Leu Pro Pro Glu Gln Asn Ala Glu		
	80 85 90	
AAA ATC GCT CTT TTA AGG GCC AGA ATA AAC GCT TAC AGC ACT TTA GAG	339	
Lys Ile Ala Leu Leu Arg Ala Arg Ile Asn Ala Tyr Ser Thr Leu Glu		
	95 100 105	
AGC ATT TTA CTC ACT AAA ATG CAC AAT CGT ATT GTT AAG GTG CTT CAA	387	
Ser Ile Leu Leu Thr Lys Met His Asn Arg Ile Val Lys Val Leu Gln		
	110 115 120	
GTT AAA AAT AAT GTT ATC AGC CAT TTA TTC GGG CTT GTT GAT TTT TTA	435	
Val Lys Asn Asn Val Ile Ser His Leu Phe Gly Leu Val Asp Phe Leu		
	125 130 135	
ACC TCT AAA TCC ATT TTG GCT AAA AGG TTC GTG GAT ACC ACA AAT CAT	483	
Thr Ser Lys Ser Ile Leu Ala Lys Arg Phe Val Asp Thr Thr Asn His		
	140 145 150 155	
CGT GTG TAT GTC ATG GTG CAA TTC CCT TTC ATT CAG CCT GAA GAC TTG	531	
Arg Val Tyr Val Met Val Gln Phe Pro Phe Ile Gln Pro Glu Asp Leu		
	160 165 170	
ATC GCT TAC TTT AAA GCC AAA CGC ATC GAC CTT TCT TCA GCG AGC GCT	579	
Ile Ala Tyr Phe Lys Ala Lys Arg Ile Asp Leu Ser Ser Ala Ser Ala		
	175 180 185	
ACC CAT CTC AGC GCC CTT TTA AAT AAG GCG TTG TTC CAC CTC TAAGAGTTT	630	
Thr His Leu Ser Ala Leu Leu Asn Lys Ala Leu Phe His Leu		
	190 195 200	
GGGATTTAAG ATGCGGTTT	649	

CGT AAG GGT CTT CCT GTG AGA GGT CAA ACC ACT AAA AAT AAC GCT AGG 339
 Arg Lys Gly Leu Pro Val Arg Gly Gln Thr Thr Lys Asn Asn Ala Arg
 95 100 105

ACT CGT AAG GGT AAG AAA AAA ACC GTG GGT AGC AAG TAGCGAATAA GGAGAT 391
 Thr Arg Lys Gly Lys Lys Lys Thr Val Gly Ser Lys
 110 115 120

GATGATTTAA TGGCTAAGAG AAATGTAACG GC 423

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

Met	Ala	Arg	Ile	Ala	Gly	Val	Asp	Leu	Pro	Lys	Lys	Lys	Arg	Val	Glu	1	5	10	15
Tyr	Ala	Leu	Thr	Tyr	Ile	Tyr	Gly	Ile	Gly	Leu	Lys	Ser	Ser	Arg	Glu	20	25	30	
Ile	Leu	Glu	Ala	Val	Gly	Ile	Ser	Phe	Asp	Lys	Arg	Val	His	Glu	Leu	35	40	45	
Ser	Glu	Asp	Glu	Val	Ser	Ser	Ile	Ala	Lys	Lys	Ile	Gln	Gln	Ser	Tyr	50	55	60	
Leu	Val	Glu	Gly	Asp	Leu	Arg	Lys	Lys	Val	Gln	Met	Asp	Ile	Lys	Ser	65	70	75	80
Leu	Met	Asp	Leu	Gly	Asn	Tyr	Arg	Gly	Ile	Arg	His	Arg	Lys	Gly	Leu	85	90	95	
Pro	Val	Arg	Gly	Gln	Thr	Thr	Lys	Asn	Asn	Ala	Arg	Thr	Arg	Lys	Gly	100	105	110	
Lys	Lys	Lys	Thr	Val	Gly	Ser	Lys									115	120		

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...621
- (D) OTHER INFORMATION:

	260		265		270										
Cys	Leu	Asp	Lys	Ile	Gly	Ile	Lys	Tyr	Val	Gly	Glu	Leu	Val	Leu	Met
	275		280		285										
Ser	Glu	Glu	Glu	Leu	Lys	Gly	Val	Lys	Asn	Met	Gly	Lys	Lys	Ser	Tyr
	290		295		300										
Asp	Glu	Ile	Ala	Glu	Lys	Leu	Asn	Asp	Leu	Gly	Tyr	Pro	Val	Gly	Thr
	305		310		315										320
Glu	Leu	Ser	Pro	Glu	Gln	Arg	Glu	Ser	Leu	Lys	Lys	Arg	Leu	Glu	Lys
			325						330					335	
Leu	Glu	Asp	Lys	Gly	Gly	Asn	Asp								
			340												

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...375
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

AGACAAGGAT AAAGC ATG GCA AGG ATT GCT GGT GTA GAT TTA CCA AAA AAG	51
Met Ala Arg Ile Ala Gly Val Asp Leu Pro Lys Lys	
1 5 10	
AAG AGA GTG GAG TAT GCC CTT ACC TAT ATT TAT GGG ATT GGG CTT AAG	99
Lys Arg Val Glu Tyr Ala Leu Thr Tyr Ile Tyr Gly Ile Gly Leu Lys	
15 20 25	
AGT TCC AGA GAG ATT TTA GAA GCG GTA GGC ATT TCT TTT GAC AAG CGC	147
Ser Ser Arg Glu Ile Leu Glu Ala Val Gly Ile Ser Phe Asp Lys Arg	
30 35 40	
GTG CAT GAA TTG AGC GAA GAT GAA GTG TCT AGC ATC GCT AAA AAA ATC	195
Val His Glu Leu Ser Glu Asp Glu Val Ser Ser Ile Ala Lys Lys Ile	
45 50 55 60	
CAA CAA AGC TAC CTA GTA GAG GGC GAT TTG CGT AAA AAA GTT CAA ATG	243
Gln Gln Ser Tyr Leu Val Glu Gly Asp Leu Arg Lys Lys Val Gln Met	
65 70 75	
GAT ATT AAA TCT TTA ATG GAC TTG GGG AAT TAT CGT GGG ATC AGG CAT	291
Asp Ile Lys Ser Leu Met Asp Leu Gly Asn Tyr Arg Gly Ile Arg His	
-- 80 85 90	

CCG GTA GGC ACA GAA TTA AGC CCT GAA CAA AGA GAG AGT TTA AAG AAA 1012
 Pro Val Gly Thr Glu Leu Ser Pro Glu Gln Arg Glu Ser Leu Lys Lys
 320 325 330

AGA TTA GAA AAA TTA GAA GAT AAA GGA GGT AAC GAC TGATGAGACA CAAACA 1064
 Arg Leu Glu Lys Leu Glu Asp Lys Gly Gly Asn Asp
 335 340

CGGATACCGC AAGCTTGGGA GAACCAGCTC GCACAGAAAG GC 1106

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

Met	Lys	Val	Ile	Lys	Thr	Ala	Pro	Leu	Ile	Pro	Ser	Glu	Ile	Lys	Val	1	5	10	15
Leu	Glu	Lys	Glu	Gly	Asn	Arg	Val	Lys	Ile	Ser	Leu	Ala	Pro	Phe	Glu	20	25	30	
Phe	Gly	Tyr	Ala	Val	Thr	Leu	Ala	His	Pro	Ile	Arg	Arg	Leu	Leu	Leu	35	40	45	
Leu	Ser	Ser	Val	Gly	Tyr	Ala	Pro	Val	Gly	Leu	Lys	Ile	Glu	Gly	Val	50	55	60	
His	His	Glu	Phe	Asp	Ser	Leu	Arg	Gly	Val	Thr	Glu	Asp	Val	Ser	Leu	65	70	75	80
Phe	Ile	Met	Asn	Leu	Lys	Asn	Ile	Arg	Phe	Ile	Ala	Lys	Ala	Leu	Val	85	90	95	
Gly	Gln	Asp	Ser	Ser	Leu	Glu	Asn	Gln	Ser	Val	Val	Val	Asp	Tyr	Ser	100	105	110	
Phe	Lys	Gly	Pro	Met	Glu	Leu	Arg	Ala	Arg	Asp	Leu	Asn	Ser	Glu	Gln	115	120	125	
Ile	Glu	Ile	Val	Asn	Pro	Glu	Met	Pro	Leu	Ala	Thr	Ile	Asn	Glu	Asp	130	135	140	
Ala	Gln	Leu	Asn	Phe	Ser	Leu	Ile	Ile	Tyr	Lys	Gly	Met	Gly	Tyr	Val	145	150	155	160
Pro	Ser	Glu	Asn	Thr	Arg	Glu	Leu	Met	Pro	Glu	Gly	Tyr	Met	Pro	Leu	165	170	175	
Asp	Gly	Ser	Phe	Thr	Pro	Ile	Lys	Lys	Val	Val	Tyr	Glu	Ile	Glu	Asn	180	185	190	
Val	Leu	Val	Glu	Gly	Asp	Pro	Asn	Tyr	Glu	Lys	Ile	Ile	Phe	Asp	Ile	195	200	205	
Glu	Thr	Asp	Gly	Gln	Ile	Asp	Pro	Tyr	Lys	Ala	Phe	Leu	Ser	Ala	Val	210	215	220	
Lys	Val	Met	Ser	Lys	Gln	Leu	Gly	Val	Phe	Gly	Glu	Arg	Pro	Ile	Ala	225	230	235	240
Asn	Thr	Glu	Tyr	Ser	Gly	Asp	Tyr	Ala	Gln	Arg	Asp	Asp	Ala	Lys	Asp	245	250	255	
Leu	Ser	Ala	Lys	Ile	Glu	Ser	Met	Asn	Leu	Ser	Ala	Arg	Cys	Phe	Asn				

Lys	Ala	Leu	Val	Gly	Gln	Asp	Ser	Ser	Leu	Glu	Asn	Gln	Ser	Val	Val	
	95						100					105				
GTG	GAT	TAT	TCT	TTT	AAA	GGG	CCT	ATG	GAG	CTT	AGG	GCT	AGG	GAT	TTG	388
Val	Asp	Tyr	Ser	Phe	Lys	Gly	Pro	Met	Glu	Leu	Arg	Ala	Arg	Asp	Leu	
	110					115					120					
AAT	TCT	GAG	CAG	ATA	GAA	ATC	GTC	AAT	CCG	GAA	ATG	CCC	CTA	GCG	ACA	436
Asn	Ser	Glu	Gln	Ile	Glu	Ile	Val	Asn	Pro	Glu	Met	Pro	Leu	Ala	Thr	
	125				130					135					140	
ATC	AAT	GAA	GAC	GCT	CAA	TTG	AAT	TTT	TCG	CTC	ATT	ATT	TAT	AAA	GGA	484
Ile	Asn	Glu	Asp	Ala	Gln	Leu	Asn	Phe	Ser	Leu	Ile	Ile	Tyr	Lys	Gly	
				145					150					155		
ATG	GGG	TAT	GTC	CCA	AGC	GAA	AAC	ACA	AGG	GAA	TTG	ATG	CCT	GAG	GGC	532
Met	Gly	Tyr	Val	Pro	Ser	Glu	Asn	Thr	Arg	Glu	Leu	Met	Pro	Glu	Gly	
			160					165					170			
TAC	ATG	CCG	CTA	GAC	GGC	TCT	TTC	ACG	CCG	ATT	AAA	AAG	GTC	GTT	TAT	580
Tyr	Met	Pro	Leu	Asp	Gly	Ser	Phe	Thr	Pro	Ile	Lys	Lys	Val	Val	Tyr	
		175					180					185				
GAG	ATT	GAA	AAC	GTT	CTG	GTT	GAG	GGC	GAT	CCC	AAC	TAT	GAA	AAA	ATC	628
Glu	Ile	Glu	Asn	Val	Leu	Val	Glu	Gly	Asp	Pro	Asn	Tyr	Glu	Lys	Ile	
	190					195					200					
ATT	TTT	GAT	ATT	GAA	ACA	GAC	GGG	CAG	ATT	GAC	CCT	TAT	AAA	GCG	TTT	676
Ile	Phe	Asp	Ile	Glu	Thr	Asp	Gly	Gln	Ile	Asp	Pro	Tyr	Lys	Ala	Phe	
	205				210					215					220	
TTA	TCA	GCG	GTG	AAA	GTG	ATG	AGC	AAG	CAA	TTG	GGT	GTT	TTT	GGC	GAA	724
Leu	Ser	Ala	Val	Lys	Val	Met	Ser	Lys	Gln	Leu	Gly	Val	Phe	Gly	Glu	
				225					230					235		
AGA	CCC	ATT	GCT	AAC	ACG	GAG	TAT	TCA	GGC	GAT	TAC	GCT	CAA	AGA	GAT	772
Arg	Pro	Ile	Ala	Asn	Thr	Glu	Tyr	Ser	Gly	Asp	Tyr	Ala	Gln	Arg	Asp	
			240					245					250			
GAC	GCT	AAA	GAC	TTG	AGC	GCT	AAG	ATT	GAA	AGC	ATG	AAT	TTG	AGC	GCT	820
Asp	Ala	Lys	Asp	Leu	Ser	Ala	Lys	Ile	Glu	Ser	Met	Asn	Leu	Ser	Ala	
		255					260					265				
AGG	TGT	TTT	AAT	TGC	TTG	GAT	AAA	ATC	GGC	ATC	AAG	TAT	GTG	GGC	GAA	868
Arg	Cys	Phe	Asn	Cys	Leu	Asp	Lys	Ile	Gly	Ile	Lys	Tyr	Val	Gly	Glu	
	270					275					280					
CTC	GTG	TTG	ATG	AGC	GAA	GAA	GAG	CTT	AAG	GGC	GTG	AAA	AAC	ATG	GGT	916
Leu	Val	Leu	Met	Ser	Glu	Glu	Glu	Leu	Lys	Gly	Val	Lys	Asn	Met	Gly	
	285				290					295					300	
AAA	AAA	TCC	TAT	GAT	GAA	ATC	GCT	GAA	AAA	TTG	AAT	GAT	TTG	GGC	TAT	964
Lys	Lys	Ser	Tyr	Asp	Glu	Ile	Ala	Glu	Lys	Leu	Asn	Asp	Leu	Gly	Tyr	
				305					310					315		

130		135		140	
Gln	Ile	Ser	Leu	Phe	Ser
145		150		155	
Asn	Leu	Lys	Tyr	Pro	Leu
		165		170	
Gly	Ser	Leu	Asn	Glu	Ala
		180		185	
Pro	Lys	Ser	Val	Val	Leu
		195		200	

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...1048
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

AGTAAGGGGT TAGAGC ATG AAA GTT ATC AAA ACA GCA CCT TTG ATC CCA TCA	52
Met Lys Val Ile Lys Thr Ala Pro Leu Ile Pro Ser	
1 5 10	
GAA ATT AAG GTG CTA GAG AAA GAG GGC AAT CGG GTT AAG ATT TCT CTG	100
Glu Ile Lys Val Leu Glu Lys Glu Gly Asn Arg Val Lys Ile Ser Leu	
15 20 25	
GCT CCA TTT GAG TTT GGT TAC GCT GTT ACG CTC GCT CAT CCT ATT AGA	148
Ala Pro Phe Glu Phe Gly Tyr Ala Val Thr Leu Ala His Pro Ile Arg	
30 35 40	
AGG CTC TTG CTT TTA AGC TCT GTG GGG TAT GCT CCT GTA GGT TTA AAG	196
Arg Leu Leu Leu Leu Ser Ser Val Gly Tyr Ala Pro Val Gly Leu Lys	
45 50 55 60	
ATT GAA GGC GTC CAT CAT GAG TTT GAC TCT TTA AGG GGG GTT ACT GAA	244
Ile Glu Gly Val His His Glu Phe Asp Ser Leu Arg Gly Val Thr Glu	
65 70 75	
GAC GTG TCG CTT TTT ATC ATG AAT TTA AAA AAT ATC CGC TTT ATA GCC	292
Asp Val Ser Leu Phe Ile Met Asn Leu Lys Asn Ile Arg Phe Ile Ala	
80 85 90	
AAG GCG TTA GTG GGG CAG GAT AGC TCT TTA GAA AAC CAA TCG GTT GTG	340

```

TTA TTG TTG GAA TAT TTT AAA TTT TGC CAA AAA ATC CAA GCC ATA AGC      387
Leu Leu Leu Glu Tyr Phe Lys Phe Cys Gln Lys Ile Gln Ala Ile Ser
    110                      115                      120

GAC TAT GGT CTT TTT AGG GTG TTA GAA ACC CCT TTC ACT TTG CCC AGT      435
Asp Tyr Gly Leu Phe Arg Val Leu Glu Thr Pro Phe Thr Leu Pro Ser
    125                      130                      135                      140

TTT AAA GGG GAA CAA ATC TCG CTT TTT AGC CTG GAT CTT AAA GCC CAA      483
Phe Lys Gly Glu Gln Ile Ser Leu Phe Ser Leu Asp Leu Lys Ala Gln
                      145                      150                      155

TTC ACT TCT AAA AAC CTC AAA TAC CCC TTA AAA AAC TTG CGT TTA AAA      531
Phe Thr Ser Lys Asn Leu Lys Tyr Pro Leu Lys Asn Leu Arg Leu Lys
                      160                      165                      170

ACG CTC TTT TCT GGC TCG CTC AAT GAA GCT ACA GAT AGT TAT TTT AGC      579
Thr Leu Phe Ser Gly Ser Leu Asn Glu Ala Thr Asp Ser Tyr Phe Ser
    175                      180                      185

CTT AGC TCT ACA CCT AAA TCG GTG GTG TTG GTG TAT CAA AAA TTC TTA T      628
Leu Ser Ser Thr Pro Lys Ser Val Val Leu Val Tyr Gln Lys Phe Leu
    190                      195                      200

AAGCGGGTTT TGTTAGGCAA GTTTTTGTCT GTATA                                663

```

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

```

Met Gln Ala Val Ile Leu Ala Asn Gly Glu Phe Pro Lys Ser Gln Lys
 1      5      10      15
Cys Leu Asp Leu Lys Asn Ala Pro Phe Leu Ile Ala Cys Asp Gly
 20      25      30
Ala Val Thr Ser Leu His Ala Leu Gln Phe Lys Pro Ser Val Val Ile
 35      40      45
Gly Asp Leu Asp Ser Ile Asp Ser His Leu Lys Ala Leu Tyr Asn Pro
 50      55      60
Ile Arg Met Ser Glu Gln Asn Ser Asn Asp Leu Ser Lys Ala Phe Phe
 65      70      75      80
Tyr Ala Leu Asn Lys Gly Cys Asp Asp Phe Ile Phe Leu Gly Leu Asn
 85      90      95
Gly Lys Arg Glu Asp His Ala Leu Ala Asn Thr Phe Leu Leu Leu Glu
 100     105     110
Tyr Phe Lys Phe Cys Gln Lys Ile Gln Ala Ile Ser Asp Tyr Gly Leu
 115     120     125
Phe Arg Val Leu Glu Thr Pro Phe Thr Leu Pro Ser Phe Lys Gly Glu

```

```

Ile Ser Lys Tyr Thr His Asn Leu Asp Gly Gln Met Phe Ala Leu Phe
  50                      55                      60
Ile Ile Ser Ile Ala Ala Ser Glu Val Ala Ile Gly Leu Gly Leu Val
65                      70                      75                      80
Ile Leu Trp Phe Lys Lys Phe Lys Ser Leu Asp Ile Asp Ser Leu Asn
                      85                      90                      95
Ala Met Lys Gly
                      100

```

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...627
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

```

CCGGTGAAT AAGTC ATG CAA GCA GTG ATT TTA GCG AAT GGG GAG TTT CCT      51
      Met Gln Ala Val Ile Leu Ala Asn Gly Glu Phe Pro
      1                      5                      10

AAA TCT CAA AAA TGC TTA GAC CTT TTA AAA AAC GCT CCC TTT TTA ATC      99
Lys Ser Gln Lys Cys Leu Asp Leu Leu Lys Asn Ala Pro Phe Leu Ile
      15                      20                      25

GCA TGC GAT GGG GCT GTT ACC TCA TTA CAT GCG CTT CAA TTC AAA CCC      147
Ala Cys Asp Gly Ala Val Thr Ser Leu His Ala Leu Gln Phe Lys Pro
      30                      35                      40

AGC GTT GTT ATA GGC GAT CTA GAT AGC ATT GAT TCG CAT TTG AAA GCT      195
Ser Val Val Ile Gly Asp Leu Asp Ser Ile Asp Ser His Leu Lys Ala
      45                      50                      55                      60

TTG TAT AAC CCT ATA CGC ATG AGT GAA CAA AAC AGC AAC GAT TTG TCC      243
Leu Tyr Asn Pro Ile Arg Met Ser Glu Gln Asn Ser Asn Asp Leu Ser
      65                      70                      75

AAA GCC TTT TTT TAT GCT TTA AAT AAA GGC TGT GAT GAC TTT ATT TTT      291
Lys Ala Phe Phe Tyr Ala Leu Asn Lys Gly Cys Asp Asp Phe Ile Phe
      80                      85                      90

TTA GGG TTG AAT GGC AAG CGA GAA GAT CAC GCT TTA GCG AAC ACT TTT      339
Leu Gly Leu Asn Gly Lys Arg Glu Asp His Ala Leu Ala Asn Thr Phe
      95                      100                      105

```


(B) LOCATION: 44...343
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

```

AAATCCATGG GAAAAATCAC ACGCAATTTA TAAAGGAATC TCT ATG ATA GGG TTA      55
                               Met Ile Gly Leu
                               1

AAC CAC TAT TTG ATT GTT TCA GGG TTG CTC TTT TGC ATT GGT TTA GCG      103
Asn His Tyr Leu Ile Val Ser Gly Leu Leu Phe Cys Ile Gly Leu Ala
  5              10              15              20

GGC ATG CTG AAA CGC AAA AAC ATT CTG TTA CTC TTT TTT TCT ACA GAA      151
Gly Met Leu Lys Arg Lys Asn Ile Leu Leu Leu Phe Phe Ser Thr Glu
              25              30              35

ATC ATG CTC AAT GCG ATC AAT ATC GGT TTT GTA GCG ATC TCT AAA TAC      199
Ile Met Leu Asn Ala Ile Asn Ile Gly Phe Val Ala Ile Ser Lys Tyr
              40              45              50

ACG CAT AAT TTA GAC GGG CAG ATG TTT GCG CTC TTT ATT ATC TCT ATT      247
Thr His Asn Leu Asp Gly Gln Met Phe Ala Leu Phe Ile Ile Ser Ile
              55              60              65

GCC GCT AGT GAG GTG GCT ATT GGT TTG GGC TTG GTG ATT TTG TGG TTT      295
Ala Ala Ser Glu Val Ala Ile Gly Leu Gly Leu Val Ile Leu Trp Phe
  70              75              80

AAG AAA TTC AAA AGC TTA GAT ATT GAT TCT TTA AAC GCT ATG AAA GGT T      344
Lys Lys Phe Lys Ser Leu Asp Ile Asp Ser Leu Asn Ala Met Lys Gly
  85              90              95              100

GAGCATGCAA TATTCTTCTT TGCTGTCA GTG GGTG      378

```

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

```

Met Ile Gly Leu Asn His Tyr Leu Ile Val Ser Gly Leu Leu Phe Cys
  1              5              10              15
Ile Gly Leu Ala Gly Met Leu Lys Arg Lys Asn Ile Leu Leu Leu Phe
              20              25              30
Phe Ser Thr Glu Ile Met Leu Asn Ala Ile Asn Ile Gly Phe Val Ala
  35              40              45

```

```

Glu Val Pro Thr Lys Thr Thr Tyr Leu Leu Leu Glu Glu Ala Gly Ile
      515                      520                      525
Asn Leu Glu Thr Tyr Glu Lys Ile Leu Ala Leu Leu Gln Lys Ser Asn
      530                      535                      540
Asn Thr Leu Leu Val Val Gly Glu Glu Ile Tyr Ser His Lys Gln Ala
545                      550                      555                      560
His Asn Ile Ala Lys Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile
      565                      570                      575
Lys Leu Ile Leu Ile Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser
      580                      585                      590
Ile Cys Gln Leu Ser Glu Glu Ile Phe Glu His Glu Lys Ile Val Gly
      595                      600                      605
Ile Arg Ala Gln Gly Asp Phe Thr Ile Asn Ser Asp Asp Arg Val Phe
      610                      615                      620
Gly Lys Asp Ala Ala Ser Lys Val Asp Phe Ile Leu Pro Ser Leu Asn
625                      630                      635                      640
Gln Leu Glu Gly Thr Ile Thr Asn Ile Glu Gly Arg Val Leu Pro Leu
      645                      650                      655
Lys Pro Ala Leu Arg Phe Glu Gly Tyr Asp Leu Ser Asp Ile Met Gln
      660                      665                      670
Gly Phe Gly Phe Val Glu Glu Asn Leu Ile Glu Cys Thr His Lys Leu
      675                      680                      685
Pro Thr Glu Ala Gly Phe Lys Ala Ile Glu Phe Asp Tyr Leu Thr Asn
      690                      695                      700
Tyr Phe Ala Asn Asp Arg Val Asn His Arg Gly Tyr Leu Leu Gly Thr
705                      710                      715                      720
Ser His Phe Glu Lys Ser Ala Lys Glu Cys Glu Thr Ile Glu Cys Glu
      725                      730                      735
Pro Ile Lys Pro Leu Lys Glu Lys Ile Ala Phe Asn Ala Tyr Leu Lys
      740                      745                      750
Tyr Pro Glu Thr Gln Phe Asn Asn Ala Thr Asn Lys Ser Glu Asn Leu
      755                      760                      765
Gln Leu Lys Ala Gly Val Tyr Val Ser Lys Ala Phe Leu Lys Lys Leu
      770                      775                      780
Asn Lys Glu Val Gly Gln Asn Ile Thr Leu Ser Lys Glu Glu Glu Glu
785                      790                      795                      800
Leu Thr Gly Val Leu Tyr Leu Asp Glu Ser Leu Asp Gln Glu Val Phe
      805                      810                      815
Val Ile Ser Pro Ser Leu Leu Lys Asn His Ser Gly Phe Phe Arg Glu
      820                      825                      830
Gly Val Phe Asp Ser Val Asp Leu Lys Glu Gln Ala
      835                      840

```

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

65					70					75				80
Arg	Lys	Ser	Ile	Met	Gln	Thr	Tyr	Asp	Val	Asn	His	Pro	Leu	Glu Cys
				85					90					95
Gly	Val	Cys	Asp	Lys	Ser	Gly	Glu	Cys	Glu	Leu	Gln	Asp	Met	Thr His
			100					105					110	
Leu	Thr	Gly	Val	Glu	His	Gln	Pro	Tyr	Ala	Val	Ala	Asp	Asp	Phe Lys
		115					120					125		
Ala	Leu	Asp	Phe	Trp	Ala	Lys	Ala	Leu	Tyr	Asp	Pro	Asn	Leu	Cys Ile
	130					135					140			
Met	Cys	Glu	Arg	Cys	Val	Thr	Thr	Cys	Lys	Asp	Asn	Val	Gly	Glu Asn
145					150					155				160
Asn	Leu	Lys	Ala	Thr	Lys	Ala	Asp	Leu	His	Ala	Pro	Asp	Lys	Phe Lys
				165					170					175
Asp	Ser	Met	Ser	Lys	Asp	Ala	Phe	Ser	Val	Trp	Ser	Arg	Lys	Gln Lys
			180					185					190	
Gly	Ile	Ile	Ser	Phe	Val	Gly	Ser	Val	Pro	Cys	Tyr	Asp	Cys	Gly Glu
		195					200					205		
Cys	Ile	Ala	Val	Cys	Pro	Val	Gly	Ala	Leu	Ser	Tyr	Lys	Asp	Phe Ala
	210					215					220			
Tyr	Thr	Ala	Asn	Ala	Trp	Glu	Leu	Lys	Lys	Ile	His	Ser	Thr	Cys Ser
225					230					235				240
His	Cys	Ser	Ala	Gly	Cys	Leu	Ile	Ser	Tyr	Asp	Val	Arg	His	Phe Asp
				245					250					255
Thr	Leu	Gly	Glu	Glu	Ser	Lys	Ile	Phe	Arg	Val	Leu	Asn	Asp	Phe Tyr
			260					265					270	
His	Asn	Pro	Ile	Cys	Gly	Ala	Gly	Arg	Phe	Ala	Phe	Asp	Val	Ser Ser
	275						280					285		
Ser	Pro	Lys	Gly	Ser	Ala	Asn	Leu	Lys	Glu	Ala	Gln	Asn	Ala	Leu Lys
	290					295					300			
Glu	Cys	Glu	Ala	Val	Arg	Ile	Gly	Gly	Asp	Ile	Thr	Asn	Glu	Glu Ala
305					310					315				320
Phe	Leu	Ile	Glu	Arg	Leu	Arg	Lys	Glu	Leu	Asp	Phe	Lys	Ile	Tyr Asn
				325					330					335
Gln	Glu	Ala	Tyr	Arg	Phe	Gln	Gln	Phe	Leu	Lys	Val	Leu	Gly	Glu Ile
			340					345					350	
Lys	Arg	Pro	Ser	Val	Glu	Glu	Ile	Lys	Thr	Ser	His	Leu	Val	Val Thr
		355					360					365		
Ile	Gly	Ser	Ser	Ile	Lys	Thr	Glu	Asn	Pro	Leu	Val	Arg	Tyr	Ala Ile
	370					375					380			
Asn	Asn	Ala	Leu	Lys	Leu	Asn	Lys	Ala	Ser	Leu	Ile	Ala	Met	His Pro
385					390					395				400
Ile	Lys	Asp	Asn	Ala	Leu	Ala	Asn	Leu	Cys	Arg	Ser	Ser	Phe	Cys Ile
				405					410					415
Thr	His	Glu	Val	Gly	Ala	Glu	Glu	Ile	Leu	Leu	Gly	Met	Leu	Leu Lys
			420					425					430	
Met	Leu	Asn	Ile	Glu	Ser	Ala	Ala	Leu	Lys	Ser	Leu	Glu	Asp	Ser Lys
		435					440					445		
Gln	Asn	Ile	Val	Asp	Glu	Ala	Ala	Leu	Lys	Ala	Leu	Glu	Glu	Glu Arg
	450					455					460			
Lys	Lys	Ala	Leu	Glu	Gln	Ala	Glu	Gln	Gly	Cys	Ser	Ile	Gly	Glu Asn
465					470					475				480
Lys	Ala	Glu	Asn	Gln	Glu	Glu	Asn	Lys	Thr	Glu	Ala	Thr	Thr	Pro Lys
				485					490					495
Glu	Glu	Asn	Gln	Glu	Glu	Asn	Lys	Thr	Glu	Val	Lys	Glu	Glu	Lys Ile
			500					505					510	

```

GAA AAG AGC GCT AAA GAA TGC GAA ACC ATA GAA TGC GAG CCT ATC AAG      2265
Glu Lys Ser Ala Lys Glu Cys Glu Thr Ile Glu Cys Glu Pro Ile Lys
    725                      730                      735

CCT TTA AAA GAA AAA ATC GCT TTC AAC GCG TAT TTA AAA TAC CCA GAA      2313
Pro Leu Lys Glu Lys Ile Ala Phe Asn Ala Tyr Leu Lys Tyr Pro Glu
    740                      745                      750                      755

ACG CAA TTC AAT AAC GCT ACT AAT AAA AGC GAG AAT TTG CAA TTA AAA      2361
Thr Gln Phe Asn Asn Ala Thr Asn Lys Ser Glu Asn Leu Gln Leu Lys
                760                      765                      770

GCC GGT GTC TAT GTG TCT AAA GCT TTC TTA AAG AAA TTG AAT AAA GAA      2409
Ala Gly Val Tyr Val Ser Lys Ala Phe Leu Lys Lys Leu Asn Lys Glu
                775                      780                      785

GTG GGG CAA AAC ATC ACT TTA TCT AAA GAA GAA GAG GAA TTA ACA GGC      2457
Val Gly Gln Asn Ile Thr Leu Ser Lys Glu Glu Glu Glu Leu Thr Gly
                790                      795                      800

GTT TTG TAT CTT GAT GAG AGC TTG GAT CAG GAA GTG TTT GTT ATC TCG      2505
Val Leu Tyr Leu Asp Glu Ser Leu Asp Gln Glu Val Phe Val Ile Ser
    805                      810                      815

CCT TCT CTT TTG AAA AAC CAT TCT GGC TTT TTT AGA GAG GGC GTG TTT      2553
Pro Ser Leu Leu Lys Asn His Ser Gly Phe Phe Arg Glu Gly Val Phe
    820                      825                      830                      835

GAT AGC GTG GAT TTA AAG GAG CAA GCA TGAGCGCTTA TATCATTGAA ACCCTGA      2607
Asp Ser Val Asp Leu Lys Glu Gln Ala
                840

TTAAAATTTT GATTTT                                                    2623

```

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

```

Met Ile Thr Met Asn Ile Asn Gly Lys Thr Ile Glu Cys Gln Glu Gly
  1                      5                      10                      15
Gln Ser Val Leu Glu Ala Ala Arg Ser Ala Gly Ile Tyr Ile Pro Thr
                20                      25                      30
Ile Cys Tyr Leu Ser Gly Cys Ser Pro Thr Val Ala Cys Lys Met Cys
    35                      40                      45
Met Val Glu Met Asp Gly Lys Arg Val Tyr Ser Cys Asn Thr Lys Ala
    50                      55                      60
Lys Asn Asn Ala Thr Ile Leu Thr Asn Thr Pro Thr Leu Met Asp Glu

```

CAA GAA GAA AAC AAG ACA GAG GTT AAA GAA GAA AAA ATT GAA GTC CCT	1593
Gln Glu Glu Asn Lys Thr Glu Val Lys Glu Glu Lys Ile Glu Val Pro	
500 505 510 515	
ACC AAA ACC ACT TAT TTG CTG CTT GAA GAA GCG GGC ATC AAT TTA GAA	1641
Thr Lys Thr Thr Tyr Leu Leu Leu Glu Glu Ala Gly Ile Asn Leu Glu	
520 525 530	
ACT TAT GAA AAA ATT CTG GCT CTT TTG CAA AAA TCA AAT AAC ACC CTG	1689
Thr Tyr Glu Lys Ile Leu Ala Leu Leu Gln Lys Ser Asn Asn Thr Leu	
535 540 545	
CTA GTG GTT GGC GAA GAA ATC TAT AGC CAT AAG CAA GCC CAC AAT ATC	1737
Leu Val Val Gly Glu Glu Ile Tyr Ser His Lys Gln Ala His Asn Ile	
550 555 560	
GCT AAA ATG TTG CGT TTG CTA GCC CAA AAA AGC GCT ATT AAA CTC ATT	1785
Ala Lys Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile Lys Leu Ile	
565 570 575	
CTT ATC CCC CCA AGC GCC AAC GCT TTA GGC ATC GCT TCT ATT TGT CAA	1833
Leu Ile Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser Ile Cys Gln	
580 585 590 595	
TTG AGC GAA GAA ATT TTT GAA CAT GAA AAA ATT GTA GGC ATT CGC GCT	1881
Leu Ser Glu Glu Ile Phe Glu His Glu Lys Ile Val Gly Ile Arg Ala	
600 605 610	
CAA GGG GAT TTC ACT ATC AAT AGC GAT GAT AGG GTT TTT GGA AAA GAC	1929
Gln Gly Asp Phe Thr Ile Asn Ser Asp Asp Arg Val Phe Gly Lys Asp	
615 620 625	
GCT GCC AGC AAA GTG GAT TTT ATT TTA CCC AGT CTC AAC CAG CTA GAA	1977
Ala Ala Ser Lys Val Asp Phe Ile Leu Pro Ser Leu Asn Gln Leu Glu	
630 635 640	
GGC ACG ATC ACC AAT ATT GAA GGG CGT GTG TTG CCC TTA AAA CCG GCT	2025
Gly Thr Ile Thr Asn Ile Glu Gly Arg Val Leu Pro Leu Lys Pro Ala	
645 650 655	
TTG AGG TTT GAG GGC TAT GAT TTG AGC GAT ATT ATG CAA GGC TTT GGC	2073
Leu Arg Phe Glu Gly Tyr Asp Leu Ser Asp Ile Met Gln Gly Phe Gly	
660 665 670 675	
TTT GTG GAA GAA AAC CTC ATA GAA TGC ACC CAC AAA CTC CCT ACA GAA	2121
Phe Val Glu Glu Asn Leu Ile Glu Cys Thr His Lys Leu Pro Thr Glu	
680 685 690	
GCG GGC TTT AAA GCC ATA GAA TTT GAT TAT TTA ACC AAC TAT TTC GCT	2169
Ala Gly Phe Lys Ala Ile Glu Phe Asp Tyr Leu Thr Asn Tyr Phe Ala	
695 700 705	
AAC GAC AGA GTC AAC CAC AGA GGC TAT CTG CTA GGA ACA AGC CAT TTT	2217
Asn Asp Arg Val Asn His Arg Gly Tyr Leu Leu Gly Thr Ser His Phe	
710 715 720	

ATT TGT GGG GCA GGC CGT TTC GCT TTT GAT GTG AGC TCT AGC CCT AAA	921
Ile Cys Gly Ala Gly Arg Phe Ala Phe Asp Val Ser Ser Ser Pro Lys	
280 285 290	
GGC AGT GCT AAT CTT AAA GAA GCG CAA AAC GCC CTC AAA GAA TGC GAA	969
Gly Ser Ala Asn Leu Lys Glu Ala Gln Asn Ala Leu Lys Glu Cys Glu	
295 300 305	
GCG GTG CGA ATA GGT GGG GAT ATT ACG AAT GAA GAG GCG TTT TTA ATA	1017
Ala Val Arg Ile Gly Gly Asp Ile Thr Asn Glu Glu Ala Phe Leu Ile	
310 315 320	
GAG CGT TTA AGA AAA GAG CTT GAT TTT AAA ATC TAC AAT CAA GAA GCG	1065
Glu Arg Leu Arg Lys Glu Leu Asp Phe Lys Ile Tyr Asn Gln Glu Ala	
325 330 335	
TAT CGT TTC CAG CAA TTC TTA AAA GTA TTG GGC GAA ATT AAA CGC CCC	1113
Tyr Arg Phe Gln Gln Phe Leu Lys Val Leu Gly Glu Ile Lys Arg Pro	
340 345 350 355	
AGC GTT GAA GAG ATT AAA ACT TCT CAT TTA GTC GTT ACG ATA GGA TCT	1161
Ser Val Glu Glu Ile Lys Thr Ser His Leu Val Val Thr Ile Gly Ser	
360 365 370	
TCT ATC AAA ACA GAA AAC CCT TTG GTG CGC TAT GCC ATC AAT AAC GCT	1209
Ser Ile Lys Thr Glu Asn Pro Leu Val Arg Tyr Ala Ile Asn Asn Ala	
375 380 385	
CTC AAA CTC AAT AAA GCT TCT TTA ATC GCT ATG CAC CCT ATT AAG GAT	1257
Leu Lys Leu Asn Lys Ala Ser Leu Ile Ala Met His Pro Ile Lys Asp	
390 395 400	
AAC GCG CTA GCG AAT TTG TGC CGA AGC TCT TTT TGC ATC ACC CAT GAA	1305
Asn Ala Leu Ala Asn Leu Cys Arg Ser Ser Phe Cys Ile Thr His Glu	
405 410 415	
GTG GGG GCT GAA GAA ATC CTT TTA GGC ATG CTT TTA AAA ATG CTT AAC	1353
Val Gly Ala Glu Glu Ile Leu Leu Gly Met Leu Leu Lys Met Leu Asn	
420 425 430 435	
ATT GAA AGC GCG GCC CTA AAA AGC TTA GAA GAT TCC AAG CAA AAT ATT	1401
Ile Glu Ser Ala Ala Leu Lys Ser Leu Glu Asp Ser Lys Gln Asn Ile	
440 445 450	
GTA GAT GAA GCG GCT CTT AAA GCC TTA GAA GAA GAG CGA AAA AAA GCT	1449
Val Asp Glu Ala Ala Leu Lys Ala Leu Glu Glu Glu Arg Lys Lys Ala	
455 460 465	
TTA GAA CAA GCC GAG CAA GGG TGC AGT ATT GGA GAA AAT AAG GCA GAA	1497
Leu Glu Gln Ala Glu Gln Gly Cys Ser Ile Gly Glu Asn Lys Ala Glu	
470 475 480	
AAT CAA GAA GAG AAT AAA ACA GAA GCG ACT ACC CCA AAA GAA GAA AAT	1545
Asn Gln Glu Glu Asn Lys Thr Glu Ala Thr Thr Pro Lys Glu Glu Asn	
485 490 495	

ATG GAT GGC AAA CGG GTT TAT AGC TGC AAC ACG AAA GCC AAA AAC AAC	249
Met Asp Gly Lys Arg Val Tyr Ser Cys Asn Thr Lys Ala Lys Asn Asn	
55 60 65	
GCC ACC ATT CTC ACT AAC ACC CCA ACG CTC ATG GAT GAA AGA AAA AGC	297
Ala Thr Ile Leu Thr Asn Thr Pro Thr Leu Met Asp Glu Arg Lys Ser	
70 75 80	
ATC ATG CAA ACT TAT GAT GTC AAC CAC CCC CTA GAG TGT GGC GTG TGC	345
Ile Met Gln Thr Tyr Asp Val Asn His Pro Leu Glu Cys Gly Val Cys	
85 90 95	
GAT AAG AGT GGG GAG TGC GAA TTG CAA GAC ATG ACG CAT TTA ACC GGC	393
Asp Lys Ser Gly Glu Cys Glu Leu Gln Asp Met Thr His Leu Thr Gly	
100 105 110 115	
GTA GAG CAC CAA CCC TAT GCG GTG GCT GAT GAT TTT AAA GCA CTG GAT	441
Val Glu His Gln Pro Tyr Ala Val Ala Asp Asp Phe Lys Ala Leu Asp	
120 125 130	
TTT TGG GCA AAA GCC TTG TAT GAT CCT AAT TTG TGC ATC ATG TGT GAA	489
Phe Trp Ala Lys Ala Leu Tyr Asp Pro Asn Leu Cys Ile Met Cys Glu	
135 140 145	
AGG TGC GTA ACC ACT TGT AAG GAC AAT GTG GGC GAA AAC AAC CTT AAA	537
Arg Cys Val Thr Thr Cys Lys Asp Asn Val Gly Glu Asn Asn Leu Lys	
150 155 160	
GCC ACT AAA GCC GAC TTG CAT GCT CCG GAT AAA TTT AAA GAC AGC ATG	585
Ala Thr Lys Ala Asp Leu His Ala Pro Asp Lys Phe Lys Asp Ser Met	
165 170 175	
TCC AAA GAC GCT TTT AGC GTG TGG AGT CGT AAG CAA AAA GGC ATT ATT	633
Ser Lys Asp Ala Phe Ser Val Trp Ser Arg Lys Gln Lys Gly Ile Ile	
180 185 190 195	
TCT TTT GTG GGC AGC GTG CCT TGC TAT GAT TGC GGG GAA TGC ATT GCA	681
Ser Phe Val Gly Ser Val Pro Cys Tyr Asp Cys Gly Glu Cys Ile Ala	
200 205 210	
GTA TGC CCT GTG GGC GCT TTG AGC TAT AAA GAT TTC GCT TAC ACG GCT	729
Val Cys Pro Val Gly Ala Leu Ser Tyr Lys Asp Phe Ala Tyr Thr Ala	
215 220 225	
AAC GCA TGG GAG TTA AAA AAG ATC CAT TCT ACT TGT TCG CAT TGC TCG	777
Asn Ala Trp Glu Leu Lys Lys Ile His Ser Thr Cys Ser His Cys Ser	
230 235 240	
GCC GGG TGT TTG ATT TCT TAT GAT GTG CGC CAT TTT GAT ACT CTA GGC	825
Ala Gly Cys Leu Ile Ser Tyr Asp Val Arg His Phe Asp Thr Leu Gly	
245 250 255	
GAA GAA TCT AAA ATT TTT AGA GTG CTT AAT GAT TTT TAC CAT AAC CCT	873
Glu Glu Ser Lys Ile Phe Arg Val Leu Asn Asp Phe Tyr His Asn Pro	
260 265 270 275	

```

Lys Asn Arg Arg Arg Xaa Arg Val Lys Cys Val Leu Leu Pro Asn Glu
      115                      120                      125
Ser Val Asp Ser Leu Ser Phe Leu Tyr Arg Ser Ala Asn Trp Ser Glu
      130                      135                      140
Arg Glu Ala Tyr Asp Met Leu Gly Ile Val Phe Asp Lys His Pro Tyr
      145                      150                      155                      160
Leu Lys Arg Leu Ile Met Pro His Asp Trp Val Gly His Pro Leu Leu
      165                      170                      175
Arg Ser Tyr Pro Leu Lys Gly Asp Glu Phe Ala Gln Trp Tyr Glu Val
      180                      185                      190
Asp Lys Ile Phe Gly Lys Glu Tyr Arg Glu Val Val Gly Lys Glu Gln
      195                      200                      205
Arg Asp Ser Ala Arg Val Asp Glu Lys Asp Thr Phe Asn Phe Ala Lys
      210                      215                      220
Ile Gly Tyr Glu Gln Gly Lys Gly Glu Glu Leu Lys Glu Val Glu Glu
      225                      230                      235                      240
Lys His Ala Phe Lys Lys Ile Pro Phe Val Lys Asp Leu His Lys Ile
      245                      250                      255
Ala Pro Thr Ile Leu Lys Lys Arg Leu
      260                      265

```

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...2580
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

```

TGACGCTTAC CCTTATATCC CTATTTTATC CCACTCTCAA GGAATTTC ATG ATC ACA      57
                                     Met Ile Thr
                                     1

ATG AAT ATC AAT GGC AAA ACG ATT GAA TGC CAA GAG GGA CAA AGC GTT      105
Met Asn Ile Asn Gly Lys Thr Ile Glu Cys Gln Glu Gly Gln Ser Val
      5                      10                      15

TTA GAG GCT GCT AGG AGC GCT GGG ATC TAC ATC CCT ACC ATT TGC TAT      153
Leu Glu Ala Ala Arg Ser Ala Gly Ile Tyr Ile Pro Thr Ile Cys Tyr
      20                      25                      30                      35

TTA AGC GGT TGC TCG CCC ACA GTC GCA TGC AAA ATG TGC ATG GTT GAA      201
Leu Ser Gly Cys Ser Pro Thr Val Ala Cys Lys Met Cys Met Val Glu
      40                      45                      50

```



```

CCG CAT GAT TGG GTA GGC CAC CCA TTA TTG CGC TCT TAC CCG CTC AAA      582
Pro His Asp Trp Val Gly His Pro Leu Leu Arg Ser Tyr Pro Leu Lys
                170                      175                  180

GGC GAT GAA TTC GCC CAA TGG TAT GAA GTG GAT AAA ATT TTT GGT AAA      630
Gly Asp Glu Phe Ala Gln Trp Tyr Glu Val Asp Lys Ile Phe Gly Lys
                185                      190                  195

GAA TAC CGA GAA GTG GTG GGT AAA GAG CAG AGA GAC AGC GCA AGA GTG      678
Glu Tyr Arg Glu Val Val Gly Lys Glu Gln Arg Asp Ser Ala Arg Val
                200                      205                  210

GAT GAA AAA GAC ACT TTC AAT TTT GCA AAA ATT GGC TAT GAA CAG GGC      726
Asp Glu Lys Asp Thr Phe Asn Phe Ala Lys Ile Gly Tyr Glu Gln Gly
                215                      220                  225                  230

AAG GGC GAA GAA TTA AAA GAA GTA GAA GAA AAG CAT GCG TTT AAG AAA      774
Lys Gly Glu Glu Leu Lys Glu Val Glu Glu Lys His Ala Phe Lys Lys
                235                      240                  245

ATC CCT TTT GTC AAA GAT TTG CAC AAA ATC GCC CCC ACT ATC TTA AAA      822
Ile Pro Phe Val Lys Asp Leu His Lys Ile Ala Pro Thr Ile Leu Lys
                250                      255                  260

AAG AGG CTA TAAATGGCT CAAAATTTC ACGAACTCAA CCC                      864
Lys Arg Leu
                265

```

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

```

Met Val Arg Lys Gln Ser Pro Tyr Glu Asp Val Gln Lys Gln Ser Arg
 1          5          10          15
Gln His Asp Pro Tyr Lys Ile Ile Glu Pro Thr Pro Lys Lys Tyr Leu
 20          25          30
Glu Gly Ser Ala Tyr Glu Val Ile Tyr Asn His Leu Ser Tyr Lys His
 35          40          45
Glu Ile Leu Asp Lys Tyr Ile Glu Thr Asn Thr Ala Val Phe Trp Ile
 50          55          60
Lys Lys Asp Asp Ile Phe Ser Val Ala Thr Ile Leu Arg His Leu Gly
 65          70          75          80
Tyr Glu Cys Leu Ser Glu Met Ser Ala Ile Asp Leu Cys Ala Lys Lys
 85          90          95
Gly His Phe Glu Leu Phe Tyr Gln Phe Val Gly Phe Ser Asp Ser Cys
100          105          110

```

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 37...831
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

AGCGATCAAA CAAGACGCTC CCAAAAGGTT AGTGTG	ATG GTA AGA AAA CAA TCC	54
	Met Val Arg Lys Gln Ser	
	1 5	
CCC TAT GAA GAT GTG CAA AAA CAA TCG CGC CAG CAT GAC CCC TAT AAA	102	
Pro Tyr Glu Asp Val Gln Lys Gln Ser Arg Gln His Asp Pro Tyr Lys		
10 15 20		
ATC ATA GAA CCC ACC CCT AAA AAA TAT TTA GAG GGC AGC GCT TAT GAG	150	
Ile Ile Glu Pro Thr Pro Lys Lys Tyr Leu Glu Gly Ser Ala Tyr Glu		
25 30 35		
GTC ATT TAC AAC CAC CTT TCT TAC AAA CAT GAG ATT TTA GAC AAA TAC	198	
Val Ile Tyr Asn His Leu Ser Tyr Lys His Glu Ile Leu Asp Lys Tyr		
40 45 50		
ATA GAG ACT AAC ACG GCT GTG TTT TGG ATC AAA AAA GAC GAT ATT TTT	246	
Ile Glu Thr Asn Thr Ala Val Phe Trp Ile Lys Lys Asp Asp Ile Phe		
55 60 65 70		
TCT GTC GCT ACG ATT TTA AGG CAT TTG GGT TAT GAG TGT TTG AGC GAA	294	
Ser Val Ala Thr Ile Leu Arg His Leu Gly Tyr Glu Cys Leu Ser Glu		
75 80 85		
ATG AGC GCG ATA GAT TTG TGC GCT AAA AAA GGG CAT TTT GAA TTG TTT	342	
Met Ser Ala Ile Asp Leu Cys Ala Lys Lys Gly His Phe Glu Leu Phe		
90 95 100		
TAT CAG TTC GTG GGC TTT AGC GAT AGC TGC AAG AAC CGC CGT AGG NTG	390	
Tyr Gln Phe Val Gly Phe Ser Asp Ser Cys Lys Asn Arg Arg Arg Xaa		
105 110 115		
CGC GTG AAG TGC GTT TTG TTG CCT AAT GAG AGC GTG GAT TCT TTG AGT	438	
Arg Val Lys Cys Val Leu Leu Pro Asn Glu Ser Val Asp Ser Leu Ser		
120 125 130		
TTT TTA TAC CGA TCG GCT AAT TGG AGC GAA AGG GAA GCG TAT GAC ATG	486	
Phe Leu Tyr Arg Ser Ala Asn Trp Ser Glu Arg Glu Ala Tyr Asp Met		
135 140 145 150		
CTT GGT ATT GTG TTT GAC AAA CAC CCC TAT TTG AAA CGC CTT ATT ATG	534	
Leu Gly Ile Val Phe Asp Lys His Pro Tyr Leu Lys Arg Leu Ile Met		
155 160 165		

75	80	85	90	
GCG ATT GGT TTT AAA AAA TTA GGC TTG TTT GGA CTC GTT GAA ATG CTA				340
Ala Ile Gly Phe Lys Lys Leu Gly Leu Phe Gly Leu Val Glu Met Leu				
	95	100	105	
GGC TTT GTC TTC TTT TTA ACC ATT GGT TTT ATT TAC GCT TTA AAG CGA				388
Gly Phe Val Phe Phe Leu Thr Ile Gly Phe Ile Tyr Ala Leu Lys Arg				
	110	115	120	
AAC GCT TTG AGC TGG CAA AAA TTA GAG GTG AAA TAATGCAACA AGCACC GGTT				441
Asn Ala Leu Ser Trp Gln Lys Leu Glu Val Lys				
	125	130		
GTTCTAAGCA CTTTGGATAA ATTATTG				468

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

Met	Gln	Gln	Ala	Thr	Glu	Ala	Leu	Asn	His	Pro	Tyr	Phe	Gly	Val	Phe
1				5					10					15	
Val	Leu	Leu	Val	Phe	Thr	Phe	Trp	Val	Phe	Asn	Leu	Thr	Leu	Arg	Ile
			20					25					30		
Gln	Arg	Phe	Leu	Ser	Arg	Lys	Met	Ala	Gln	Lys	Lys	Gly	Glu	Lys	Leu
		35					40					45			
Lys	Leu	Ala	Pro	Tyr	Glu	Cys	Gly	Pro	Val	Ala	Leu	Lys	Gln	Pro	Asn
		50				55					60				
Arg	Val	Ser	His	His	Phe	Tyr	Ile	Met	Ala	Met	Leu	Phe	Ile	Leu	Phe
65					70				75					80	
Asp	Val	Glu	Ile	Val	Phe	Met	Phe	Pro	Trp	Ala	Ile	Gly	Phe	Lys	Lys
				85				90					95		
Leu	Gly	Leu	Phe	Gly	Leu	Val	Glu	Met	Leu	Gly	Phe	Val	Phe	Phe	Leu
			100				105						110		
Thr	Ile	Gly	Phe	Ile	Tyr	Ala	Leu	Lys	Arg	Asn	Ala	Leu	Ser	Trp	Gln
		115					120					125			
Lys	Leu	Glu	Val	Lys											
															130

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

			100					105					110			
Gln	Leu	Arg	Pro	Asp	Ile	Val	Trp	Phe	Gly	Glu	Ala	Val	Pro	Leu	Leu	
			115					120					125			
Lys	Glu	Ala	Ile	Ser	Leu	Val	Lys	Gln	Ala	His	Leu	Leu	Ile	Ile	Ile	
			130					135					140			
Gly	Thr	Ser	Leu	Gln	Val	Tyr	Pro	Ala	Ala	Ser	Leu	Tyr	Thr	His	Ala	
145					150					155					160	
His	Lys	Asp	Ala	Leu	Ile	Tyr	Tyr	Ile	Asp	Pro	Lys	Ala	Lys	Asn	Ala	
			165					170					175			
His	Leu	Pro	Gln	Asn	Val	Gln	Cys	Ile	Asn	Glu	Ser	Ala	Val	His	Ala	
			180					185					190			
Met	Gln	Asp	Leu	Met	Pro	Lys	Leu	Ile	Glu	Met	Ala	Ser				
		195					200					205				

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 23...421
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

ATTAAAGGAG	TTTGAGAGTC	TG	ATG	CAA	CAA	GCC	ACA	GAA	GCA	TTG	AAT	CAC				52
			Met	Gln	Gln	Ala	Thr	Glu	Ala	Leu	Asn	His				
			1				5					10				
CCC	TAT	TTT	GGC	GTT	TTT	GTT	TTA	TTG	GTA	TTC	ACC	TTT	TGG	GTG	TTT	100
Pro	Tyr	Phe	Gly	Val	Phe	Val	Leu	Leu	Val	Phe	Thr	Phe	Trp	Val	Phe	
			15						20					25		
AAC	TTA	ACC	TTA	AGG	ATC	CAA	AGG	TTT	TTA	AGC	CGT	AAA	ATG	GCT	CAA	148
Asn	Leu	Thr	Leu	Arg	Ile	Gln	Arg	Phe	Leu	Ser	Arg	Lys	Met	Ala	Gln	
			30					35					40			
AAA	AAG	GGC	GAA	AAG	CTC	AAG	CTC	GCT	CCC	TAT	GAA	TGC	GGG	CCT	GTG	196
Lys	Lys	Gly	Glu	Lys	Leu	Lys	Leu	Ala	Pro	Tyr	Glu	Cys	Gly	Pro	Val	
		45					50					55				
GCT	CTC	AAA	CAG	CCT	AAT	AGG	GTG	TCG	CAC	CAT	TTC	TAT	ATC	ATG	GCC	244
Ala	Leu	Lys	Gln	Pro	Asn	Arg	Val	Ser	His	His	Phe	Tyr	Ile	Met	Ala	
	60					65					70					
ATG	CTT	TTT	ATT	TTA	TTT	GAT	GTA	GAA	ATC	GTT	TTC	ATG	TTC	CCT	TGG	292
Met	Leu	Phe	Ile	Leu	Phe	Asp	Val	Glu	Ile	Val	Phe	Met	Phe	Pro	Trp	

GAA AAG GAC TTG AAT TTA GGC GAC TTG GCC AAA GAC AAA TCG CAA TTA	394
Glu Lys Asp Leu Asn Leu Gly Asp Leu Ala Lys Asp Lys Ser Gln Leu	
100 105 110	
CGC CCT GAT ATT GTG TGG TTT GGC GAA GCG GTG CCT TTG CTT AAA GAA	442
Arg Pro Asp Ile Val Trp Phe Gly Glu Ala Val Pro Leu Leu Lys Glu	
115 120 125 130	
GCG ATT TCT TTA GTC AAA CAA GCG CAT CTT TTA ATC ATC ATT GGC ACT	490
Ala Ile Ser Leu Val Lys Gln Ala His Leu Leu Ile Ile Ile Gly Thr	
135 140 145	
TCT TTG CAA GTC TAT CCC GCC GCT AGC CTC TAC ACG CAT GCG CAT AAA	538
Ser Leu Gln Val Tyr Pro Ala Ala Ser Leu Tyr Thr His Ala His Lys	
150 155 160	
GAC GCT CTC ATT TAT TAC ATT GAC CCT AAG GCT AAA AAC GCC CAT TTA	586
Asp Ala Leu Ile Tyr Tyr Ile Asp Pro Lys Ala Lys Asn Ala His Leu	
165 170 175	
CCC CAG AAT GTC CAA TGC ATT AAT GAA AGC GCG GTG CAT GCC ATG CAA	634
Pro Gln Asn Val Gln Cys Ile Asn Glu Ser Ala Val His Ala Met Gln	
180 185 190	
GAT TTA ATG CCC AAA CTC ATA GAA ATG GCT TCT TAAGAAATGT TAAAATAATT	687
Asp Leu Met Pro Lys Leu Ile Glu Met Ala Ser	
195 200 205	
TTTATTTT CAGCTAACGA TTAGCAAAAA	717

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

Met	Ala	Cys	Gly	Lys	Gly	His	Asp	Ile	Met	Glu	Val	Ala	Ser	Pro	Tyr
1				5					10					15	
Gly	Trp	Lys	Lys	Asn	Pro	Gln	Lys	Val	Leu	Asp	Phe	Tyr	Asn	Gln	Arg
		20						25					30		
Arg	Arg	Gln	Leu	Phe	Glu	Val	Tyr	Pro	Asn	Lys	Ala	His	Lys	Ala	Leu
		35					40					45			
Ala	Glu	Leu	Glu	Lys	His	Tyr	Gln	Val	Asn	Ile	Ile	Thr	Gln	Asn	Val
	50					55					60				
Asp	Asp	Leu	His	Glu	Arg	Ala	Gly	Ser	Ser	Arg	Ile	Leu	His	Leu	His
65					70					75				80	
Gly	Glu	Leu	Leu	Ser	Val	Arg	Ser	Glu	Lys	Asp	Pro	Asn	Leu	Val	Tyr
			85					90					95		
Arg	Trp	Glu	Lys	Asp	Leu	Asn	Leu	Gly	Asp	Leu	Ala	Lys	Asp	Lys	Ser

```

65          70          75          80
Leu Ser Met Gly Leu Leu Ile Gly Phe Val Thr Pro Phe Ile Phe Lys
          85          90          95
Phe Phe Leu His Asp Lys Leu Ser Gly Thr His Ile Glu Thr Ile Lys
          100          105          110
Glu Ala Thr
          115

```

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...667
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

```

AGCGGGGCTG GTATTTTCAGC AGAAAGCGGG ATTAAAACCT TTAGAGACGC TG ATG GCT      58
                               Met Ala
                               1

TGT GGG AAA GGG CAT GAC ATC ATG GAA GTT GCC TCG CCT TAT GGC TGG      106
Cys Gly Lys Gly His Asp Ile Met Glu Val Ala Ser Pro Tyr Gly Trp
      5              10              15

AAA AAG AAC CCG CAA AAG GTG TTG GAT TTT TAC AAC CAA AGG CGC CGA      154
Lys Lys Asn Pro Gln Lys Val Leu Asp Phe Tyr Asn Gln Arg Arg Arg
      20              25              30

CAG CTT TTT GAA GTT TAT CCT AAC AAA GCC CAT AAG GCT TTA GCG GAA      202
Gln Leu Phe Glu Val Tyr Pro Asn Lys Ala His Lys Ala Leu Ala Glu
      35              40              45              50

TTG GAA AAA CAC TAT CAA GTC AAT ATC ATC ACC CAA AAT GTA GAT GAT      250
Leu Glu Lys His Tyr Gln Val Asn Ile Ile Thr Gln Asn Val Asp Asp
              55              60              65

TTG CAT GAA AGA GCG GGT TCT TCT CGC ATT TTG CAC TTG CAT GGC GAA      298
Leu His Glu Arg Ala Gly Ser Ser Arg Ile Leu His Leu His Gly Glu
              70              75              80

TTA TTG AGC GTT CGC AGC GAG AAA GAT CCT AAT TTA GTT TAT AGG TGG      346
Leu Leu Ser Val Arg Ser Glu Lys Asp Pro Asn Leu Val Tyr Arg Trp
      85              90              95

```

```

CTCTCTTTGCGCCTAAAGGCCTTTATCACC GATATTTTT ATG ATT TAT ACC CCC      54
                               Met Ile Tyr Thr Pro
                               1             5

ATG CTT TAT ATA ATG ACT TAT GCG ATT TTA GGG AGC GCG AAG GAT TTT      102
Met Leu Tyr Ile Met Thr Tyr Ala Ile Leu Gly Ser Ala Lys Asp Phe
          10             15             20

AGG GAA AAC CAG AGC GCG ATT TTT TTA TGC CTG CTT TTT TAC GCC CTA      150
Arg Glu Asn Gln Ser Ala Ile Phe Leu Cys Leu Leu Phe Tyr Ala Leu
          25             30             35

ACA CAC AGC TTT TTT ATC GCT TTT AAA TCC CAA AGC CCT GGC ATG CGT      198
Thr His Ser Phe Phe Ile Ala Phe Lys Ser Gln Ser Pro Gly Met Arg
          40             45             50

TAC GCT CGG TTT AAA TTA ATC AAA AAT AAT GGC GAA AAA GTG GGC TTT      246
Tyr Ala Arg Phe Lys Leu Ile Lys Asn Asn Gly Glu Lys Val Gly Phe
          55             60             65

TTT TTA GCT TTG TGG CGC TTT GTT TTG TGG GTG TTG AGC ATG GGG TTA      294
Phe Leu Ala Leu Trp Arg Phe Val Leu Trp Val Leu Ser Met Gly Leu
          70             75             80             85

CTC ATA GGG TTT GTT ACG CCT TTT ATT TTT AAG TTT TTT TTG CAT GAC      342
Leu Ile Gly Phe Val Thr Pro Phe Ile Phe Lys Phe Phe Leu His Asp
          90             95             100

AAA CTC AGC GGC ACT CAT ATT GAA ACC ATC AAG GAG GCA ACA TGAAAAATT      393
Lys Leu Ser Gly Thr His Ile Glu Thr Ile Lys Glu Ala Thr
          105             110             115

TAGTAATC                                                                401

```

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

```

Met Ile Tyr Thr Pro Met Leu Tyr Ile Met Thr Tyr Ala Ile Leu Gly
 1             5             10             15
Ser Ala Lys Asp Phe Arg Glu Asn Gln Ser Ala Ile Phe Leu Cys Leu
          20             25             30
Leu Phe Tyr Ala Leu Thr His Ser Phe Phe Ile Ala Phe Lys Ser Gln
          35             40             45
Ser Pro Gly Met Arg Tyr Ala Arg Phe Lys Leu Ile Lys Asn Asn Gly
          50             55             60
Glu Lys Val Gly Phe Phe Leu Ala Leu Trp Arg Phe Val Leu Trp Val

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

```

Met Asp Ile Lys Ala Cys Tyr Gln Asn Ala Lys Ala Leu Leu Glu Gly
 1           5           10           15
His Phe Leu Leu Ser Ser Gly Phe His Ser Asn Tyr Tyr Leu Gln Ser
          20           25           30
Ala Lys Val Leu Glu Asp Pro Lys Leu Ala Glu Gln Leu Ala Leu Glu
          35           40           45
Leu Ala Lys Gln Ile Gln Glu Ala His Leu Asn Ile Glu Cys Val Cys
          50           55           60
Ser Pro Ala Ile Gly Gly Ile Leu Ala Gly Tyr Glu Leu Ala Arg Ala
65           70           75           80
Leu Gly Val Arg Phe Ile Phe Thr Glu Arg Val Asp Asn Thr Met Ala
          85           90           95
Leu Arg Arg Gly Phe Glu Val Lys Lys Asn Glu Lys Ile Leu Val Cys
          100          105          110
Glu Asp Ile Ile Thr Thr Gly Lys Ser Ala Met Glu Cys Ala Lys Val
          115          120          125
Leu Glu Glu Lys Gly Ala Gln Ile Val Ala Phe Gly Ala Leu Ala Asn
          130          135          140
Arg Gly Ile Cys Lys Arg Ala His Ser His Leu Lys Ala Gln Glu Gly
145          150          155          160
Ala Cys Leu Pro Ser His Leu Pro Leu Phe Ala Leu Glu Asp Phe Val
          165          170          175
Phe Asp Met His Lys Pro Ser Ser Cys Pro Leu Cys Ala Thr Ser Val
          180          185          190
Ala Ile Lys Pro Gly Ser Arg Gly Asn
          195          200

```

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...384
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

Met	Asp	Ile	Lys	Ala	Cys	Tyr	Gln	Asn	Ala	Lys	Ala					
1				5						10						
TTA	TTA	GAG	GGG	CAT	TTC	TTG	CTC	AGC	AGT	GGG	TTT	CAT	TCC	AAT	TAT	99
Leu	Leu	Glu	Gly	His	Phe	Leu	Leu	Ser	Ser	Gly	Phe	His	Ser	Asn	Tyr	
	15					20					25					
TAT	TTG	CAA	TCC	GCT	AAA	GTT	TTA	GAA	GAT	CCC	AAA	CTA	GCC	GAA	CAA	147
Tyr	Leu	Gln	Ser	Ala	Lys	Val	Leu	Glu	Asp	Pro	Lys	Leu	Ala	Glu	Gln	
	30				35					40						
TTA	GCG	CTA	GAA	TTA	GCC	AAA	CAA	ATC	CAA	GAA	GCT	CAT	TTG	AAT	ATT	195
Leu	Ala	Leu	Glu	Leu	Ala	Lys	Gln	Ile	Gln	Glu	Ala	His	Leu	Asn	Ile	
45					50					55				60		
GAA	TGC	GTG	TGC	TCA	CCG	GCT	ATT	GGG	GGG	ATT	TTG	GCT	GGG	TAT	GAG	243
Glu	Cys	Val	Cys	Ser	Pro	Ala	Ile	Gly	Gly	Ile	Leu	Ala	Gly	Tyr	Glu	
				65				70						75		
CTT	GCA	AGG	GCT	TTG	GGC	GTG	CGT	TTT	ATC	TTC	ACC	GAA	AGG	GTG	GAT	291
Leu	Ala	Arg	Ala	Leu	Gly	Val	Arg	Phe	Ile	Phe	Thr	Glu	Arg	Val	Asp	
		80						85						90		
AAT	ACC	ATG	GCG	TTA	AGG	CGT	GGC	TTT	GAA	GTC	AAA	AAA	AAC	GAA	AAA	339
Asn	Thr	Met	Ala	Leu	Arg	Arg	Gly	Phe	Glu	Val	Lys	Lys	Asn	Glu	Lys	
	95						100					105				
ATT	TTA	GTG	TGT	GAG	GAC	ATT	ATC	ACT	ACG	GGA	AAA	TCC	GCT	ATG	GAA	387
Ile	Leu	Val	Cys	Glu	Asp	Ile	Ile	Thr	Thr	Gly	Lys	Ser	Ala	Met	Glu	
	110					115					120					
TGC	GCT	AAA	GTT	TTA	GAA	GAA	AAG	GGT	GCT	CAA	ATC	GTG	GCT	TTT	GGT	435
Cys	Ala	Lys	Val	Leu	Glu	Glu	Lys	Gly	Ala	Gln	Ile	Val	Ala	Phe	Gly	
125					130					135				140		
GCT	TTA	GCT	AAT	CGG	GGC	ATT	TGC	AAG	CGT	GCT	CAT	TCT	CAT	TTA	AAA	483
Ala	Leu	Ala	Asn	Arg	Gly	Ile	Cys	Lys	Arg	Ala	His	Ser	His	Leu	Lys	
				145					150					155		
GCC	CAA	GAG	GGA	GCG	TGT	TTG	CCT	AGC	CAT	TTG	CCC	CTT	TTT	GCT	TTA	531
Ala	Gln	Glu	Gly	Ala	Cys	Leu	Pro	Ser	His	Leu	Pro	Leu	Phe	Ala	Leu	
			160						165					170		
GAA	GAT	TTT	GTT	TTT	GAC	ATG	CAC	AAG	CCT	AGT	TCT	TGC	CCT	TTA	TGC	579
Glu	Asp	Phe	Val	Phe	Asp	Met	His	Lys	Pro	Ser	Ser	Cys	Pro	Leu	Cys	
	175							180				185				
GCT	ACT	AGC	GTT	GCT	ATA	AAG	CCA	GGA	AGT	CGT	GGC	AAC	TAAAAAAACA	AA		630
Ala	Thr	Ser	Val	Ala	Ile	Lys	Pro	Gly	Ser	Arg	Gly	Asn				
	190					195					200					
AAAAAATAAA	ACCCCAAAAA	AAAAGCAAGC	GT													662

(2) INFORMATION FOR SEQ ID NO:1032:

```

Lys Pro Ile Gly Glu Arg Tyr Leu Leu Met Leu Lys Lys Tyr Leu Gln
                        85                      90                      95
Phe Asp Phe Gly Glu Ser Phe Tyr Arg Gln Ile Lys Val Ile Asp Leu
                        100                     105                     110
Ile Lys Glu Lys Leu Pro Val Ser Ile Ser Leu Gly Leu Phe Ser Thr
                        115                     120                     125
Leu Leu Ile Tyr Leu Ile Ser Ile Pro Leu Gly Ile Phe Lys Ala Lys
                        130                     135                     140
Arg Asn Asn Glu Pro Leu Asp Val Leu Ser Ser Val Val Ile Ile Val
145                      150                      155                      160
Ala Asn Ala Ile Pro Ala Phe Leu Phe Ala Val Val Leu Ile Val Phe
                        165                     170                     175
Phe Ala Gly Gly Asn Tyr Trp His Trp Phe Pro Leu Lys Gly Leu Val
                        180                     185                     190
Ser Asp Asn Phe Glu Ser Leu Ser Ala Leu Gly Lys Ile Lys Asp Tyr
                        195                     200                     205
Leu Trp His Ile Thr Leu Pro Val Leu Cys Ile Ser Leu Gly Gly Phe
                        210                     215                     220
Ala Ser Leu Thr Leu Leu Val Lys Asn Ser Phe Leu Asp Glu Met Gly
225                      230                      235                      240
Lys Leu Tyr Val Leu Ser Ala Lys Ala Lys Gly Cys Ser Val Gly Arg
                        245                     250                     255
Ile Phe Tyr Ala His Val Phe Arg Asn Ala Ile Leu Leu Val Val Ala
                        260                     265                     270
Gly Phe Pro Gln Ala Phe Leu Gly Met Phe Phe Ser Ser Ser Leu Leu
                        275                     280                     285
Ile Glu Ile Val Phe Ser Leu Asp Gly Leu Gly Leu Gly Tyr Glu
                        290                     295                     300
Ser Ile Val Ser Arg Asp Tyr Pro Val Val Phe Gly Ser Leu Tyr Ile
305                      310                      315                      320
Phe Thr Leu Leu Gly Leu Val Ala Ser Leu Ile Ser Asp Leu Leu Cys
                        325                     330                     335
Val Val Ile Asp Pro Arg Ile Asp Phe Glu Lys Arg
                        340                     345

```

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...618
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

TTAAAGGTCT AAACC ATG GAT ATT AAG GCA TGT TAT CAA AAC GCT AAA GCG

51

```

Leu Thr Leu Leu Val Lys Asn Ser Phe Leu Asp Glu Met Gly Lys Leu
      230                      235                      240

TAT GTA CTG AGC GCT AAG GCT AAG GGT TGT TCA GTG GGG CGT ATT TTT      825
Tyr Val Leu Ser Ala Lys Ala Lys Gly Cys Ser Val Gly Arg Ile Phe
      245                      250                      255

TAT GCG CAT GTG TTC CGT AAT GCG ATT TTA TTA GTG GTG GCG GGT TTC      873
Tyr Ala His Val Phe Arg Asn Ala Ile Leu Leu Val Val Ala Gly Phe
      260                      265                      270

CCG CAA GCT TTT TTG GGC ATG TTC TTT AGC TCA AGT TTG TTG ATA GAG      921
Pro Gln Ala Phe Leu Gly Met Phe Phe Ser Ser Ser Leu Leu Ile Glu
      275                      280                      285                      290

ATT GTT TTT AGC CTA GAC GGG TTA GGG CTT TTA GGG TAT GAA AGC ATT      969
Ile Val Phe Ser Leu Asp Gly Leu Gly Leu Leu Gly Tyr Glu Ser Ile
      295                      300                      305

GTG AGT AGG GAT TAT CCC GTT GTG TTT GGT TCG CTT TAT ATT TTC ACG      1017
Val Ser Arg Asp Tyr Pro Val Val Phe Gly Ser Leu Tyr Ile Phe Thr
      310                      315                      320

CTT TTA GGT TTG GTA GCG AGT TTG ATA AGC GAT TTG CTC TGT GTG GTG      1065
Leu Leu Gly Leu Val Ala Ser Leu Ile Ser Asp Leu Leu Cys Val Val
      325                      330                      335

ATT GAC CCT AGG ATT GAT TTT GAA AAG CGT TGAGGGTAGG AATGAAAAC T GAG      1118
Ile Asp Pro Arg Ile Asp Phe Glu Lys Arg
      340                      345

ATGAAATCTT CTTTAAAACT TTTTATGCGG CCTT      1152

```

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

```

Met Ile Ala Tyr Ile Leu Lys Arg Leu Leu Leu Ile Ile Pro Thr Leu
 1           5           10           15
Leu Ala Ile Met Thr Ile Asn Phe Phe Leu Ile Gln Ser Ala Pro Gly
      20           25           30
Gly Pro Ile Glu Gln Met Met Ala Lys Ile Asn Asn Thr Gln Ser Lys
      35           40           45
Glu Ile Gln Gly Val Val Lys Glu Arg Ser Tyr Arg Ala Ser Gln Gly
      50           55           60
Leu Glu Ser Asp Leu Leu Glu Asn Leu Lys Lys Leu Tyr Gly Phe Asp
65           70           75           80

```

5	10	15	
ATC ATG ACC ATT AAT TTC TTT TTG ATC CAA TCG GCT CCT GGA GGC CCT			153
Ile Met Thr Ile Asn Phe Phe Leu Ile Gln Ser Ala Pro Gly Gly Pro			
20	25	30	
ATA GAG CAG ATG ATG GCT AAA ATC AAT AAC ACG CAG TCC AAA GAG ATT			201
Ile Glu Gln Met Met Ala Lys Ile Asn Asn Thr Gln Ser Lys Glu Ile			
35	40	45	50
CAA GGC GTT GTT AAA GAG CGT TCG TAT AGG GCG TCT CAA GGG TTG GAG			249
Gln Gly Val Val Lys Glu Arg Ser Tyr Arg Ala Ser Gln Gly Leu Glu			
55	60	65	
AGC GAT TTG TTA GAA AAT TTA AAA AAA CTC TAT GGT TTT GAC AAG CCC			297
Ser Asp Leu Leu Glu Asn Leu Lys Lys Leu Tyr Gly Phe Asp Lys Pro			
70	75	80	
ATA GGG GAG CGC TAC CTT CTC ATG CTC AAA AAA TAT CTG CAA TTT GAT			345
Ile Gly Glu Arg Tyr Leu Leu Met Leu Lys Lys Tyr Leu Gln Phe Asp			
85	90	95	
TTT GGG GAG AGC TTT TAT CGC CAG ATT AAA GTG ATA GAT TTG ATT AAG			393
Phe Gly Glu Ser Phe Tyr Arg Gln Ile Lys Val Ile Asp Leu Ile Lys			
100	105	110	
GAA AAA TTG CCC GTA TCC ATT TCG TTA GGG CTT TTT AGC ACG CTT TTG			441
Glu Lys Leu Pro Val Ser Ile Ser Leu Gly Leu Phe Ser Thr Leu Leu			
115	120	125	130
ATT TAT CTT ATT TCT ATC CCT TTA GGG ATT TTC AAG GCC AAA CGC AAT			489
Ile Tyr Leu Ile Ser Ile Pro Leu Gly Ile Phe Lys Ala Lys Arg Asn			
135	140	145	
AAC GAG CCT TTA GAC GTG TTA AGC AGC GTG GTG ATC ATT GTC GCT AAC			537
Asn Glu Pro Leu Asp Val Leu Ser Ser Val Val Ile Ile Val Ala Asn			
150	155	160	
GCT ATC CCG GCC TTT TTG TTT GCG GTG GTG TTG ATC GTG TTT TTT GCT			585
Ala Ile Pro Ala Phe Leu Phe Ala Val Val Leu Ile Val Phe Phe Ala			
165	170	175	
GGA GGG AAT TAT TGG CAT TGG TTC CCT TTA AAG GGG CTA GTG AGC GAT			633
Gly Gly Asn Tyr Trp His Trp Phe Pro Leu Lys Gly Leu Val Ser Asp			
180	185	190	
AAT TTT GAA AGT TTG AGC GCG TTA GGT AAA ATC AAG GAT TAT TTA TGG			681
Asn Phe Glu Ser Leu Ser Ala Leu Gly Lys Ile Lys Asp Tyr Leu Trp			
195	200	205	210
CAT ATC ACT TTG CCC GTT CTT TGC ATT TCT TTA GGG GGT TTT GCA AGC			729
His Ile Thr Leu Pro Val Leu Cys Ile Ser Leu Gly Gly Phe Ala Ser			
215	220	225	
CTT ACG CTT TTA GTG AAA AAC TCT TTT TTA GAT GAA ATG GGC AAG CTC			777

			100					105				110			
Asn	Pro	Tyr	Asn	Thr	Ala	Ile	Ile	Ile	Asp	Pro	Gln	Gly	Glu	Ile	Ile
			115					120				125			
Leu	Lys	Tyr	Arg	Lys	Leu	Phe	Pro	Trp	Asn	Pro	Ile	Glu	Pro	Trp	Tyr
			130					135				140			
Pro	Gly	Asp	Leu	Gly	Met	Pro	Val	Cys	Glu	Gly	Pro	Gly	Gly	Ser	Lys
145					150					155				160	
Leu	Ala	Val	Cys	Ile	Cys	His	Asp	Gly	Met	Ile	Pro	Glu	Leu	Ala	Arg
			165						170					175	
Glu	Ala	Ala	Tyr	Lys	Gly	Cys	Asn	Val	Tyr	Ile	Arg	Ile	Ser	Gly	Tyr
			180						185				190		
Ser	Thr	Gln	Val	Asn	Asp	Gln	Trp	Ile	Leu	Thr	Asn	Arg	Ser	Asn	Ala
			195				200					205			
Trp	His	Asn	Leu	Met	Tyr	Thr	Val	Ser	Val	Asn	Leu	Ala	Gly	Tyr	Asp
			210				215				220				
Asn	Val	Phe	Tyr	Tyr	Phe	Gly	Glu	Gly	Gln	Ile	Cys	Asn	Phe	Asp	Gly
225					230					235				240	
Thr	Thr	Leu	Val	Gln	Gly	His	Arg	Asn	Pro	Trp	Glu	Ile	Val	Thr	Gly
			245						250				255		
Glu	Ile	Tyr	Pro	Lys	Met	Ala	Asp	Asn	Ala	Arg	Leu	Ser	Trp	Gly	Leu
			260					265					270		
Glu	Asn	Asn	Ile	Tyr	Asn	Leu	Gly	His	Arg	Gly	Tyr	Val	Ala	Lys	Pro
			275				280					285			
Gly	Gly	Glu	His	Asp	Ala	Gly	Leu	Thr	Tyr	Ile	Lys	Asp	Leu	Ala	Ala
			290				295				300				
Gly	Lys	Tyr	Lys	Leu	Pro	Trp	Glu	Asp	His	Met	Lys	Ile	Lys	Asp	Gly
305				310					315				320		
Ser	Ile	Tyr	Gly	Tyr	Pro	Thr	Thr	Gly	Gly	Arg	Phe	Gly	Lys		
			325					330							

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1095
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

TAGCTATGGA	TTTTCGCCGT	ATTGTGGTG	GATAAAAGAA	AAGGATCTTC	A	ATG	ATT	57
						Met	Ile	
						1		
GCT	TAC	ATT	CTC	AAA	CGC	TTG	CTT	105
Ala	Tyr	Ile	Leu	Lys	Arg	Leu	Leu	
						Ile	Ile	
						Pro	Thr	
						Leu	Leu	
						Ala		

```

GTC TTT TAC TAC TTT GGT GAG GGG CAA ATC TGT AAC TTT GAT GGC ACG      780
Val Phe Tyr Tyr Phe Gly Glu Gly Gln Ile Cys Asn Phe Asp Gly Thr
                230                      235                      240

ACT CTT GTT CAA GGG CAC CGC AAC CCT TGG GAG ATT GTA ACC GGG GAA      828
Thr Leu Val Gln Gly His Arg Asn Pro Trp Glu Ile Val Thr Gly Glu
                245                      250                      255

ATC TAT CCC AAA ATG GCA GAC AAC GCT CGC TTA AGC TGG GGA TTA GAA      876
Ile Tyr Pro Lys Met Ala Asp Asn Ala Arg Leu Ser Trp Gly Leu Glu
                260                      265                      270

AAC AAC ATT TAC AAC CTA GGC CAT AGA GGG TAT GTG GCT AAA CCG GGC      924
Asn Asn Ile Tyr Asn Leu Gly His Arg Gly Tyr Val Ala Lys Pro Gly
                275                      280                      285

GGA GAA CAT GAC GCA GGC TTA ACC TAT ATC AAA GAC TTA GCG GCC GGT      972
Gly Glu His Asp Ala Gly Leu Thr Tyr Ile Lys Asp Leu Ala Ala Gly
                290                      295                      300                      305

AAA TAC AAA TTG CCT TGG GAA GAT CAC ATG AAA ATC AAA GAC GGC TCT      1020
Lys Tyr Lys Leu Pro Trp Glu Asp His Met Lys Ile Lys Asp Gly Ser
                310                      315                      320

ATT TAT GGC TAC CCT ACC ACC GGT GGG CGT TTT GGG AAA TAATCCCTAA CC  1071
Ile Tyr Gly Tyr Pro Thr Thr Gly Gly Arg Phe Gly Lys
                325                      330

TTGCATTTTT GCTAGAACCC GTTTTAAAGG G      1102

```

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

```

Met Gly Ser Ile Gly Ser Met Gly Lys Pro Ile Glu Gly Phe Leu Val
 1           5           10           15
Ala Ala Ile Gln Phe Pro Val Pro Ile Val Asn Ser Arg Lys Asp Ile
 20           25           30
Asp His Asn Ile Glu Ser Ile Ile Arg Thr Leu His Ala Thr Lys Ala
 35           40           45
Gly Tyr Pro Gly Val Glu Leu Ile Ile Phe Pro Glu Tyr Ser Thr Gln
 50           55           60
Gly Leu Asn Thr Ala Lys Trp Leu Ser Glu Glu Phe Leu Leu Asp Val
 65           70           75           80
Pro Gly Lys Glu Thr Glu Leu Tyr Ala Lys Ala Cys Lys Glu Ala Lys
 85           90           95
Val Tyr Gly Val Phe Ser Ile Met Glu Arg Asn Pro Asp Ser Asn Lys

```

GGA AGT ATC GGT AGT ATG GGC AAA CCT ATT GAA GGG TTT TTA GTG GCA	108
Gly Ser Ile Gly Ser Met Gly Lys Pro Ile Glu Gly Phe Leu Val Ala	
5 10 15	
GCC ATT CAG TTT CCT GTG CCA ATT GTC AAT AGC CGT AAG GAT ATT GAT	156
Ala Ile Gln Phe Pro Val Pro Ile Val Asn Ser Arg Lys Asp Ile Asp	
20 25 30	
CAC AAT ATT GAA AGC ATT ATT AGA ACC TTG CAT GCG ACT AAA GCG GGG	204
His Asn Ile Glu Ser Ile Ile Arg Thr Leu His Ala Thr Lys Ala Gly	
35 40 45	
TAT CCG GGA GTG GAG CTT ATC ATT TTC CCT GAG TAT AGC ACG CAA GGT	252
Tyr Pro Gly Val Glu Leu Ile Ile Phe Pro Glu Tyr Ser Thr Gln Gly	
50 55 60 65	
TTG AAT ACC GCT AAG TGG CTT AGC GAA GAG TTT TTA TTA GAT GTC CCG	300
Leu Asn Thr Ala Lys Trp Leu Ser Glu Glu Phe Leu Leu Asp Val Pro	
70 75 80	
GGT AAA GAG ACA GAG CTA TAC GCT AAG GCG TGT AAA GAG GCG AAA GTT	348
Gly Lys Glu Thr Glu Leu Tyr Ala Lys Ala Cys Lys Glu Ala Lys Val	
85 90 95	
TAT GGT GTT TTT TCA ATC ATG GAA CGC AAT CCT GAT TCT AAC AAA AAC	396
Tyr Gly Val Phe Ser Ile Met Glu Arg Asn Pro Asp Ser Asn Lys Asn	
100 105 110	
CCC TAC AAC ACC GCC ATT ATC ATT GAT CCG CAA GGT GAA ATC ATT TTA	444
Pro Tyr Asn Thr Ala Ile Ile Ile Asp Pro Gln Gly Glu Ile Ile Leu	
115 120 125	
AAA TAC CGC AAG CTA TTC CCA TGG AAT CCC ATT GAG CCA TGG TAT CCT	492
Lys Tyr Arg Lys Leu Phe Pro Trp Asn Pro Ile Glu Pro Trp Tyr Pro	
130 135 140 145	
GGG GAT TTA GGA ATG CCT GTG TGC GAG GGT CCG GGC GGA TCA AAA TTA	540
Gly Asp Leu Gly Met Pro Val Cys Glu Gly Pro Gly Gly Ser Lys Leu	
150 155 160	
GCC GTG TGC ATT TGC CAT GAC GGC ATG ATT CCA GAG CTC GCC AGA GAA	588
Ala Val Cys Ile Cys His Asp Gly Met Ile Pro Glu Leu Ala Arg Glu	
165 170 175	
GCG GCC TAT AAA GGG TGC AAT GTG TAT ATC CGC ATT TCA GGC TAT AGC	636
Ala Ala Tyr Lys Gly Cys Asn Val Tyr Ile Arg Ile Ser Gly Tyr Ser	
180 185 190	
ACT CAA GTC AAT GAT CAA TGG ATT TTG ACC AAC CGC TCC AAC GCA TGG	684
Thr Gln Val Asn Asp Gln Trp Ile Leu Thr Asn Arg Ser Asn Ala Trp	
195 200 205	
CAC AAT TTG ATG TAT ACC GTG AGC GTG AAT TTA GCC GGC TAT GAT AAT	732
His Asn Leu Met Tyr Thr Val Ser Val Asn Leu Ala Gly Tyr Asp Asn	
210 215 220 225	

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

Gly	Tyr	Ser	Val	Lys	Asn	Ser	Asn	Arg	Leu	Ile	Tyr	Thr	Asp	Asn	Leu
1				5				10						15	
Glu	Glu	Ser	Leu	Glu	Glu	Thr	Ala	Ser	Leu	Phe	Glu	His	His	Ile	Lys
			20					25					30		
Phe	Tyr	Thr	Glu	Ile	Ile	Glu	Lys	Asp	Lys	Lys	Val	Ile	Lys	Thr	Phe
		35					40					45			
Asn	Lys	Asp	Phe	Lys	Ile	Glu	His	Ala	Lys	Glu	Val	Ile	Ser	Lys	Ala
		50					55				60				
His	Leu	Lys	His	Ser	Glu	Leu	Asn	Ala	Phe	Leu	Ile	Ala	Ala	Pro	Ser
65					70					75				80	
Tyr	Gly	Ile	Glu	Ala	Gln	Asn	Ala	Leu	Leu	Lys	Ile	Leu	Glu	Glu	Pro
				85				90						95	
Pro	Asn	Asn	Val	Cys	Phe	Ile	Met	Phe	Ala	Lys	Ser	Gln	Asn	His	Val
			100					105					110		
Leu	Ala	Thr	Ile	Lys	Ser	Arg	Leu	Ile	Lys	Glu	Asp	Lys	Arg	Gln	Lys
		115					120					125			
Ile	Pro	Leu	Lys	Pro	Leu	Asp	Leu	Asp	Leu	Ser	Lys	Leu	Asp	Leu	Lys
		130				135					140				
Asp	Ile	Tyr	Ala	Phe	Leu	Lys	Asn	Leu	Asp	Lys	Glu	Asn	Phe	Asp	Ser
145					150					155				160	
Arg	Glu	Asn	Gln	Arg	Glu	Arg	Ile	Glu	Ser	Leu	Leu	Glu	Ser	Val	Asn
				165				170						175	
Arg	His	Lys	Ile	Pro	Leu	Asn	Glu	Gln	Glu	Leu	Gln	Ala	Phe	Asp	Leu
			180					185					190		
Ala	Ile	Lys	Ala	Asn	Ser	Ser	Tyr	Tyr	Lys	Leu	Ser	Tyr	Asn	Leu	Leu
		195					200					205			
Pro	Leu	Leu	Leu	Ser	Leu	Leu	Ser	Lys	Lys	Lys	Thr	Pro			
		210					215					220			

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...1059
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

TATTCTCTCG	CAATAATTGT	TATTGTTATT	GCGACAAAAC	TTT TAGAAGG	AGTTATT	ATG	60
						Met	
						1	

35	40	45	
AAC AAG GAT TTT AAA ATA GAG CAT GCC AAA GAA GTC ATT TCC AAA GCT			192
Asn Lys Asp Phe Lys Ile Glu His Ala Lys Glu Val Ile Ser Lys Ala			
50	55	60	
CAC CTA AAA CAC AGC GAA TTA AAC GCT TTT TTA ATC GCC GCT CCT AGT			240
His Leu Lys His Ser Glu Leu Asn Ala Phe Leu Ile Ala Ala Pro Ser			
65	70	75	80
TAT GGT ATA GAA GCC CAA AAC GCG CTT TTA AAA ATC TTA GAA GAA CCC			288
Tyr Gly Ile Glu Ala Gln Asn Ala Leu Leu Lys Ile Leu Glu Glu Pro			
85	90	95	
CCG AAT AAC GTT TGT TTT ATC ATG TTC GCT AAA AGC CAA AAC CAT GTG			336
Pro Asn Asn Val Cys Phe Ile Met Phe Ala Lys Ser Gln Asn His Val			
100	105	110	
TTA GCC ACC ATT AAA TCC CGC CTA ATT AAA GAA GAC AAA CGC CAA AAA			384
Leu Ala Thr Ile Lys Ser Arg Leu Ile Lys Glu Asp Lys Arg Gln Lys			
115	120	125	
ATC CCC CTA AAA CCT TTA GAT TTG GAT TTA TCC AAG CTG GAT TTG AAA			432
Ile Pro Leu Lys Pro Leu Asp Leu Asp Leu Ser Lys Leu Asp Leu Lys			
130	135	140	
GAC ATT TAT GCG TTT TTA AAA AAT TTA GAC AAA GAA AAT TTT GAT TCC			480
Asp Ile Tyr Ala Phe Leu Lys Asn Leu Asp Lys Glu Asn Phe Asp Ser			
145	150	155	160
AGA GAA AAT CAG AGG GAA AGG ATT GAA AGC CTG TTA GAG AGC GTT AAC			528
Arg Glu Asn Gln Arg Glu Arg Ile Glu Ser Leu Leu Glu Ser Val Asn			
165	170	175	
AGG CAT AAG ATC CCC TTA AAC GAG CAA GAA TTG CAA GCC TTT GAT TTA			576
Arg His Lys Ile Pro Leu Asn Glu Gln Glu Leu Gln Ala Phe Asp Leu			
180	185	190	
GCG ATC AAG GCT AAC AGC TCT TAT TAC AAG CTC AGC TAT AAT CTT TTA			624
Ala Ile Lys Ala Asn Ser Ser Tyr Tyr Lys Leu Ser Tyr Asn Leu Leu			
195	200	205	
CCC CTG CTT TTA AGC CTT TTA TCC AAA AAG AAA ACG CCA TGATTGTAAA AC			675
Pro Leu Leu Leu Ser Leu Leu Ser Lys Lys Lys Thr Pro			
210	215	220	
GCCTTAACCC TGATGCGCTC AAAAAACGCTC T			706

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```

      195              200              205
Lys Leu Ser Val Lys Leu Val Thr Arg Asn Ser Phe Asn His Ser Glu
  210              215              220
Gly Thr Leu Ile Val Ala Glu Lys Asp Phe Lys Gly Glu Arg Met Glu
  225              230              235              240
Thr Pro Ile Val Ser Gly Ile Ala Leu Asp Lys Asn Gln Ala Arg Val
      245              250              255
Ser Met Glu Gly Val Glu Asp Arg Pro Gly Ile Ala Ala Glu Ile Phe
      260              265              270
Gly Ala Leu Ala Glu Tyr Arg Ile Asn Val Asp Met Ile Val Gln Thr
      275              280              285
Ile Gly Arg Asp Gly Lys Thr Asp Leu Asp Phe Thr Ile Val Lys Thr
      290              295              300
Gln Ile Glu Glu Thr Lys Gln Ala Leu Lys Pro Phe Leu Ala Gln Met
  305              310              315              320
Asp Ser Ile Asp Tyr Asp Glu Asn Ile Ala Lys Val Ser Ile Val Gly
      325              330              335
Val Gly Met Lys Ser His Ser Gly Val Ala Ser Ile Ala Phe Lys Ala
      340              345              350
Leu Ala Lys Asp Asn Ile Asn Ile Met Met Ile Ser Thr Ser Glu Ile
      355              360              365
Lys Ile Ser Val Leu Ile Asp Ile Lys Tyr Ala Glu Leu Ala Val Arg
      370              375              380
Thr Leu His Ala Val Tyr Gln Leu Asp Gln
  385              390

```

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...663
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

```

GGT TAC TCT GTG AAA AAC TCC AAC CGC CTT ATT TAT ACG GAC AAT CTT      48
Gly Tyr Ser Val Lys Asn Ser Asn Arg Leu Ile Tyr Thr Asp Asn Leu
  1              5              10              15

GAA GAG AGC CTA GAA GAG ACT GCA AGC CTT TTT GAA CAC CAC ATT AAA      96
Glu Glu Ser Leu Glu Glu Thr Ala Ser Leu Phe Glu His His Ile Lys
      20              25              30

TTC TAC ACG GAG ATT ATT GAA AAA GAC AAA AAG GTG ATC AAA ACT TTC      144
Phe Tyr Thr Glu Ile Ile Glu Lys Asp Lys Lys Val Ile Lys Thr Phe

```

```

TCC ATA GTG GGC GTG GGC ATG AAG TCG CAT TCT GGG GTG GCG AGT ATC      1119
Ser Ile Val Gly Val Gly Met Lys Ser His Ser Gly Val Ala Ser Ile
      335                      340                      345

GCT TTT AAA GCC CTA GCC AAA GAC AAT ATC AAT ATC ATG ATG ATT TCT      1167
Ala Phe Lys Ala Leu Ala Lys Asp Asn Ile Asn Ile Met Met Ile Ser
      350                      355                      360

ACA AGC GAG ATT AAA ATT TCG GTT TTG ATT GAC ATT AAA TAC GCT GAA      1215
Thr Ser Glu Ile Lys Ile Ser Val Leu Ile Asp Ile Lys Tyr Ala Glu
      365                      370                      375                      380

TTA GCT GTT AGA ACT TTG CAT GCG GTG TAT CAA TTA GAT CAA TGAAAAATT  1266
Leu Ala Val Arg Thr Leu His Ala Val Tyr Gln Leu Asp Gln
      385                      390

TCTACGATTG GATCAAGGAA TTTGT                                          1291

```

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

```

Met Gly Ser Ile Glu Arg Ile His Asn Val Ala Gln Arg Val Leu Glu
 1           5           10           15
Ser Val Thr Leu Gly His Gln Val Val Val Val Val Ser Ala Met Ser
      20           25           30
Gly Glu Thr Asp Arg Leu Leu Glu Phe Gly Lys Asn Phe Ser His Asn
      35           40           45
Pro Asn Lys Arg Glu Met Asp Arg Ile Val Ser Val Gly Glu Leu Val
      50           55           60
Ser Ser Ala Ala Leu Ser Met Ala Leu Glu Arg Tyr Gly His Arg Ala
      65           70           75           80
Ile Ser Leu Ser Gly Lys Glu Ala Gly Ile Leu Thr Ser Ser His Phe
      85           90           95
Gln Asn Ala Val Ile Gln Ser Ile Asp Thr Lys Arg Ile Thr Glu Leu
      100          105          110
Leu Glu Lys Asn Tyr Ile Val Val Ile Ala Gly Phe Gln Gly Ala Asp
      115          120          125
Ile Gln Gly Glu Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Leu Ser
      130          135          140
Ala Val Ala Leu Ala Gly Ala Leu Lys Ala His Leu Cys Glu Ile Tyr
      145          150          155          160
Thr Asp Val Asp Gly Val Tyr Thr Thr Asp Pro Arg Ile Glu Glu Lys
      165          170          175
Ala Gln Lys Ile Ala Gln Ile Ser Tyr Asp Glu Met Leu Glu Leu Ala
      180          185          190
Ser Met Gly Ala Lys Val Leu Leu Asn Arg Ser Val Glu Leu Ala Lys

```

ATC ACA GAG CTT TTA GAA AAA AAC TAC ATT GTG GTG ATC GCT GGG TTT	447
Ile Thr Glu Leu Leu Glu Lys Asn Tyr Ile Val Val Ile Ala Gly Phe	
110 115 120	
CAA GGC GCT GAT ATT CAA GGT GAA ACA ACG ACT TTA GGG CGT GGG GGG	495
Gln Gly Ala Asp Ile Gln Gly Glu Thr Thr Thr Leu Gly Arg Gly Gly	
125 130 135 140	
AGC GAT TTG AGC GCG GTT GCT TTG GCC GGG GCT TTA AAA GCG CAT TTG	543
Ser Asp Leu Ser Ala Val Ala Leu Ala Gly Ala Leu Lys Ala His Leu	
145 150 155	
TGC GAA ATC TAT ACG GAT GTG GAT GGC GTT TAT ACC ACC GAT CCG CGC	591
Cys Glu Ile Tyr Thr Asp Val Asp Gly Val Tyr Thr Thr Asp Pro Arg	
160 165 170	
ATT GAA GAA AAG GCT CAA AAA ATC GCG CAA ATC AGC TAT GAT GAA ATG	639
Ile Glu Glu Lys Ala Gln Lys Ile Ala Gln Ile Ser Tyr Asp Glu Met	
175 180 185	
CTT GAA CTG GCT TCT ATG GGG GCT AAA GTT TTA TTA AAC CGC TCG GTG	687
Leu Glu Leu Ala Ser Met Gly Ala Lys Val Leu Leu Asn Arg Ser Val	
190 195 200	
GAA TTA GCC AAA AAG CTC AGC GTG AAG TTA GTG ACT CGC AAT TCG TTT	735
Glu Leu Ala Lys Lys Leu Ser Val Lys Leu Val Thr Arg Asn Ser Phe	
205 210 215 220	
AAC CAT AGC GAA GGC ACG CTC ATT GTG GCT GAA AAA GAC TTT AAA GGA	783
Asn His Ser Glu Gly Thr Leu Ile Val Ala Glu Lys Asp Phe Lys Gly	
225 230 235	
GAA CGC ATG GAA ACC CCT ATA GTG AGT GGG ATC GCA TTG GAT AAA AAT	831
Glu Arg Met Glu Thr Pro Ile Val Ser Gly Ile Ala Leu Asp Lys Asn	
240 245 250	
CAG GCT CGT GTG AGC ATG GAG GGC GTG GAA GAT CGG CCA GGC ATT GCC	879
Gln Ala Arg Val Ser Met Glu Gly Val Glu Asp Arg Pro Gly Ile Ala	
255 260 265	
GCT GAA ATC TTT GGC GCT TTA GCG GAG TAT CGC ATT AAC GTG GAT ATG	927
Ala Glu Ile Phe Gly Ala Leu Ala Glu Tyr Arg Ile Asn Val Asp Met	
270 275 280	
ATC GTC CAA ACG ATC GGC AGA GAC GGC AAA ACC GAT TTG GAT TTT ACG	975
Ile Val Gln Thr Ile Gly Arg Asp Gly Lys Thr Asp Leu Asp Phe Thr	
285 290 295 300	
ATC GTT AAA ACC CAA ATA GAA GAA ACC AAG CAA GCC TTA AAG CCT TTT	1023
Ile Val Lys Thr Gln Ile Glu Glu Thr Lys Gln Ala Leu Lys Pro Phe	
305 310 315	
TTA GCG CAA ATG GAT TCC ATT GAT TAT GAT GAA AAT ATC GCT AAA GTC	1071
Leu Ala Gln Met Asp Ser Ile Asp Tyr Asp Glu Asn Ile Ala Lys Val	
320 325 330	

```

Cys Ala His Phe Asp Asn Val Val Arg Glu Ile Leu Glu Gly Phe Ser
  210                215                220
Phe Lys Gln Tyr Glu Cys Leu Ile Thr Leu Glu Ile Ile Lys Ser Asn
  225                230                235                240
Thr Thr Trp Leu Thr Gly Gly Leu Lys Ile Ile
                245                250

```

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 76...1257
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

```

GCCAAGTCAT TGCTTATTTT AAAAGAGAGG GGTATTTTATA GGGTGTTAAT CGTTCAAAAA      60
TACGGCGGCA CGAGC ATG GGC AGC ATA GAA AGG ATC CAC AAT GTC GCT CAA      111
      Met Gly Ser Ile Glu Arg Ile His Asn Val Ala Gln
            1                5                10

AGG GTT TTA GAA AGC GTT ACA TTA GGG CAT CAA GTC GTG GTG GTG GTT      159
Arg Val Leu Glu Ser Val Thr Leu Gly His Gln Val Val Val Val Val
      15                20                25

TCA GCG ATG AGC GGC GAA ACC GAC AGG CTT TTA GAA TTT GGC AAG AAT      207
Ser Ala Met Ser Gly Glu Thr Asp Arg Leu Leu Glu Phe Gly Lys Asn
      30                35                40

TTT AGC CAT AAC CCT AAC AAG CGA GAG ATG GAC AGG ATT GTA AGC GTG      255
Phe Ser His Asn Pro Asn Lys Arg Glu Met Asp Arg Ile Val Ser Val
      45                50                55                60

GGG GAA TTG GTT TCA AGT GCG GCT TTG AGC ATG GCG TTA GAA AGG TAT      303
Gly Glu Leu Val Ser Ser Ala Ala Leu Ser Met Ala Leu Glu Arg Tyr
            65                70                75

GGG CAT AGA GCC ATT TCC TTG AGC GGG AAA GAA GCG GGC ATT TTA ACC      351
Gly His Arg Ala Ile Ser Leu Ser Gly Lys Glu Ala Gly Ile Leu Thr
            80                85                90

AGC TCG CAT TTT CAA AAC GCC GTG ATC CAA TCC ATT GAC ACC AAA CGC      399
Ser Ser His Phe Gln Asn Ala Val Ile Gln Ser Ile Asp Thr Lys Arg
      95                100                105

```

```

Ala Tyr Ala Leu Ser Val Glu Lys Asn Thr Asn Leu Glu Lys Asn Ala
  190                      195                      200

AAA AAA CCC TCA TGC GCT CAT TTT GAC AAT GTG GTG AGA GAG ATT TTA      676
Lys Lys Pro Ser Cys Ala His Phe Asp Asn Val Val Arg Glu Ile Leu
205                      210                      215                      220

GAG GGC TTT TCT TTC AAG CAA TAC GAG TGT CTA ATT ACG CTA GAA ATT      724
Glu Gly Phe Ser Phe Lys Gln Tyr Glu Cys Leu Ile Thr Leu Glu Ile
                225                      230                      235

ATC AAG TCA AAC ACA ACT TGG CTT ACT GGG GGG CTA AAG ATT ATT TAGGG      774
Ile Lys Ser Asn Thr Thr Trp Leu Thr Gly Gly Leu Lys Ile Ile
                240                      245                      250

TGCGGGGCTG GGGCTGTGGG CTGCGTGGCG AATGAGCGCT TTTTTCGAAA AAA      827

```

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

```

Met Arg Glu Ile Asn Met Ile Leu Tyr Ile His Ile Pro Phe Cys Glu
  1             5             10             15
Asn Lys Cys Gly Tyr Cys Ala Phe Asn Ser Tyr Glu Asn Lys His Gly
                20             25             30
Leu Lys Glu Glu Tyr Thr Gln Ala Leu Cys Leu Asp Leu Lys His Ala
                35             40             45
Leu Ser Gln Thr Asp Glu Pro Ile Glu Ser Val Phe Ile Gly Gly Gly
                50             55             60
Thr Pro Asn Thr Leu Ser Val Lys Ala Phe Glu Arg Ile Phe Glu Ser
                65             70             75             80
Ile Tyr Gln His Ala Ser Leu Ser Leu Asp Cys Glu Ile Thr Thr Glu
                85             90             95
Ala Asn Pro Glu Leu Ile Thr Lys Ala Trp Cys Gln Gly Leu Lys Gly
                100            105            110
Leu Gly Ile Asn Arg Leu Ser Leu Gly Val Gln Ser Phe Arg Glu Asp
                115            120            125
Lys Leu Leu Phe Leu Glu Arg Gln His Ser Lys Asn Ile Ala Pro Ala
                130            135            140
Ile Glu Thr Ile Leu Lys Ser Gly Ile Glu Asn Ile Ser Ile Asp Leu
                145            150            155            160
Ile Tyr Asn Thr Pro Leu Asp Asn Glu Asn Ser Leu Lys Glu Glu Leu
                165            170            175
Lys Leu Ala Lys Glu Leu Pro Ile Asn His Leu Ser Ala Tyr Ala Leu
                180            185            190
Ser Val Glu Lys Asn Thr Asn Leu Glu Lys Asn Ala Lys Lys Pro Ser
                195            200            205

```

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

TTAAATGAA GTGAAA ATG AGA GAA ATA AAT ATG ATT TTA TAC ATT CAT ATC	52
Met Arg Glu Ile Asn Met Ile Leu Tyr Ile His Ile	
1 5 10	
CCC TTT TGT GAA AAT AAA TGC GGC TAT TGC GCT TTC AAT TCC TAT GAA	100
Pro Phe Cys Glu Asn Lys Cys Gly Tyr Cys Ala Phe Asn Ser Tyr Glu	
15 20 25	
AAC AAG CAT GGG TTA AAA GAA GAA TAC ACT CAA GCG TTA TGC CTG GAT	148
Asn Lys His Gly Leu Lys Glu Glu Tyr Thr Gln Ala Leu Cys Leu Asp	
30 35 40	
TTA AAG CAT GCG TTA AGT CAA ACT GAC GAA CCA ATT GAA AGC GTT TTT	196
Leu Lys His Ala Leu Ser Gln Thr Asp Glu Pro Ile Glu Ser Val Phe	
45 50 55 60	
ATT GGT GGC GGC ACG CCT AAC ACT TTA AGC GTG AAG GCT TTT GAA AGG	244
Ile Gly Gly Gly Thr Pro Asn Thr Leu Ser Val Lys Ala Phe Glu Arg	
65 70 75	
ATT TTT GAA AGC ATT TAT CAA CAT GCG AGC TTG AGC TTG GAT TGT GAG	292
Ile Phe Glu Ser Ile Tyr Gln His Ala Ser Leu Ser Leu Asp Cys Glu	
80 85 90	
ATC ACC ACT GAA GCT AAC CCC GAA TTG ATT ACT AAA GCT TGG TGT CAA	340
Ile Thr Thr Glu Ala Asn Pro Glu Leu Ile Thr Lys Ala Trp Cys Gln	
95 100 105	
GGC TTA AAA GGT TTA GGG ATC AAC CGC TTG AGT TTA GGG GTG CAA AGT	388
Gly Leu Lys Gly Leu Gly Ile Asn Arg Leu Ser Leu Gly Val Gln Ser	
110 115 120	
TTT AGG GAA GAT AAA TTA TTG TTT TTA GAG CGC CAA CAT TCC AAA AAT	436
Phe Arg Glu Asp Lys Leu Leu Phe Leu Glu Arg Gln His Ser Lys Asn	
125 130 135 140	
ATC GCT CCT GCG ATA GAA ACT ATT TTA AAA AGC GGG ATT GAA AAT ATC	484
Ile Ala Pro Ala Ile Glu Thr Ile Leu Lys Ser Gly Ile Glu Asn Ile	
145 150 155	
AGC ATT GAT TTG ATT TAT AAC ACC CCA TTA GAC AAT GAA AAC TCT CTA	532
Ser Ile Asp Leu Ile Tyr Asn Thr Pro Leu Asp Asn Glu Asn Ser Leu	
160 165 170	
AAA GAA GAA TTA AAA CTC GCT AAA GAA CTC CCT ATC AAC CAC TTG AGC	580
Lys Glu Glu Leu Lys Leu Ala Lys Glu Leu Pro Ile Asn His Leu Ser	
175 180 185	
GCT TAC GCT TTG AGC GTT GAA AAA AAC ACG AAT TTA GAA AAA AAC GCC	628

```

      100      105      110
Phe Val Lys Glu Cys Gly Ile Lys Ser Ala Ser Tyr Phe Glu Thr Asn
      115      120      125
Asp Leu Lys Glu Ala Leu Ser Tyr Ile Gln Asn Ala Ser Phe Pro Leu
      130      135      140
Val Ile Lys Ala Leu Asn Lys Asn Thr Ser Ile Val Tyr Gln Glu Glu
      145      150      155      160
Glu Ala Ile Lys Ile Leu Glu Asp Ala Phe Lys Gln Ser Asn Glu Pro
      165      170      175
Val Ile Ile Glu Pro Phe Leu Glu Gly Phe Glu Leu Ser Val Thr Ala
      180      185      190
Leu Ile Ala Asn Asp Asp Phe Ile Leu Leu Pro Phe Cys Gln Asn Tyr
      195      200      205
Lys Arg Leu Leu Glu Gly Asp Asn Gly Val Asn Thr Gly Gly Met Gly
      210      215      220
Ala Ile Ala Pro Ala Asn Phe Phe Ser Asn Glu Leu Glu Glu Lys Ile
      225      230      235      240
Lys Asn His Ile Phe Lys Pro Thr Leu Glu Lys Leu Gln Ala Asp Asn
      245      250      255
Thr Pro Phe Lys Gly Val Leu Leu Ala Glu Ile Val Ile Ile Glu Glu
      260      265      270
Lys Gly Val Leu Glu Pro Tyr Leu Leu Asp Phe Ser Val Arg Phe Lys
      275      280      285
Asp Ile Glu Cys Gln Thr Ile Leu Pro Leu Leu Glu Ser Ser Leu Leu
      290      295      300
Asp Leu Cys Leu Ala Thr Ala Lys Gly Glu Leu His Ser Leu Glu Leu
      305      310      315      320
Val Phe Ser Lys Glu Phe Val Met Ser Val Ala Leu Val Ser Arg Asn
      325      330      335
Tyr Pro Thr Ser Ser Ser Pro Lys Gln Thr Leu Tyr Ile Asp Pro Val
      340      345      350
Asp Glu Lys Lys Gly His Leu Ile Leu Gly Glu Val Glu Gln Asp Asn
      355      360      365
Gly Val Phe Glu Ser Ser Gly Gly Arg Val Ile Phe Ala Ile Gly Arg
      370      375      380
Gly Lys Ser Leu Leu Glu Ala Arg Asn His Ala Tyr Glu Ile Ala Gln
      385      390      395      400
Lys Val His Phe Glu Gly Met Phe Tyr Arg Lys Asp Ile Gly Phe Lys
      405      410      415
Val Leu Asp Leu Lys Glu Tyr Ser
      420

```

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...769

GAA TTA CAT TCT CTT GAA TTG GTG TTT TCT AAA GAA TTT GTG ATG AGT	1011
Glu Leu His Ser Leu Glu Leu Val Phe Ser Lys Glu Phe Val Met Ser	
315 320 325	
GTG GCG CTT GTT TCT AGG AAT TAC CCC ACT AGC TCT TCG CCC AAA CAA	1059
Val Ala Leu Val Ser Arg Asn Tyr Pro Thr Ser Ser Ser Pro Lys Gln	
330 335 340 345	
ACC CTT TAT ATT GAT CCG GTT GAT GAA AAA AAG GGT CAT TTG ATT TTA	1107
Thr Leu Tyr Ile Asp Pro Val Asp Glu Lys Lys Gly His Leu Ile Leu	
350 355 360	
GGG GAG GTG GAG CAG GAT AAT GGC GTG TTT GAA AGC AGT GGG GGG AGG	1155
Gly Glu Val Glu Gln Asp Asn Gly Val Phe Glu Ser Ser Gly Gly Arg	
365 370 375	
GTG ATC TTT GCC ATT GGT AGG GGA AAA TCC TTA TTA GAA GCC AGA AAC	1203
Val Ile Phe Ala Ile Gly Arg Gly Lys Ser Leu Leu Glu Ala Arg Asn	
380 385 390	
CAT GCT TAT GAA ATC GCT CAA AAG GTG CAT TTT GAA GGC ATG TTT TAT	1251
His Ala Tyr Glu Ile Ala Gln Lys Val His Phe Glu Gly Met Phe Tyr	
395 400 405	
CGC AAG GAT ATT GGT TTT AAG GTG TTA GAT TTG AAA GAA TAT TCT TAAAG	1301
Arg Lys Asp Ile Gly Phe Lys Val Leu Asp Leu Lys Glu Tyr Ser	
410 415 420	
GTAAAGTTT AAGACAAACC AAAGAGTTTG TCTTGTTTG	1340

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

Met Lys Asp Asn Asn Asn Tyr Asn Val Leu Ile Val Gly Asn Lys Gly	
1 5 10 15	
Arg Glu Tyr Ala Leu Ala Gln Arg Leu Gln Gln Asp Glu Arg Val Asn	
20 25 30	
Ala Leu Tyr Phe Cys Leu Gly Asn Gly Gly Thr Gln Asp Leu Gly Glu	
35 40 45	
Asn Leu Glu Cys Glu His Tyr Glu His Ile Val Glu Leu Ala Leu Lys	
50 55 60	
Lys Gln Ile His Leu Ala Ile Ile Ser Glu Glu Glu Phe Leu Val Leu	
65 70 75 80	
Gly Leu Thr Glu Met Leu Glu Lys Ala Gly Ile Leu Val Phe Gly Ala	
85 90 95	
Ser Lys Glu Ala Ala Lys Leu Glu Ala Ser Lys Ser Tyr Met Lys Ala	

Gly Ile Leu Val Phe Gly Ala Ser Lys Glu Ala Ala Lys Leu Glu Ala	
90 95 100 105	
TCT AAA AGC TAT ATG AAA GCT TTT GTT AAA GAG TGT GGC ATC AAA AGT	387
Ser Lys Ser Tyr Met Lys Ala Phe Val Lys Glu Cys Gly Ile Lys Ser	
110 115 120	
GCG TCT TAC TTT GAA ACA AAC GAC TTA AAA GAA GCT TTG AGT TAC ATT	435
Ala Ser Tyr Phe Glu Thr Asn Asp Leu Lys Glu Ala Leu Ser Tyr Ile	
125 130 135	
CAA AAC GCT TCT TTC CCC TTA GTC ATT AAA GCG TTG AAT AAA AAC ACA	483
Gln Asn Ala Ser Phe Pro Leu Val Ile Lys Ala Leu Asn Lys Asn Thr	
140 145 150	
AGC ATT GTC TAT CAA GAA GAA GAA GCG ATA AAA ATC CTT GAA GAC GCT	531
Ser Ile Val Tyr Gln Glu Glu Glu Ala Ile Lys Ile Leu Glu Asp Ala	
155 160 165	
TTC AAA CAA AGC AAT GAG CCT GTG ATT ATA GAG CCT TTT TTA GAG GGA	579
Phe Lys Gln Ser Asn Glu Pro Val Ile Ile Glu Pro Phe Leu Glu Gly	
170 175 180 185	
TTT GAG CTT TCA GTT ACA GCG CTC ATA GCC AAT GAT GAT TTT ATC TTG	627
Phe Glu Leu Ser Val Thr Ala Leu Ile Ala Asn Asp Asp Phe Ile Leu	
190 195 200	
TTG CCC TTT TGC CAA AAC TAC AAA CGC TTA TTA GAG GGG GAT AAT GGG	675
Leu Pro Phe Cys Gln Asn Tyr Lys Arg Leu Leu Glu Gly Asp Asn Gly	
205 210 215	
GTC AAT ACG GGG GGT ATG GGG GCC ATC GCT CCT GCA AAC TTT TTC TCT	723
Val Asn Thr Gly Gly Met Gly Ala Ile Ala Pro Ala Asn Phe Phe Ser	
220 225 230	
AAT GAA TTA GAA GAG AAA ATA AAA AAT CAT ATC TTT AAA CCC ACT TTA	771
Asn Glu Leu Glu Glu Lys Ile Lys Asn His Ile Phe Lys Pro Thr Leu	
235 240 245	
GAG AAA CTT CAG GCT GAC AAC ACG CCT TTT AAA GGG GTT TTA CTC GCT	819
Glu Lys Leu Gln Ala Asp Asn Thr Pro Phe Lys Gly Val Leu Leu Ala	
250 255 260 265	
GAA ATT GTA ATC ATA GAA GAA AAA GGC GTT TTA GAG CCG TAT TTA TTG	867
Glu Ile Val Ile Ile Glu Glu Lys Gly Val Leu Glu Pro Tyr Leu Leu	
270 275 280	
GAT TTT AGC GTG CGT TTT AAA GAC ATT GAA TGC CAG ACG ATT TTA CCC	915
Asp Phe Ser Val Arg Phe Lys Asp Ile Glu Cys Gln Thr Ile Leu Pro	
285 290 295	
CTT TTA GAA AGC TCG CTT TTA GAT TTG TGT TTG GCC ACA GCC AAA GGG	963
Leu Leu Glu Ser Ser Leu Leu Asp Leu Cys Leu Ala Thr Ala Lys Gly	
300 305 310	

```

Ile Leu Asn Tyr Leu His Ser Leu Asp Gln Glu Leu Glu Gln Tyr Ala
  610                      615                      620
Ile Asp Glu Val Leu Glu Ala Gln Val Lys Arg Ile Val Asp Phe Gly
625                      630                      635                      640
Ala Phe Leu Ser Leu Pro Lys Gly Gly Glu Gly Leu Leu Arg Lys Gln
                      645                      650                      655
Asn Met Asp Lys Cys Gln Val Val Leu Lys Glu Gly Asp Ser Ile Arg
                      660                      665                      670
Cys Arg Val Ile Ser Phe Asn Lys Gly Lys Ile Ala Leu Asp Leu Ala
                      675                      680                      685

```

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1296
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

```

AAACAACCAC ATTGCAGGAA AGAC ATG AAA GAT AAC AAT AAC TAT AAT GTT      51
                      Met Lys Asp Asn Asn Asn Tyr Asn Val
                      1                      5

TTA ATT GTG GGG AAT AAG GGG CGA GAG TAT GCT TTG GCT CAA AGG CTT      99
Leu Ile Val Gly Asn Lys Gly Arg Glu Tyr Ala Leu Ala Gln Arg Leu
10                      15                      20                      25

CAG CAA GAT GAG CGA GTG AAT GCT TTG TAT TTT TGT TTG GGT AAT GGT      147
Gln Gln Asp Glu Arg Val Asn Ala Leu Tyr Phe Cys Leu Gly Asn Gly
                      30                      35                      40

GGC ACT CAA GAT TTA GGC GAG AAT CTG GAA TGC GAA CAT TAC GAG CAT      195
Gly Thr Gln Asp Leu Gly Glu Asn Leu Glu Cys Glu His Tyr Glu His
                      45                      50                      55

ATC GTG GAA TTA GCC CTG AAA AAA CAG ATC CAT TTA GCC ATC ATT TCA      243
Ile Val Glu Leu Ala Leu Lys Lys Gln Ile His Leu Ala Ile Ile Ser
                      60                      65                      70

GAA GAA GAG TTT TTG GTT TTA GGG CTT ACA GAA ATG CTA GAA AAA GCG      291
Glu Glu Glu Phe Leu Val Leu Gly Leu Thr Glu Met Leu Glu Lys Ala
                      75                      80                      85

GGG ATT TTA GTG TTT GGG GCT TCT AAA GAA GCG GCT AAG TTA GAG GCT      339

```

				165					170					175		
Gly	Thr	Lys	Glu	Ser	Leu	Asn	Met	Ile	Glu	Met	Arg	Ser	Leu	Gly	Gln	
			180					185					190			
Lys	Leu	Asn	Ala	Leu	Glu	Glu	Pro	Leu	Met	Leu	Glu	Ala	Leu	Glu	Leu	
		195					200					205				
Ala	Gln	Lys	Ser	Leu	Glu	Glu	Thr	Cys	Thr	Leu	Tyr	Glu	Glu	Ile	Phe	
	210					215					220					
Thr	Pro	His	Gln	Asn	Glu	Leu	Phe	Phe	Lys	Glu	Ser	Gln	Gly	Ile	Val	
225					230					235					240	
Phe	Asn	Glu	Arg	Leu	Leu	Asp	Leu	Leu	Lys	Asn	Gln	Tyr	Phe	Asp	Glu	
			245						250					255		
Ile	Ile	Lys	Gly	Ile	Glu	Ser	Ser	Ala	Leu	Ser	Glu	Arg	Glu	Asn	Val	
		260						265					270			
Phe	Asn	Glu	Ile	Ala	Arg	Lys	Ile	Ser	Glu	Ala	His	Ser	Glu	Phe	Ser	
	275						280					285				
Leu	Glu	Glu	Ile	Glu	Leu	Ser	Leu	Glu	Lys	Val	Lys	Lys	Thr	Glu	Ile	
	290					295					300					
Arg	Arg	Met	Ile	Ile	Lys	Asp	Lys	Ile	Arg	Pro	Asp	Lys	Arg	Ala	Leu	
305					310					315					320	
Glu	Glu	Val	Arg	Pro	Ile	Leu	Ile	Glu	Ser	Asp	Leu	Leu	Pro	Met	Ala	
				325					330						335	
His	Ser	Ser	Ile	Leu	Phe	Thr	Arg	Gly	Gln	Thr	Gln	Ser	Leu	Val	Val	
			340					345					350			
Gly	Val	Leu	Gly	Thr	Asp	Asn	Asp	Ala	Gln	Thr	His	Glu	Ser	Leu	Glu	
		355				360						365				
His	Lys	Ala	Pro	Ile	Lys	Glu	Arg	Phe	Met	Phe	His	Tyr	Asn	Phe	Pro	
	370					375					380					
Pro	Phe	Cys	Val	Gly	Glu	Ala	Ser	Ser	Ile	Gly	Ala	Ala	Ser	Arg	Arg	
385					390					395					400	
Glu	Leu	Gly	His	Gly	Asn	Leu	Ala	Lys	Arg	Ala	Leu	Glu	Thr	Ser	Ile	
			405						410					415		
Lys	Asn	Lys	Glu	Gln	Val	Ile	Arg	Leu	Val	Ser	Glu	Ile	Leu	Glu	Ser	
			420					425					430			
Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys	Ala	Gly	Ser	Leu	Ala	Leu	
		435					440					445				
Tyr	Ala	Ser	Gly	Val	Glu	Ile	Tyr	Asp	Leu	Val	Ala	Gly	Val	Ala	Met	
	450					455					460					
Gly	Met	Val	Ser	Glu	Gly	Gln	Asp	His	Ala	Ile	Leu	Ser	Asp	Ile	Ser	
465					470					475					480	
Gly	Leu	Glu	Asp	Ala	Glu	Gly	Asp	Met	Asp	Phe	Lys	Ile	Ala	Gly	Asn	
			485						490					495		
Leu	Glu	Gly	Ile	Thr	Ala	Met	Gln	Met	Asp	Thr	Lys	Met	Ser	Gly	Ile	
			500					505								

CAA GAA TTG GAG CAA TAC GCT ATT GAT GAG GTA TTA GAA GCT CAA GTG	1923
Gln Glu Leu Glu Gln Tyr Ala Ile Asp Glu Val Leu Glu Ala Gln Val	
620 625 630	
AAA CGA ATC GTG GAT TTT GGG GCG TTT TTA AGC TTG CCT AAG GGG GGC	1971
Lys Arg Ile Val Asp Phe Gly Ala Phe Leu Ser Leu Pro Lys Gly Gly	
635 640 645	
GAA GGC TTG TTA AGA AAG CAA AAC ATG GAC AAG TGT CAA GTG GTT TTA	2019
Glu Gly Leu Leu Arg Lys Gln Asn Met Asp Lys Cys Gln Val Val Leu	
650 655 660 665	
AAA GAA GGC GAT AGC ATC AGG TGT AGG GTG ATT AGC TTC AAT AAG GGT	2067
Lys Glu Gly Asp Ser Ile Arg Cys Arg Val Ile Ser Phe Asn Lys Gly	
670 675 680	
AAA ATC GCT TTA GAT TTG GCT TAAAATTTTA AAAAGCGTTT TTTAAAAGCG TTTT	2122
Lys Ile Ala Leu Asp Leu Ala	
685	
TAAGCTAGTT T	2133

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

Met Asp Phe Ile Thr Ile Asn Ser Ser Asn Lys Thr Glu Glu Phe Ala	
1 5 10 15	
Leu Lys Gln Val Ala Lys Gln Ala Thr Ser Ser Leu Leu Tyr Arg Leu	
20 25 30	
Gly Lys Thr Ile Ile Leu Ala Ser Val Cys Val Glu Arg Glu Pro Val	
35 40 45	
Ser Glu Asp Phe Leu Pro Leu Val Val Gln Phe Leu Glu Lys Ser Tyr	
50 55 60	
Ala Ala Gly Lys Ile Pro Gly Gly Phe Val Lys Arg Glu Gly Arg Ala	
65 70 75 80	
Gln Asp Phe Glu Ile Leu Thr Ser Arg Leu Ile Asp Arg Thr Leu Arg	
85 90 95	
Pro Leu Phe Pro Lys Asp Tyr Arg Tyr Pro Thr Gln Ile Thr Leu Met	
100 105 110	
Val Leu Ser His Asp Ile Glu Asn Asp Leu Gln Val Ser Ala Leu Asn	
115 120 125	
Ala Ala Ser Ala Ala Leu Phe Leu Ala His Ile Ala Pro Ile Lys Ser	
130 135 140	
Val Ser Ala Cys Arg Ile Ala Arg Met Asp Asn Glu Phe Ile Ile Asn	
145 150 155 160	
Pro Ser Ala Ser Leu Leu Asn Gln Ser Ser Leu Asp Leu Phe Val Ser	

ATT GGC GCG GCT TCA AGG CGT GAA TTA GGG CAT GGG AAT TTG GCT AAA	1251
Ile Gly Ala Ala Ser Arg Arg Glu Leu Gly His Gly Asn Leu Ala Lys	
395 400 405	
AGA GCC TTA GAA ACG AGC ATT AAA AAT AAA GAG CAG GTG ATA CGA TTG	1299
Arg Ala Leu Glu Thr Ser Ile Lys Asn Lys Glu Gln Val Ile Arg Leu	
410 415 420 425	
GTT TCT GAG ATT TTA GAA AGC AAT GGT TCA AGC TCA ATG GCG AGC GTG	1347
Val Ser Glu Ile Leu Glu Ser Asn Gly Ser Ser Met Ala Ser Val	
430 435 440	
TGC GCA GGC TCT TTA GCC CTT TAT GCA AGC GGT GTG GAA ATT TAC GAT	1395
Cys Ala Gly Ser Leu Ala Leu Tyr Ala Ser Gly Val Glu Ile Tyr Asp	
445 450 455	
TTA GTC GCT GGG GTG GCT ATG GGC ATG GTG AGC GAA GGG CAA GAT CAC	1443
Leu Val Ala Gly Val Ala Met Gly Met Val Ser Glu Gly Gln Asp His	
460 465 470	
GCT ATT TTA AGC GAT ATT AGC GGC TTA GAA GAC GCA GAA GGC GAT ATG	1491
Ala Ile Leu Ser Asp Ile Ser Gly Leu Glu Asp Ala Glu Gly Asp Met	
475 480 485	
GAT TTT AAG ATT GCT GGG AAT TTA GAA GGC ATT ACG GCC ATG CAA ATG	1539
Asp Phe Lys Ile Ala Gly Asn Leu Glu Gly Ile Thr Ala Met Gln Met	
490 495 500 505	
GAT ACC AAA ATG AGC GGT ATC AAG CTA GAA ATT TTA TAC CAA GCC TTA	1587
Asp Thr Lys Met Ser Gly Ile Lys Leu Glu Ile Leu Tyr Gln Ala Leu	
510 515 520	
CTC CAA GCC AAA GAA GCA CGG AAA CAT ATT TTA AAA ATC ATG CAT GAA	1635
Leu Gln Ala Lys Glu Ala Arg Lys His Ile Leu Lys Ile Met His Glu	
525 530 535	
GCG AAA GAA AAG ATT GTG ATC AAT TTT TCC CAT TTG CCC ACA ACG GAG	1683
Ala Lys Glu Lys Ile Val Ile Asn Phe Ser His Leu Pro Thr Thr Glu	
540 545 550	
ATT TTT AAT GTC GCA CCC GAT AAA ATT GTA GAA ATT ATC GGT CAA GGG	1731
Ile Phe Asn Val Ala Pro Asp Lys Ile Val Glu Ile Ile Gly Gln Gly	
555 560 565	
GGG CGT GTG ATT AAA GAG ATA GTA GAA AAG TTT GAA GTT AAA ATT GAT	1779
Gly Arg Val Ile Lys Glu Ile Val Glu Lys Phe Glu Val Lys Ile Asp	
570 575 580 585	
TTG AAC AAA CCG AGC GGT GAA GTG AAA ATC ATG GGG AAT AAA GAG CGC	1827
Leu Asn Lys Pro Ser Gly Glu Val Lys Ile Met Gly Asn Lys Glu Arg	
590 595 600	
GTT TTA AAG ACT AAG GAA TTT ATT TTA AAC TAC TTG CAT TCT TTA GAT	1875
Val Leu Lys Thr Lys Glu Phe Ile Leu Asn Tyr Leu His Ser Leu Asp	
605 610 615	

AGT TTG GAT TTG TTC GTG TCT GGA ACG AAA GAG AGT TTG AAC ATG ATA	579
Ser Leu Asp Leu Phe Val Ser Gly Thr Lys Glu Ser Leu Asn Met Ile	
170 175 180 185	
GAA ATG CGC TCT TTG GGG CAA AAA TTG AAC GCT TTA GAA GAG CCT TTA	627
Glu Met Arg Ser Leu Gly Gln Lys Leu Asn Ala Leu Glu Glu Pro Leu	
190 195 200	
ATG TTA GAA GCT TTA GAA TTG GCT CAA AAA AGT TTG GAA GAA ACT TGC	675
Met Leu Glu Ala Leu Glu Leu Ala Gln Lys Ser Leu Glu Glu Thr Cys	
205 210 215	
ACG CTT TAT GAA GAG ATT TTC ACG CCC CAC CAA AAC GAG CTG TTT TTC	723
Thr Leu Tyr Glu Glu Ile Phe Thr Pro His Gln Asn Glu Leu Phe Phe	
220 225 230	
AAA GAG AGC CAA GGA ATA GTC TTT AAT GAA AGG CTG TTA GAT TTA TTG	771
Lys Glu Ser Gln Gly Ile Val Phe Asn Glu Arg Leu Leu Asp Leu Leu	
235 240 245	
AAA AAT CAG TAT TTT GAT GAA ATC ATC AAA GGC ATT GAA AGT TCT GCT	819
Lys Asn Gln Tyr Phe Asp Glu Ile Ile Lys Gly Ile Glu Ser Ser Ala	
250 255 260 265	
TTG AGC GAG CGA GAA AAT GTT TTC AAT GAA ATT GCC AGA AAA ATC AGT	867
Leu Ser Glu Arg Glu Asn Val Phe Asn Glu Ile Ala Arg Lys Ile Ser	
270 275 280	
GAA GCC CAC TCA GAA TTC AGT TTA GAA GAA ATT GAA TTG TCT TTA GAA	915
Glu Ala His Ser Glu Phe Ser Leu Glu Glu Ile Glu Leu Ser Leu Glu	
285 290 295	
AAA GTG AAA AAG ACT GAG ATA AGA CGC ATG ATC ATT AAG GAT AAA ATC	963
Lys Val Lys Lys Thr Glu Ile Arg Arg Met Ile Ile Lys Asp Lys Ile	
300 305 310	
CGC CCG GAT AAG CGC GCG TTA GAA GAA GTG CGG CCC ATT TTG ATA GAG	1011
Arg Pro Asp Lys Arg Ala Leu Glu Glu Val Arg Pro Ile Leu Ile Glu	
315 320 325	
AGC GAT TTG CTC CCT ATG GCG CAT AGC TCC ATT TTA TTC ACT AGG GGG	1059
Ser Asp Leu Leu Pro Met Ala His Ser Ser Ile Leu Phe Thr Arg Gly	
330 335 340 345	
CAA ACT CAA AGC TTA GTG GTA GGG GTT TTA GGC ACG GAT AAT GAC GCT	1107
Gln Thr Gln Ser Leu Val Val Gly Val Leu Gly Thr Asp Asn Asp Ala	
350 355 360	
CAA ACC CAT GAG AGT TTG GAG CAT AAA GCT CCC ATT AAA GAG CGC TTC	1155
Gln Thr His Glu Ser Leu Glu His Lys Ala Pro Ile Lys Glu Arg Phe	
365 370 375	
ATG TTT CAT TAT AAT TTC CCT CCT TTC TGC GTG GGC GAA GCG AGT TCT	1203
Met Phe His Tyr Asn Phe Pro Pro Phe Cys Val Gly Glu Ala Ser Ser	
380 385 390	

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 25...2088
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

TAATTTAAAA AAGGAACATT AAAT ATG GAT TTT ATC ACC ATC AAT TCT AGT	51
Met Asp Phe Ile Thr Ile Asn Ser Ser	
1 5	
AAC AAA ACC GAA GAG TTC GCT CTC AAA CAA GTG GCC AAA CAA GCC ACC	99
Asn Lys Thr Glu Glu Phe Ala Leu Lys Gln Val Ala Lys Gln Ala Thr	
10 15 20 25	
AGC TCT CTT TTA TAC CGA TTA GGA AAA ACC ATT ATT TTA GCG AGC GTG	147
Ser Ser Leu Leu Tyr Arg Leu Gly Lys Thr Ile Ile Leu Ala Ser Val	
30 35 40	
TGC GTG GAA AGA GAG CCT GTG AGT GAA GAT TTT CTG CCT TTA GTG GTG	195
Cys Val Glu Arg Glu Pro Val Ser Glu Asp Phe Leu Pro Leu Val Val	
45 50 55	
CAG TTT TTA GAA AAA TCT TAT GCA GCC GGA AAG ATC CCG GGC GGT TTT	243
Gln Phe Leu Glu Lys Ser Tyr Ala Ala Gly Lys Ile Pro Gly Gly Phe	
60 65 70	
GTT AAA AGA GAA GGC AGG GCG CAA GAT TTT GAA ATC TTA ACC TCT AGG	291
Val Lys Arg Glu Gly Arg Ala Gln Asp Phe Glu Ile Leu Thr Ser Arg	
75 80 85	
CTC ATA GAC AGG ACT TTA CGC CCT TTA TTC CCT AAA GAC TAC CGC TAC	339
Leu Ile Asp Arg Thr Leu Arg Pro Leu Phe Pro Lys Asp Tyr Arg Tyr	
90 95 100 105	
CCT ACA CAG ATC ACT TTA ATG GTT TTA AGC CAT GAT ATT GAA AAT GAC	387
Pro Thr Gln Ile Thr Leu Met Val Leu Ser His Asp Ile Glu Asn Asp	
110 115 120	
TTG CAG GTT TCT GCT TTA AAC GCC GCT TCA GCC GCT CTC TTT TTG GCC	435
Leu Gln Val Ser Ala Leu Asn Ala Ala Ser Ala Ala Leu Phe Leu Ala	
125 130 135	
CAT ATC GCT CCT ATT AAA AGC GTG AGC GCT TGC AGG ATC GCT AGG ATG	483
His Ile Ala Pro Ile Lys Ser Val Ser Ala Cys Arg Ile Ala Arg Met	
140 145 150	
GAT AAC GAA TTT ATC ATT AAC CCT AGC GCA AGC CTT TTG AAT CAA TCC	531
Asp Asn Glu Phe Ile Ile Asn Pro Ser Ala Ser Leu Leu Asn Gln Ser	
155 160 165	

TCT TGG AGT CAA AAA GAA TTG GAG ATT TTC CAA AAA GAA TTG ACT GCA 543
 Ser Trp Ser Gln Lys Glu Leu Glu Ile Phe Gln Lys Glu Leu Thr Ala
 145 150 155

ATC AAA ATA GAA GGG GCC CGC TAC CCT GAA AGA ATC AAT GAA ATG GTG 591
 Ile Lys Ile Glu Gly Ala Arg Tyr Pro Glu Arg Ile Asn Glu Met Val
 160 165 170

AAT CAA TAAAAGTATT GGGTATTTAT AATTGCATTG GCTCTTTTAA AA 639
 Asn Gln
 175

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

Met Ser Glu Ala Gly Leu Ser Ser Ile Gln Lys Ala His Gln Ile Cys
 1 5 10 15
 Pro Leu Ser Ala Leu Gln Ser Glu Tyr Ser Leu Trp Trp Arg Glu Pro
 20 25 30
 Glu Lys Glu Ile Leu Gly Phe Leu Glu Lys Glu Lys Ile Gly Phe Val
 35 40 45
 Ala Phe Ser Pro Leu Gly Lys Gly Phe Leu Gly Ala Lys Phe Glu Lys
 50 55 60
 Asn Ala Thr Phe Ala Ser Glu Asp Phe Arg Ser Val Ser Pro Arg Phe
 65 70 75 80
 Asn Gln Glu Asn Leu Ala Lys Asn Tyr Ala Leu Val Glu Leu Ile Gln
 85 90 95
 Asp His Ala His Ala Lys Gly Val Thr Pro Ala Gln Leu Ala Leu Ser
 100 105 110
 Trp Ile Leu His Thr Gln Lys Ile Ile Val Pro Leu Phe Gly Thr Thr
 115 120 125
 Lys Glu Ser Arg Leu Ile Glu Asn Ile Gly Ala Leu Gln Val Ser Trp
 130 135 140
 Ser Gln Lys Glu Leu Glu Ile Phe Gln Lys Glu Leu Thr Ala Ile Lys
 145 150 155 160
 Ile Glu Gly Ala Arg Tyr Pro Glu Arg Ile Asn Glu Met Val Asn Gln
 165 170 175

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...597
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

```

CACGCCCCATA GGAGAAGTGG CAGAAGTTAT GCAGCTCTTA TTAAAGAAGG AAAAATTAAA      60
GCTTGGGGG ATG ACT GAG GCA GGG TTA TCT AGC ATC CAA AAA GCC CAT CAA      111
  Met Ser Glu Ala Gly Leu Ser Ser Ile Gln Lys Ala His Gln
    1             5             10

ATT TGC CCT TTA AGC GCG TTG CAG AGC GAA TAT TCC TTG TGG TGG CGC      159
Ile Cys Pro Leu Ser Ala Leu Gln Ser Glu Tyr Ser Leu Trp Trp Arg
  15             20             25             30

GAA CCT GAA AAA GAG ATT TTA GGT TTT TTA GAA AAA GAA AAA ATT GGA      207
Glu Pro Glu Lys Glu Ile Leu Gly Phe Leu Glu Lys Glu Lys Ile Gly
           35             40             45

TTT GTC GCT TTT TCG CCT TTG GGT AAG GGG TTT TTA GGC GCG AAA TTT      255
Phe Val Ala Phe Ser Pro Leu Gly Lys Gly Phe Leu Gly Ala Lys Phe
           50             55             60

GAA AAA AAT GCC ACT TTC GCT AGT GAG GAT TTT AGA AGC GTT TCT CCT      303
Glu Lys Asn Ala Thr Phe Ala Ser Glu Asp Phe Arg Ser Val Ser Pro
           65             70             75

AGG TTT AAT CAA GAA AAT CTA GCC AAA AAT TAC GCC TTG GTG GAA TTA      351
Arg Phe Asn Gln Glu Asn Leu Ala Lys Asn Tyr Ala Leu Val Glu Leu
          80             85             90

ATC CAA GAT CAT GCA CAC GCT AAA GGC GTT ACA CCA GCC CAA CTG GCT      399
Ile Gln Asp His Ala His Ala Lys Gly Val Thr Pro Ala Gln Leu Ala
          95             100            105            110

CTC TCA TGG ATT TTG CAC ACG CAA AAA ATC ATT GTC CCT CTC TTT GGC      447
Leu Ser Trp Ile Leu His Thr Gln Lys Ile Ile Val Pro Leu Phe Gly
           115            120            125

ACC ACC AAA GAA TCT AGG CTC ATA GAA AAT ATA GGG GCT TTG CAG GTT      495
Thr Thr Lys Glu Ser Arg Leu Ile Glu Asn Ile Gly Ala Leu Gln Val
           130            135            140

```

```

Asp Ala Ile Gln Lys Ala Gln Leu Leu Ala Lys Val Ser Val Val Phe
      20      25      30
Gln Ser Phe Gly Phe Val Pro Ile Glu Thr Pro His Leu Glu Tyr Ala
      35      40      45
Gln Thr Leu Leu Pro Asp Ala Ser Ser Asp Ile Gln Lys Glu Ile Tyr
      50      55      60
Arg Phe Lys Asp His Gly Asp Arg Asp Val Ala Leu Arg Phe Asp Leu
      65      70      75      80
Thr Val Pro Leu Ala Arg Phe Val Ser Leu His His Gln Thr Leu Gly
      85      90      95
Met Pro Phe Lys Arg Tyr Ala Ile Gly Asn Val Phe Arg Gly Glu Arg
      100      105      110
Ala Gln Lys Gly Arg Tyr Arg Glu Phe Thr Gln Cys Asp Phe Asp Phe
      115      120      125
Ile Gly Ser Glu Ser Leu Val Cys Asp Ala Glu Ile Ile Gln Val Ile
      130      135      140
Val Ala Ser Leu Lys Ala Leu Asp Leu Glu Asp Phe Cys Val Ser Ile
      145      150      155      160
Asn His Arg Lys Ile Leu Asn Gly Ile Cys Glu Tyr Phe Gly Ile Ser
      165      170      175
Gln Val Asn Glu Ala Leu Arg Ile Val Asp Lys Leu Glu Lys Ile Gly
      180      185      190
Leu Asn Gly Val Glu Glu Glu Leu Lys Lys Glu Cys Gly Leu Asn Ser
      195      200      205
Asn Thr Ile Lys Glu Leu Leu Glu Leu Ile Gln Ile Lys Gln Asn Asp
      210      215      220
Leu Ser His Ala Glu Phe Glu Lys Ile Ala Tyr Leu Lys Asp Tyr
      225      230      235      240
Asn Glu Asn Leu Lys Lys Gly Ile Gln Asp Leu Glu Arg Leu Tyr Gln
      245      250      255
Leu Leu Gly Asp Leu Gln Ile Ser Gln Asn Leu Tyr Lys Ile Asp Phe
      260      265      270
Ser Ile Ala Arg Gly Leu Gly Tyr Tyr Thr Gly Ile Val Tyr Glu Thr
      275      280      285
Thr Leu Asn Glu Met Lys Ser Leu Gly Ser Val Cys Ser Gly Gly Arg
      290      295      300
Tyr Asp His Leu Thr Lys Asn Phe Ser Lys Glu Asn Leu Gln Gly Val
      305      310      315      320
Gly Ala Ser Ile Gly Ile Asp Arg Leu Ile Val Ala Leu Ser Glu Met
      325      330      335
Gln Leu Leu Asp Glu Arg Ser Thr Gln Ala Lys Val Leu Ile Ala Cys
      340      345      350
Met His Glu Glu Tyr Phe Ser Tyr Ala Asn Arg Leu Ala Glu Ser Leu
      355      360      365
Arg Gln Ser Gly Ile Phe Ser Glu Val Tyr Pro Glu Ala Gln Lys Ile
      370      375      380
Lys Lys Pro Phe Ser Tyr Ala Asn His Lys Gly His Glu Phe Val Ala
      385      390      395      400
Val Ile Gly Glu Glu Glu Phe Lys Ser Glu Thr Leu Ser Leu Lys Asn
      405      410      415
Met His Ser Gly Met Gln Leu Asn Cys Leu Ser Phe Leu Lys Ala Leu
      420      425      430
Glu Ile Ile Gly Glu Asn Asp Glu Asp Leu
      435      440

```

TTA GGG AGC GTG TGT TCA GGG GGG CGT TAT GAT CAT TTG ACT AAA AAT	966
Leu Gly Ser Val Cys Ser Gly Gly Arg Tyr Asp His Leu Thr Lys Asn	
300 305 310	
TTT TCT AAA GAG AAT TTA CAA GGG GTA GGG GCT TCT ATT GGG ATT GAT	1014
Phe Ser Lys Glu Asn Leu Gln Gly Val Gly Ala Ser Ile Gly Ile Asp	
315 320 325	
CGA TTG ATT GTG GCT TTG AGT GAA ATG CAA TTA TTA GAC GAG CGC TCC	1062
Arg Leu Ile Val Ala Leu Ser Glu Met Gln Leu Leu Asp Glu Arg Ser	
330 335 340	
ACC CAA GCC AAA GTT TTA ATC GCT TGC ATG CAT GAA GAG TAT TTT TCT	1110
Thr Gln Ala Lys Val Leu Ile Ala Cys Met His Glu Glu Tyr Phe Ser	
345 350 355	
TAC GCC AAC CGC TTA GCG GAG TCT TTA AGG CAA AGC GGG ATT TTT AGT	1158
Tyr Ala Asn Arg Leu Ala Glu Ser Leu Arg Gln Ser Gly Ile Phe Ser	
360 365 370 375	
GAA GTC TAT CCA GAA GCT CAA AAA ATC AAA AAA CCC TTT TCT TAT GCC	1206
Glu Val Tyr Pro Glu Ala Gln Lys Ile Lys Lys Pro Phe Ser Tyr Ala	
380 385 390	
AAC CAT AAA GGG CAT GAG TTT GTG GCT GTC ATT GGC GAA GAA GAA TTT	1254
Asn His Lys Gly His Glu Phe Val Ala Val Ile Gly Glu Glu Glu Phe	
395 400 405	
AAA AGC GAA ACT TTA AGC TTG AAA AAC ATG CAT TCA GGC ATG CAG TTG	1302
Lys Ser Glu Thr Leu Ser Leu Lys Asn Met His Ser Gly Met Gln Leu	
410 415 420	
AAT TGC TTG AGT TTT TTA AAA GCC CTT GAA ATC ATT GGA GAA AAC GAT	1350
Asn Cys Leu Ser Phe Leu Lys Ala Leu Glu Ile Ile Gly Glu Asn Asp	
425 430 435	
GAA GAC TTA TAATGTCGCT ATTGTTGGGG CCAGTGGGGC GGTAGG	1395
Glu Asp Leu	
440	

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

Met	Ile	Thr	Pro	Lys	Val	Leu	Ser	Gly	Phe	Lys	Asp	Arg	Leu	Pro	Lys
1				5				10					15		

Arg	Asp	Val	Ala	Leu	Arg	Phe	Asp	Leu	Thr	Val	Pro	Leu	Ala	Arg	Phe	
			75					80					85			
GTC	TCT	TTG	CAC	CAC	CAA	ACG	CTA	GGC	ATG	CCC	TTT	AAA	CGC	TAC	GCT	342
Val	Ser	Leu	His	His	Gln	Thr	Leu	Gly	Met	Pro	Phe	Lys	Arg	Tyr	Ala	
		90					95					100				
ATA	GGC	AAT	GTC	TTT	AGG	GGC	GAA	AGG	GCG	CAA	AAA	GGG	CGT	TAT	AGG	390
Ile	Gly	Asn	Val	Phe	Arg	Gly	Glu	Arg	Ala	Gln	Lys	Gly	Arg	Tyr	Arg	
		105				110					115					
GAA	TTT	ACG	CAA	TGC	GAT	TTT	GAT	TTT	ATA	GGG	AGC	GAG	AGT	TTG	GTG	438
Glu	Phe	Thr	Gln	Cys	Asp	Phe	Asp	Phe	Ile	Gly	Ser	Glu	Ser	Leu	Val	
120					125					130					135	
TGC	GAT	GCT	GAG	ATC	ATT	CAA	GTG	ATT	GTC	GCT	TCT	TTA	AAA	GCC	CTA	486
Cys	Asp	Ala	Glu	Ile	Ile	Gln	Val	Ile	Val	Ala	Ser	Leu	Lys	Ala	Leu	
				140					145					150		
GAT	TTA	GAA	GAT	TTT	TGC	GTC	TCT	ATC	AAC	CAC	AGA	AAA	ATT	TTG	AAC	534
Asp	Leu	Glu	Asp	Phe	Cys	Val	Ser	Ile	Asn	His	Arg	Lys	Ile	Leu	Asn	
			155					160					165			
GGG	ATA	TGC	GAA	TAT	TTT	GGG	ATC	TCT	CAA	GTG	AAT	GAA	GCG	TTG	CGC	582
Gly	Ile	Cys	Glu	Tyr	Phe	Gly	Ile	Ser	Gln	Val	Asn	Glu	Ala	Leu	Arg	
		170					175					180				
ATT	GTG	GAT	AAA	TTG	GAA	AAA	ATT	GGC	TTG	AAT	GGG	GTT	GAA	GAA	GAA	630
Ile	Val	Asp	Lys	Leu	Glu	Lys	Ile	Gly	Leu	Asn	Gly	Val	Glu	Glu	Glu	
	185					190					195					
TTA	AAA	AAA	GAG	TGC	GGT	TTA	AAT	TCA	AAC	ACC	ATT	AAA	GAG	CTT	TTA	678
Leu	Lys	Lys	Glu	Cys	Gly	Leu	Asn	Ser	Asn	Thr	Ile	Lys	Glu	Leu	Leu	
200					205					210					215	
GAA	TTA	ATT	CAA	ATC	AAA	CAA	AAC	GAT	TTA	AGC	CAT	GCG	GAA	TTT	TTT	726
Glu	Leu	Ile	Gln	Ile	Lys	Gln	Asn	Asp	Leu	Ser	His	Ala	Glu	Phe	Phe	
				220					225					230		
GAA	AAA	ATT	GCT	TAT	TTG	AAA	GAC	TAT	AAT	GAA	AAT	CTA	AAA	AAA	GGC	774
Glu	Lys	Ile	Ala	Tyr	Leu	Lys	Asp	Tyr	Asn	Glu	Asn	Leu	Lys	Lys	Gly	
			235					240					245			
ATA	CAG	GAT	TTA	GAA	AGG	CTA	TAC	CAG	TTG	CTA	GGG	GAT	TTG	CAA	ATT	822
Ile	Gln	Asp	Leu	Glu	Arg	Leu	Tyr	Gln	Leu	Leu	Gly	Asp	Leu	Gln	Ile	
		250					255					260				
TCT	CAA	AAC	CTG	TAT	AAA	ATT	GAT	TTT	TCT	ATC	GCT	AGG	GGA	TTA	GGG	870
Ser	Gln	Asn	Leu	Tyr	Lys	Ile	Asp	Phe	Ser	Ile	Ala	Arg	Gly	Leu	Gly	
	265					270					275					
TAT	TAT	ACA	GGG	ATT	GTG	TAT	GAA	ACC	ACG	CTT	AAT	GAA	ATG	AAG	TCT	918
Tyr	Tyr	Thr	Gly	Ile	Val	Tyr	Glu	Thr	Thr	Leu	Asn	Glu	Met	Lys	Ser	
280					285					290					295	

```

Ser Ala Thr Cys Val Arg Val Pro Val Leu Arg Ser His Ser Glu Ser
                245                250                255
Leu Ser Ile Ala Phe Glu Lys Glu Phe Asp Leu Lys Glu Val Tyr Glu
                260                265                270
Val Leu Lys Asn Ala Pro Ser Val Ala Val Cys Asp Asp Pro Ser His
                275                280                285
Asn Leu Tyr Pro Thr Pro Leu Lys Ala Ser His Thr Asp Ser Val Phe
                290                295                300
Ile Gly Arg Leu Arg Lys Asp Leu Phe Asp Lys Lys Thr Leu His Gly
305                310                315                320
Phe Cys Val Ala Asp Gln Leu Arg Val Gly Ala Ala Thr Asn Ala Leu
                325                330                335
Lys Ile Ala Leu His Tyr Ile Lys Asn Ala
                340                345

```

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1359
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

```

TAAAATTTTA GCATACAAAT ACAAGGAAAT GGA ATG ATT ACC CCT AAA GTG TTG      54
                Met Ile Thr Pro Lys Val Leu
                1                5

AGC GGG TTT AAA GAC CGC TTG CCT AAA GAT GCG ATA CAA AAA GCC CAG      102
Ser Gly Phe Lys Asp Arg Leu Pro Lys Asp Ala Ile Gln Lys Ala Gln
                10                15                20

TTG CTT GCG AAA GTT TCA GTC GTG TTT CAA AGT TTT GGT TTT GTG CCG      150
Leu Leu Ala Lys Val Ser Val Val Phe Gln Ser Phe Gly Phe Val Pro
                25                30                35

ATT GAA ACC CCT CAT TTG GAA TAC GCT CAA ACG TTA TTG CCT GAT GCG      198
Ile Glu Thr Pro His Leu Glu Tyr Ala Gln Thr Leu Leu Pro Asp Ala
40                45                50                55

AGC AGT GAT ATT CAA AAA GAA ATT TAT CGT TTT AAA GAC CAT GGG GAT      246
Ser Ser Asp Ile Gln Lys Glu Ile Tyr Arg Phe Lys Asp His Gly Asp
                60                65                70

AGA GAT GTG GCT TTA AGG TTT GAT TTG ACT GTG CCA TTA GCC CGC TTT      294

```

GAT AAG AAA ACT TTG CAT GGC TTT TGT GTG GCG GAT CAA TTG AGA GTG 1014
 Asp Lys Lys Thr Leu His Gly Phe Cys Val Ala Asp Gln Leu Arg Val
 315 320 325

GGG GCA GCC ACC AAC GCA CTC AAA ATC GCT CTG CAT TAC ATT AAG AAC 1062
 Gly Ala Ala Thr Asn Ala Leu Lys Ile Ala Leu His Tyr Ile Lys Asn
 330 335 340 345

GCT TGAGTTTATT CAAAGATAAC AAAGATGAAT GT 1097
 Ala

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

Met Lys Thr Tyr Asn Val Ala Ile Val Gly Ala Ser Gly Ala Val Gly
 1 5 10 15
 Gln Glu Leu Ile Lys Gly Leu Glu Asn Ser Phe Phe Pro Ile Lys Lys
 20 25 30
 Phe Val Pro Leu Ala Ser Thr Arg Ser Ala Gly Lys Lys Ile Lys Ala
 35 40 45
 Phe Asn Lys Asp Tyr Glu Ile Leu Glu Thr Thr His Glu Val Phe Glu
 50 55 60
 Arg Glu Lys Ile Asp Ile Ala Phe Phe Ser Ala Gly Gly Ser Val Ser
 65 70 75 80
 Xaa Glu Phe Ala Thr Ser Ala Ser Lys Thr Ala Leu Val Val Asp Asn
 85 90 95
 Thr Ser Phe Phe Arg Leu Asn Lys Asp Val Pro Leu Val Val Pro Glu
 100 105 110
 Ile Asn Ala Lys Glu Ile Phe Asn Ala Pro Leu Asn Ile Ile Ala Asn
 115 120 125
 Pro Asn Cys Ser Thr Ile Gln Met Thr Gln Ile Leu Asn Pro Leu His
 130 135 140
 Leu His Phe Lys Ile Lys Ser Val Ile Val Ser Thr Tyr Gln Ala Val
 145 150 155 160
 Ser Gly Ala Gly Asn Lys Gly Ile Glu Ser Leu Lys Asn Glu Leu Lys
 165 170 175
 Thr Ala Leu Glu Cys Leu Glu Lys Asp Pro Thr Ile Asp Leu Asn Gln
 180 185 190
 Val Leu Gln Ala Gly Ala Phe Ala Tyr Pro Ile Ala Phe Asn Ala Ile
 195 200 205
 Ala His Ile Asp Thr Phe Lys Glu Asn Gly Tyr Thr Lys Glu Glu Leu
 210 215 220
 Lys Met Leu His Glu Thr His Lys Ile Met Gly Val Asp Phe Pro Ile
 225 230 235 240

Thr	Ala	Leu	Val	Val	Asp	Asn	Thr	Ser	Phe	Phe	Arg	Leu	Asn	Lys	Asp	
90					95					100					105	
GTG	CCT	TTA	GTC	GTT	CCT	GAA	ATC	AAC	GCT	AAA	GAA	ATT	TTT	AAC	GCT	390
Val	Pro	Leu	Val	Val	Pro	Glu	Ile	Asn	Ala	Lys	Glu	Ile	Phe	Asn	Ala	
			110						115					120		
CCC	TTG	AAT	ATC	ATC	GCT	AAC	CCT	AAT	TGC	TCC	ACC	ATT	CAA	ATG	ACG	438
Pro	Leu	Asn	Ile	Ile	Ala	Asn	Pro	Asn	Cys	Ser	Thr	Ile	Gln	Met	Thr	
			125					130					135			
CAA	ATC	TTA	AAC	CCC	TTA	CAT	CTC	CAT	TTT	AAG	ATA	AAA	AGC	GTG	ATT	486
Gln	Ile	Leu	Asn	Pro	Leu	His	Leu	His	Phe	Lys	Ile	Lys	Ser	Val	Ile	
		140					145					150				
GTT	AGC	ACC	TAT	CAA	GCC	GTG	AGT	GGG	GCA	GGG	AAC	AAG	GGC	ATA	GAG	534
Val	Ser	Thr	Tyr	Gln	Ala	Val	Ser	Gly	Ala	Gly	Asn	Lys	Gly	Ile	Glu	
	155					160					165					
AGT	TTA	AAA	AAT	GAG	TTA	AAA	ACC	GCT	TTA	GAG	TGT	TTG	GAA	AAA	GAC	582
Ser	Leu	Lys	Asn	Glu	Leu	Lys	Thr	Ala	Leu	Glu	Cys	Leu	Glu	Lys	Asp	
170					175					180					185	
CCC	ACT	ATT	GAT	TTA	AAC	CAA	GTC	TTG	CAA	GCT	GGG	GCT	TTC	GCT	TAT	630
Pro	Thr	Ile	Asp	Leu	Asn	Gln	Val	Leu	Gln	Ala	Gly	Ala	Phe	Ala	Tyr	
				190					195					200		
CCG	ATC	GCT	TTC	AAT	GCG	ATC	GCT	CAT	ATT	GAT	ACT	TTT	AAG	GAG	AAT	678
Pro	Ile	Ala	Phe	Asn	Ala	Ile	Ala	His	Ile	Asp	Thr	Phe	Lys	Glu	Asn	
			205					210					215			
GGT	TAC	ACG	AAA	GAA	GAG	CTA	AAA	ATG	CTG	CAT	GAA	ACC	CAT	AAA	ATC	726
Gly	Tyr	Thr	Lys	Glu	Glu	Leu	Lys	Met	Leu	His	Glu	Thr	His	Lys	Ile	
		220					225					230				
ATG	GGC	GTG	GAT	TTC	CCT	ATC	AGC	GCG	ACT	TGC	GTG	CGC	GTG	CCG	GTA	774
Met	Gly	Val	Asp	Phe	Pro	Ile	Ser	Ala	Thr	Cys	Val	Arg	Val	Pro	Val	
	235					240					245					
TTG	AGG	AGC	CAT	AGC	GAG	AGT	TTG	AGT	ATC	GCT	TTT	GAA	AAA	GAA	TTC	822
Leu	Arg	Ser	His	Ser	Glu	Ser	Leu	Ser	Ile	Ala	Phe	Glu	Lys	Glu	Phe	
250					255				260						265	
GAT	CTC	AAA	GAA	GTC	TAT	GAA	GTT	TTA	AAA	AAC	GCC	CCT	AGC	GTG	GCT	870
Asp	Leu	Lys	Glu	Val	Tyr	Glu	Val	Leu	Lys	Asn	Ala	Pro	Ser	Val	Ala	
				270					275					280		
GTT	TGC	GAT	GAT	CCC	AGT	CAT	AAT	CTT	TAC	CCC	ACG	CCC	CTA	AAA	GCG	918
Val	Cys	Asp	Asp	Pro	Ser	His	Asn	Leu	Tyr	Pro	Thr	Pro	Leu	Lys	Ala	
			285					290					295			
AGC	CAC	ACG	GAT	AGC	GTC	TTT	ATA	GGG	CGC	TTG	AGG	AAG	GAT	TTG	TTT	966
Ser	His	Thr	Asp	Ser	Val	Phe	Ile	Gly	Arg	Leu	Arg	Lys	Asp	Leu	Phe	
		300					305					310				


```

Ile Ser Leu Gln Met Arg Val Leu Gln Leu Ala Pro Asp Ala Thr Asp
  210                      215                      220
Val Ala Ser Ala Ile Tyr Ser Gly Ser Tyr Asn Val Gly Ile Gly Ser
  225                      230                      235                      240
Gly Ala Leu Phe Gly Ser Ile Val Ile His Gln Leu Gly Leu Gly Tyr
                      245                      250                      255
Ile Gly Phe Val Gly Gly Ala Leu Gly Leu Leu Ala Leu Phe Trp Leu
                      260                      265                      270
Arg Phe Ile Thr Ile Lys Phe Lys Lys Thr
  275                      280

```

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1065
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

```

AAGCCCTTGA AATCATTGGA GAAAACG ATG AAG ACT TAT AAT GTC GCT ATT GTT      54
                      Met Lys Thr Tyr Asn Val Ala Ile Val
                      1                      5

GGG GCC AGT GGG GCG GTA GGC CAA GAG CTG ATT AAG GGT TTA GAA AAT      102
Gly Ala Ser Gly Ala Val Gly Gln Glu Leu Ile Lys Gly Leu Glu Asn
10                      15                      20                      25

TCT TTT TTC CCA ATT AAA AAA TTT GTC CCG CTC GCT AGC ACT AGG AGT      150
Ser Phe Phe Pro Ile Lys Lys Phe Val Pro Leu Ala Ser Thr Arg Ser
                      30                      35                      40

GCT GGT AAA AAG ATC AAA GCT TTC AAT AAA GAC TAT GAA ATT TTA GAA      198
Ala Gly Lys Lys Ile Lys Ala Phe Asn Lys Asp Tyr Glu Ile Leu Glu
                      45                      50                      55

ACC ACG CAT GAA GTT TTT GAA AGA GAA AAA ATA GAC ATC GCC TTT TTT      246
Thr Thr His Glu Val Phe Glu Arg Glu Lys Ile Asp Ile Ala Phe Phe
                      60                      65                      70

AGC GCT GGG GGG AGC GTG AGC GMA GAA TTT GCT ACA AGC GCT TCA AAA      294
Ser Ala Gly Gly Ser Val Ser Xaa Glu Phe Ala Thr Ser Ala Ser Lys
75                      80                      85

ACG GCC TTA GTG GTT GAT AAC ACG AGC TTT TTT AGA TTG AAT AAA GAT      342

```

```

AGC TAT AAT GTG GGG ATT GGA TCA GGA GCG CTG TTT GGC AGT ATT GTG      773
Ser Tyr Asn Val Gly Ile Gly Ser Gly Ala Leu Phe Gly Ser Ile Val
      235                      240                      245

ATC CAC CAA CTA GGG CTA GGA TAT ATT GGC TTT GTG GGT GGG GCT TTA      821
Ile His Gln Leu Gly Leu Gly Tyr Ile Gly Phe Val Gly Gly Ala Leu
      250                      255                      260

GGT TTG TTG GCG CTC TTT TGG CTT AGA TTC ATT ACG ATA AAG TTT AAA      869
Gly Leu Leu Ala Leu Phe Trp Leu Arg Phe Ile Thr Ile Lys Phe Lys
      265                      270                      275                      280

AAA ACA TAAAGAGCGT TAAAAGGATT AGCCCAATAA AGGAGAATCC CTTTCGCACT      925
Lys Thr

```

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

```

Met Gly Ile Ala Phe Ala His Ser Ile Phe Trp Ser Ile Thr Ala Ser
 1           5           10           15
Leu Val Ile Arg Val Ala Pro Arg Asn Lys Lys Gln Gln Ala Leu Gly
      20           25           30
Leu Leu Ala Leu Gly Ser Ser Leu Ala Met Ile Leu Gly Leu Pro Leu
      35           40           45
Gly Arg Ile Ile Gly Gln Ile Leu Asp Trp Arg Ser Thr Phe Gly Val
      50           55           60
Ile Gly Gly Val Ala Thr Leu Ile Ala Leu Leu Met Trp Lys Leu Leu
      65           70           75           80
Pro His Leu Pro Ser Arg Asn Ala Gly Thr Leu Ala Ser Val Pro Val
      85           90           95
Leu Met Lys Arg Pro Leu Leu Met Gly Ile Tyr Leu Leu Val Ile Met
      100          105          110
Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe Ile
      115          120          125
Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu Phe
      130          135          140
Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg Leu
      145          150          155          160
Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu Val
      165          170          175
Ile Cys Pro Gln Leu Leu Leu Phe Val Phe Lys Asn Leu Glu Trp Val
      180          185          190
Val Phe Leu Gln Ile Phe Leu Trp Gly Ile Gly Ile Thr Ser Leu Gly
      195          200          205

```

ATT TTT TGG TCC ATC ACG GCT TCT TTA GTC ATT CGT GTC GCG CCA AGA	101
Ile Phe Trp Ser Ile Thr Ala Ser Leu Val Ile Arg Val Ala Pro Arg	
10 15 20	
AAT AAA AAA CAA CAG GCC TTA GGG CTG TTA GCG TTA GGG AGT TCG TTA	149
Asn Lys Lys Gln Gln Ala Leu Gly Leu Leu Ala Leu Gly Ser Ser Leu	
25 30 35 40	
GCG ATG ATT TTA GGG TTG CCG CTT GGG AGG ATC ATT GGG CAA ATT CTA	197
Ala Met Ile Leu Gly Leu Pro Leu Gly Arg Ile Ile Gly Gln Ile Leu	
45 50 55	
GAT TGG CGT TCC ACT TTT GGC GTG ATC GGG GGC GTT GCG ACC CTT ATA	245
Asp Trp Arg Ser Thr Phe Gly Val Ile Gly Gly Val Ala Thr Leu Ile	
60 65 70	
GCG TTG CTT ATG TGG AAA TTG CTC CCG CAT CTA CCC AGT AGA AAC GCA	293
Ala Leu Leu Met Trp Lys Leu Leu Pro His Leu Pro Ser Arg Asn Ala	
75 80 85	
GGC ACG CTC GCA AGT GTC CCT GTA TTA ATG AAA CGG CCG CTT TTA ATG	341
Gly Thr Leu Ala Ser Val Pro Val Leu Met Lys Arg Pro Leu Leu Met	
90 95 100	
GGG ATT TAT TTG CTT GTG ATC ATG GTC ATC TCT GGG CAT TTC ACC ACT	389
Gly Ile Tyr Leu Leu Val Ile Met Val Ile Ser Gly His Phe Thr Thr	
105 110 115 120	
TAT AGT TAT ATT GAG CCT TTT ATC ATT CAA ATC AGC CAA TTT TCT CCT	437
Tyr Ser Tyr Ile Glu Pro Phe Ile Ile Gln Ile Ser Gln Phe Ser Pro	
125 130 135	
GAC ATT ACA ACG CTA ATG TTG TTT GTG TTT GGG TTA GCG GGC GTG GTG	485
Asp Ile Thr Thr Leu Met Leu Phe Val Phe Gly Leu Ala Gly Val Val	
140 145 150	
GGG AGT TTT TTG TTC GGC CGT TTG TAT GCA AAA AAT TCA AGA AAA TTT	533
Gly Ser Phe Leu Phe Gly Arg Leu Tyr Ala Lys Asn Ser Arg Lys Phe	
155 160 165	
ATC GCT TTT GCG ATG GTT TTA GTC ATT TGC CCG CAA CTC TTG CTT TTT	581
Ile Ala Phe Ala Met Val Leu Val Ile Cys Pro Gln Leu Leu Leu Phe	
170 175 180	
GTG TTT AAA AAC TTA GAG TGG GTG GTT TTC TTG CAA ATT TTC TTA TGG	629
Val Phe Lys Asn Leu Glu Trp Val Val Phe Leu Gln Ile Phe Leu Trp	
185 190 195 200	
GGG ATT GGG ATC ACT TCG CTT GGG ATT TCC TTG CAA ATG AGG GTG TTG	677
Gly Ile Gly Ile Thr Ser Leu Gly Ile Ser Leu Gln Met Arg Val Leu	
205 210 215	
CAG CTT GCG CCG GAT GCC ACG GAT GTT GCG AGT GCG ATT TAC TCA GGG	725
Gln Leu Ala Pro Asp Ala Thr Asp Val Ala Ser Ala Ile Tyr Ser Gly	
220 225 230	

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

```

Met Ser Tyr Phe Tyr Lys His Cys Leu Lys Phe Ser Leu Val Gly Leu
 1           5           10           15
Leu Gly Leu Leu Ser Val Gln Leu Asp Ala Arg Ser Phe Val Asp Gly
 20           25           30
Asp Leu Asp Ile Gln Lys Phe Ser Tyr Glu Asp Ser Leu Leu Lys Lys
 35           40           45
Gly Asp Pro Asn Gly Val His Lys Val Gln Val Arg Asp Tyr Lys Gly
 50           55           60
Lys Met Gln Glu Ala Glu Ile His Ser Glu Ile Arg Ile Ala Leu Lys
 65           70           75           80
Pro Gly Val Lys Lys Glu Val Lys Lys Gly Lys Ile Tyr Ser Ala Gln
 85           90           95
Ile Asn Asp Gly Met Cys Tyr Ala Phe Arg Met Leu Gln Thr Gly Asp
100          105          110
Asn Thr Thr Gly Leu Asp Ser Lys Glu Phe Pro Lys Gln Ser Arg Glu
115          120          125
Lys Lys Gly Arg Val Ile Thr Leu Ile Gly Lys Gly Glu Val Pro Tyr
130          135          140
Leu Ile Leu Glu Thr Asp Cys Gln Val Gly Asp Ile Ala Lys Ile Ser
145          150          155          160
Leu Val Gly Asn Phe Asp Gly Thr Gly Phe Leu Thr Glu Tyr Lys Phe
165          170          175
Lys Asp Ala Lys Pro Ile Tyr
180

```

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 925 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 30...875
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

```

GGAATTTTTTG GGTGCTACTC CTTTCTCGT ATG GGT ATC GCT TTT GCC CAC TCT
Met Gly Ile Ala Phe Ala His Ser
 1           5

```

53

AAGGATTTGT TG ATG AGT TAT TTT TAT AAG CAC TGT TTG AAA TTT TCG TTG	51
Met Ser Tyr Phe Tyr Lys His Cys Leu Lys Phe Ser Leu	
1 5 10	
GTT GGG TTG CTA GGG CTT TTG AGC GTT CAG CTT GAC GCT AGG AGT TTT	99
Val Gly Leu Leu Gly Leu Ser Val Gln Leu Asp Ala Arg Ser Phe	
15 20 25	
GTT GAT GGG GAT TTA GAC ATT CAG AAA TTC AGC TAT GAA GAT TCT CTA	147
Val Asp Gly Asp Leu Asp Ile Gln Lys Phe Ser Tyr Glu Asp Ser Leu	
30 35 40 45	
CTT AAA AAG GGA GAC CCT AAT GGC GTG CAT AAA GTG CAG GTG CGA GAT	195
Leu Lys Lys Gly Asp Pro Asn Gly Val His Lys Val Gln Val Arg Asp	
50 55 60	
TAT AAA GGC AAA ATG CAA GAA GCT GAG ATC CAC TCA GAA ATA CGC ATT	243
Tyr Lys Gly Lys Met Gln Glu Ala Glu Ile His Ser Glu Ile Arg Ile	
65 70 75	
GCG CTT AAA CCG GGG GTT AAA AAA GAA GTT AAA AAA GGC AAG ATT TAT	291
Ala Leu Lys Pro Gly Val Lys Lys Glu Val Lys Lys Gly Lys Ile Tyr	
80 85 90	
AGC GCT CAA ATC AAT GAT GGC ATG TGC TAT GCT TTT AGA ATG CTC CAA	339
Ser Ala Gln Ile Asn Asp Gly Met Cys Tyr Ala Phe Arg Met Leu Gln	
95 100 105	
ACC GGC GAT AAT ACC ACA GGC CTT GAT TCT AAA GAG TTC CCC AAG CAA	387
Thr Gly Asp Asn Thr Thr Gly Leu Asp Ser Lys Glu Phe Pro Lys Gln	
110 115 120 125	
AGT CGT GAG AAA AAG GGC CGA GTG ATC ACT TTA ATC GGT AAA GGT GAA	435
Ser Arg Glu Lys Lys Gly Arg Val Ile Thr Leu Ile Gly Lys Gly Glu	
130 135 140	
GTG CCT TAT CTT ATT TTA GAA ACC GAT TGC CAA GTG GGT GAT ATT GCA	483
Val Pro Tyr Leu Ile Leu Glu Thr Asp Cys Gln Val Gly Asp Ile Ala	
145 150 155	
AAG ATC TCT TTG GTG GGT AAT TTT GAT GGC ACT GGG TTT CTT ACG GAA	531
Lys Ile Ser Leu Val Gly Asn Phe Asp Gly Thr Gly Phe Leu Thr Glu	
160 165 170	
TAT AAA TTC AAA GAC GCT AAA CCC ATT TAC TAGTCTTTAT TCTTCGCTTC ATT	584
Tyr Lys Phe Lys Asp Ala Lys Pro Ile Tyr	
175 180	
CTTAA	589

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

```

Met Ser Val Ile Leu Glu Thr Lys Gly Leu Lys Lys Thr Tyr Gln Asn
 1           5           10           15
His Leu Val Leu Asp Gly Ile Asn Phe Thr Leu Asn Lys Gly Glu Val
      20           25           30
Ala Val Ile Leu Gly Pro Ser Gly Cys Gly Lys Ser Thr Phe Leu Lys
      35           40           45
Cys Leu Asn Gly Leu Glu Lys Ile Asn Glu Gly Glu Ile Leu Phe Glu
      50           55           60
Asn Thr Asn Leu Asn Asn Lys Ala Thr Asn Trp Asn Gln Met Arg Gln
65           70           75           80
Lys Ile Gly Met Val Phe Gln Asn Tyr Glu Leu Phe Pro His Leu Asn
      85           90           95
Val Leu Asp Asn Ile Leu Leu Ala Pro Met Lys Val Gln Lys Arg Ser
      100          105          110
Lys Asp Glu Val Ile Ser Gln Ala Ile Glu Leu Leu Lys Arg Val Gly
      115          120          125
Leu Glu His Lys Gln Gln Ala Tyr Pro Lys Glu Leu Ser Gly Gly Gln
      130          135          140
Lys Gln Arg Val Ala Ile Val Arg Ser Leu Cys Met Arg Pro Lys Ile
145          150          155          160
Met Leu Phe Asp Glu Val Thr Ala Ser Leu Asp Pro Glu Met Val Lys
      165          170          175
Glu Val Leu Glu Val Ile Leu Glu Leu Ala Thr Thr Gly Met Ser Met
      180          185          190
Val Ile Val Thr His Glu Met Lys Phe Ala Gln Lys Ile Ala His Lys
      195          200          205
Ile Val Phe Phe Asp Ser Gly Lys Ile Ala Glu Glu Asn Asn Ala Lys
      210          215          220
Glu Phe Phe Asn His Pro Lys Ser Gln Arg Ala Gln Lys Phe Leu Glu
225          230          235          240
Thr Phe His Phe Leu Gly Ser Cys
      245

```

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...561
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

60										65					70					
ACT	AAC	TGG	AAT	CAA	ATG	CGC	CAA	AAA	ATA	GGC	ATG	GTG	TTT	CAA	AAT	294				
Thr	Asn	Trp	Asn	Gln	Met	Arg	Gln	Lys	Ile	Gly	Met	Val	Phe	Gln	Asn					
75			80			85														
TAT	GAA	TTG	TTC	CCG	CAT	TTA	AAT	GTG	TTA	GAT	AAT	ATC	TTA	CTC	GCT	342				
Tyr	Glu	Leu	Phe	Pro	His	Leu	Asn	Val	Leu	Asp	Asn	Ile	Leu	Leu	Ala					
90			95			100														
CCT	ATG	AAA	GTG	CAA	AAA	CGA	TCC	AAA	GAT	GAG	GTT	ATT	TCT	CAA	GCC	390				
Pro	Met	Lys	Val	Gln	Lys	Arg	Ser	Lys	Asp	Glu	Val	Ile	Ser	Gln	Ala					
105			110			115			120											
ATA	GAG	CTT	TTA	AAG	CGA	GTG	GGT	TTG	GAG	CAT	AAA	CAA	CAA	GCT	TAC	438				
Ile	Glu	Leu	Leu	Lys	Arg	Val	Gly	Leu	Glu	His	Lys	Gln	Gln	Ala	Tyr					
125			130			135														
CCT	AAA	GAA	TTG	AGC	GGC	GGA	CAA	AAA	CAA	CGA	GTA	GCG	ATC	GTG	CGC	486				
Pro	Lys	Glu	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val	Ala	Ile	Val	Arg					
140			145			150														
TCT	TTA	TGC	ATG	CGA	CCA	AAA	ATC	ATG	CTT	TTT	GAT	GAA	GTA	ACC	GCC	534				
Ser	Leu	Cys	Met	Arg	Pro	Lys	Ile	Met	Leu	Phe	Asp	Glu	Val	Thr	Ala					
155			160			165														
TCT	TTA	GAC	CCT	GAA	ATG	GTT	AAA	GAA	GTT	TTA	GAA	GTG	ATT	TTA	GAA	582				
Ser	Leu	Asp	Pro	Glu	Met	Val	Lys	Glu	Val	Leu	Glu	Val	Ile	Leu	Glu					
170			175			180														
TTA	GCC	ACA	ACA	GGC	ATG	AGC	ATG	GTG	ATT	GTA	ACG	CAT	GAA	ATG	AAA	630				
Leu	Ala	Thr	Thr	Gly	Met	Ser	Met	Val	Ile	Val	Thr	His	Glu	Met	Lys					
185			190			195			200											
TTC	GCG	CAA	AAA	ATC	GCT	CAT	AAA	ATC	GTG	TTT	TTT	GAT	AGC	GGT	AAA	678				
Phe	Ala	Gln	Lys	Ile	Ala	His	Lys	Ile	Val	Phe	Phe	Asp	Ser	Gly	Lys					
205			210			215														
ATC	GCT	GAA	GAA	AAC	AAC	GCT	AAA	GAA	TTT	TTT	AAC	CAC	CCG	AAA	TCT	726				
Ile	Ala	Glu	Glu	Asn	Asn	Ala	Lys	Glu	Phe	Phe	Asn	His	Pro	Lys	Ser					
220			225			230														
CAA	AGA	GCG	CAA	AAA	TTT	TTA	GAA	ACT	TTC	CAT	TTT	TTA	GGG	AGC	TGT	775				
Gln	Arg	Ala	Gln	Lys	Phe	Leu	Glu	Thr	Phe	His	Phe	Leu	Gly	Ser	Cys					
235			240			245														
AAATAAAGTT TGCTAAAAAG ATGATTCTAA TT															807					

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) INFORMATION FOR SEO ID NO:1005:

(A) LENGTH: 807 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 31...774
(D) OTHER INFORMATION:

AAAAAAAAATT CCAACACATT AGAGGGTAAA																54
Met Ser Val Ile Leu Glu Thr Lys																
1 5																
GGG	TTA	AAA	AAA	ACC	TAT	CAA	AAC	CAT	TTG	GTT	TTA	GAC	GGC	ATC	AAT	102
Gly	Leu	Lys	Lys	Thr	Tyr	Gln	Asn	His	Leu	Val	Leu	Asp	Gly	Ile	Asn	
10 15 20																
TTC	ACT	TTA	AAT	AAG	GGT	GAA	GTG	GCA	GTG	ATT	TTA	GGG	CCT	AGC	GGG	150
Phe	Thr	Leu	Asn	Lys	Gly	Glu	Val	Ala	Val	Ile	Leu	Gly	Pro	Ser	Gly	
25 30 35 40																
TGC	GGG	AAA	AGC	ACT	TTT	TTA	AAA	TGC	CTA	AAC	GGG	CTT	GAA	AAG	ATT	198
Cys	Gly	Lys	Ser	Thr	Phe	Leu	Lys	Cys	Leu	Asn	Gly	Leu	Glu	Lys	Ile	
45 50 55																
AAT	GAA	GGT	GAA	ATC	CTT	TTT	GAA	AAC	ACT	AAC	CTT	AAC	AAT	AAG	GCC	246
Asn	Glu	Gly	Glu	Ile	Leu	Phe	Glu	Asn	Thr	Asn	Leu	Asn	Asn	Lys	Ala	

105	110	115	120	
GCT CTG GCT TTA GGC TTA GAT TCA AAA AAG GTG ATT TTT AAT ATT ATT				438
Ala Leu Ala Leu Gly Leu Asp Ser Lys Lys Val Ile Phe Asn Ile Ile				
	125	130	135	
TTC CCT CAA AGC TTT TTG TCT TTA TTG CCC TCA AGC CTT AAT TTG TTC				486
Phe Pro Gln Ser Phe Leu Ser Leu Leu Pro Ser Ser Leu Asn Leu Phe				
	140	145	150	
ACG CGC ATG ATC AAA ACC ACG GCT TTA GTT TCT CTC ATT GGA GCG ATT				534
Thr Arg Met Ile Lys Thr Thr Ala Leu Val Ser Leu Ile Gly Ala Ile				
	155	160	165	
GAT TTG CTA AAA GTG GGC CAG CAA ATC ATA GAG CTT AAC CTC TTA CGC				582
Asp Leu Leu Lys Val Gly Gln Gln Ile Ile Glu Leu Asn Leu Leu Arg				
	170	175	180	
ATG CCT AAT GCG AGC TTT GTG GTT TAT GGC GTT ATC TTA ATG TTT TAT				630
Met Pro Asn Ala Ser Phe Val Val Tyr Gly Val Ile Leu Met Phe Tyr				
	185	190	195	200
TTT AGT TTA TGC TAT AGT TTG AGC CTG TAT AGT TCC TAT TTA GAA AAA				678
Phe Ser Leu Cys Tyr Ser Leu Ser Leu Tyr Ser Ser Tyr Leu Glu Lys				
	205	210	215	
AAA TTC CAA CAC ATT AGA GGG TAAATGAGC GTGATTTTAG AAACCAAAGG GTTA				733
Lys Phe Gln His Ile Arg Gly				
	220			
AAAA				737

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

Met Gly Val Leu Leu Glu Leu Asp Asn Leu Lys Arg Leu Leu Glu Gly																			
1				5				10					15						
Phe Glu Thr Thr Leu Leu Ile Ala Leu Ser Ser Ala Met Ile Ser Ile																			
			20				25					30							
Ile Val Gly Met Leu Leu Gly Ser Leu Met Ala Phe Gly Ser Gln Ile																			
		35				40				45									
Val Val Leu Ala Cys Arg Val Tyr Leu Glu Ser Ile Arg Ile Ile Pro																			
	50				55				60										
Leu Leu Ala Trp Leu Phe Ile Val Tyr Phe Gly Leu Ala Ser Trp Phe																			
65				70			75					80							
Asp Leu His Ile Ser Ala Val Leu Ala Ser Val Ile Val Phe Ser Leu																			

	180		185		190
Thr Tyr Leu	Ile Ala Leu	Leu Pro Leu	Ser Val Leu	Phe Val Ile	Leu
	195		200		205
Glu Arg Phe	Phe Lys Lys	Lys Val Ala			
	210		215		

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...699
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

AGCGTTTCTT TAAAAAGAAA GTGGCTTAAA	ATG GGA GTT TTA CTA GAA TTA GAC	54
	Met Gly Val Leu Leu Glu Leu Asp	
	1 5	
AAC CTT AAG CGT TTG TTA GAA GGG TTT GAA ACC ACT CTT TTG ATC GCT	102	
Asn Leu Lys Arg Leu Leu Glu Gly Phe Glu Thr Thr Leu Leu Ile Ala		
10 15 20		
CTT AGC TCT GCA ATG ATT TCA ATC ATT GTT GGA ATG CTT TTG GGG AGC	150	
Leu Ser Ser Ala Met Ile Ser Ile Ile Val Gly Met Leu Leu Gly Ser		
25 30 35 40		
TTG ATG GCG TTT GGT TCT CAA ATA GTG GTT TTG GCG TGT CGT GTG TAT	198	
Leu Met Ala Phe Gly Ser Gln Ile Val Val Leu Ala Cys Arg Val Tyr		
45 50 55		
TTA GAA AGC ATT CGC ATC ATC CCG CTT TTA GCA TGG CTT TTT ATT GTG	246	
Leu Glu Ser Ile Arg Ile Ile Pro Leu Leu Ala Trp Leu Phe Ile Val		
60 65 70		
TAT TTC GGG TTA GCG AGC TGG TTT GAT TTG CAT ATT AGC GCG GTT TTG	294	
Tyr Phe Gly Leu Ala Ser Trp Phe Asp Leu His Ile Ser Ala Val Leu		
75 80 85		
GCA AGC GTT ATT GTT TTT AGC TTG TGG GGT GGC GCT GAA ATG ATG GAT	342	
Ala Ser Val Ile Val Phe Ser Leu Trp Gly Gly Ala Glu Met Met Asp		
90 95 100		
TTA ACT AGG GGG GTT TTA ACT TCC GTG AGC AAA CAC CAA ATA GAA AGC	390	
Leu Thr Arg Gly Val Leu Thr Ser Val Ser Lys His Gln Ile Glu Ser		

140	145	150	155	
AAA GAA ACT TCG GTG GTG GGC GCG ATA GCC CTA ACC GAT ATT ATG TTT				532
Lys Glu Thr Ser Val Val Gly Ala Ile Ala Leu Thr Asp Ile Met Phe				
	160	165	170	
GTG GCG AAA GAT TTT ATT GGC ATT TAT TAT AAA ACG ACT GAA AGC CTT				580
Val Ala Lys Asp Phe Ile Gly Ile Tyr Tyr Lys Thr Thr Glu Ser Leu				
	175	180	185	
TTG ATG TTA AGC CTC ACT TAT TTG ATC GCT TTA CTC CCT TTA AGC GTT				628
Leu Met Leu Ser Leu Thr Tyr Leu Ile Ala Leu Leu Pro Leu Ser Val				
	190	195	200	
TTG TTT GTG ATC TTA GAG CGT TTC TTT AAA AAG AAA GTG GCT TAAAATGGG				679
Leu Phe Val Ile Leu Glu Arg Phe Phe Lys Lys Lys Val Ala				
	205	210	215	
AGTTTTACTA GAATTAGACA ACCTT				704

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

Met	Ala	Leu	Asp	Trp	Asp	Phe	Met	Phe	His	Ser	Ile	Pro	Ala	Phe	Phe
1				5					10					15	
Lys	Gly	Leu	Glu	Leu	Thr	Leu	Tyr	Ile	Ser	Phe	Phe	Gly	Ile	Leu	Leu
			20					25					30		
Ser	Leu	Leu	Val	Gly	Phe	Leu	Cys	Ala	Ile	Val	Leu	Tyr	Phe	Lys	Thr
			35				40					45			
Arg	Phe	Leu	Ser	Pro	Val	Val	Tyr	Ile	Tyr	Gly	Glu	Ile	Ala	Arg	Asn
			50				55				60				
Thr	Pro	Leu	Leu	Ile	Gln	Leu	Phe	Phe	Leu	Tyr	Tyr	Gly	Leu	Asn	Glu
					70					75				80	
Ile	Gly	Leu	Ser	Ala	Leu	Glu	Cys	Ala	Ile	Leu	Ala	Leu	Gly	Phe	Leu
				85					90				95		
Gly	Gly	Gly	Tyr	Met	Ser	Gln	Ser	Phe	Leu	Leu	Gly	Phe	Lys	Ser	Leu
			100					105					110		
Ala	Ser	Ile	Gln	Arg	Glu	Ser	Ala	Leu	Ser	Leu	Gly	Phe	Ser	Pro	Leu
			115				120					125			
Lys	Met	Met	Tyr	Tyr	Ile	Ile	Leu	Pro	Gln	Ser	Leu	Ser	Val	Ser	Met
			130				135				140				
Pro	Ser	Ile	Gly	Ala	Asn	Val	Ile	Phe	Leu	Leu	Lys	Glu	Thr	Ser	Val
					150					155				160	
Val	Gly	Ala	Ile	Ala	Leu	Thr	Asp	Ile	Met	Phe	Val	Ala	Lys	Asp	Phe
				165					170					175	
Ile	Gly	Ile	Tyr	Tyr	Lys	Thr	Thr	Glu	Ser	Leu	Leu	Met	Leu	Ser	Leu

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 20...670
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

ATTTTAAAGG TATAGCGTT ATG GCA TTA GAT TGG GAT TTT ATG TTT CAC TCC	52
Met Ala Leu Asp Trp Asp Phe Met Phe His Ser	
1 5 10	
ATC CCT GCG TTT TTT AAG GGG TTA GAA CTC ACG CTT TAT ATT TCT TTC	100
Ile Pro Ala Phe Phe Lys Gly Leu Glu Leu Thr Leu Tyr Ile Ser Phe	
15 20 25	
TTT GGG ATT TTG CTC TCT CTT TTG GTG GGG TTT TTG TGC GCG ATC GTT	148
Phe Gly Ile Leu Leu Ser Leu Leu Val Gly Phe Leu Cys Ala Ile Val	
30 35 40	
TTG TAT TTT AAA ACG CGC TTT CTC TCT CCT GTT GTC TAT ATC TAT GGC	196
Leu Tyr Phe Lys Thr Arg Phe Leu Ser Pro Val Val Tyr Ile Tyr Gly	
45 50 55	
GAA ATC GCT AGG AAC ACG CCC CTG CTC ATC CAG CTT TTC TTT TTG TAT	244
Glu Ile Ala Arg Asn Thr Pro Leu Leu Ile Gln Leu Phe Phe Leu Tyr	
60 65 70 75	
TAC GGG TTG AAT GAA ATC GGT TTG AGC GCT TTA GAG TGC GCG ATT TTA	292
Tyr Gly Leu Asn Glu Ile Gly Leu Ser Ala Leu Glu Cys Ala Ile Leu	
80 85 90	
GCG TTA GGG TTT TTG GGT GGG GGG TAT ATG AGT CAA AGT TTT TTG CTT	340
Ala Leu Gly Phe Leu Gly Gly Gly Tyr Met Ser Gln Ser Phe Leu Leu	
95 100 105	
GGG TTT AAG AGC CTA GCT TCC ATT CAA AGA GAA AGC GCT TTG AGT TTG	388
Gly Phe Lys Ser Leu Ala Ser Ile Gln Arg Glu Ser Ala Leu Ser Leu	
110 115 120	
GGG TTT AGC CCT TTG AAA ATG ATG TAT TAT ATT ATT CTG CCT CAA AGT	436
Gly Phe Ser Pro Leu Lys Met Met Tyr Tyr Ile Ile Leu Pro Gln Ser	
125 130 135	
TTA AGC GTT TCT ATG CCT TCC ATA GGG GCG AAT GTG ATT TTT TTA CTC	484
Leu Ser Val Ser Met Pro Ser Ile Gly Ala Asn Val Ile Phe Leu Leu	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

```

Met Asn Gln Glu Ile Leu Asp Val Leu Ile Val Gly Ala Gly Pro Gly
 1           5           10           15
Gly Ile Ala Thr Ala Val Glu Cys Glu Ile Ala Gly Val Lys Lys Val
 20           25           30
Leu Leu Cys Glu Lys Thr Glu Ser His Ser Gly Met Leu Glu Lys Phe
 35           40           45
Tyr Lys Ala Gly Lys Arg Ile Asp Lys Asp Tyr Lys Lys Gln Val Val
 50           55           60
Glu Leu Lys Gly His Ile Pro Phe Lys Asp Ser Phe Lys Glu Glu Thr
 65           70           75           80
Leu Glu Asn Phe Thr Asn Leu Leu Lys Glu His His Ile Thr Pro Ser
 85           90           95
Tyr Lys Thr Asp Ile Glu Ser Val Lys Lys Glu Gly Glu Tyr Phe Lys
100          105          110
Ile Thr Thr Thr Ser Asn Thr Thr Tyr His Ala Lys Phe Val Val Val
115          120          125
Ala Ile Gly Lys Met Gly Gln Pro Asn Arg Pro Thr Ala Tyr Lys Ile
130          135          140
Pro Val Ala Leu Ser Lys Gln Val Val Phe Ser Ile Asn Asp Cys Lys
145          150          155          160
Glu Asn Glu Lys Thr Leu Val Ile Gly Gly Gly Asn Ser Ala Val Glu
165          170          175
Tyr Ala Ile Ala Leu Cys Lys Thr Thr Pro Thr Thr Leu Asn Tyr Arg
180          185          190
Lys Lys Glu Phe Ser Arg Ile Asn Glu Asp Asn Ala Lys Asn Leu Gln
195          200          205
Glu Val Leu Asn Asn Asn Thr Leu Lys Ser Lys Leu Gly Val Asp Ile
210          215          220
Glu Ser Leu Glu Glu Asp Asn Thr Gln Ile Lys Val Asn Phe Thr Asp
225          230          235          240
Asn Thr Ser Glu Ser Phe Asp Arg Leu Leu Tyr Ala Ile Gly Gly Ser
245          250          255
Thr Pro Leu Glu Phe Phe Lys Arg Cys Ser Leu Glu Leu Asp Pro Ser
260          265          270
Thr Asn Ile Pro Val Val Lys Glu Asn Leu Glu Ser Asn Asn Ile Pro
275          280          285
Asn Leu Phe Ile Val Gly Asp Ile Leu Phe Lys Ser Gly Ala Ser Ile
290          295          300
Ala Thr Ala Leu Asn His Gly Tyr Asp Val Ala Ile Glu Ile Ala Lys
305          310          315          320
Arg Leu His Ser

```

(2) INFORMATION FOR SEQ ID NO:1001:

CAT GCT AAA TTC GTG GTG GTT GCG ATC GGG AAA ATG GGC CAG CCA AAC	435
His Ala Lys Phe Val Val Val Ala Ile Gly Lys Met Gly Gln Pro Asn	
125 130 135	
CGC CCT ACT GCT TAT AAA ATC CCT GTT GCG CTC TCT AAA CAA GTG GTT	483
Arg Pro Thr Ala Tyr Lys Ile Pro Val Ala Leu Ser Lys Gln Val Val	
140 145 150	
TTT AGC ATC AAT GAT TGT AAG GAA AAT GAA AAA ACC CTT GTG ATC GGC	531
Phe Ser Ile Asn Asp Cys Lys Glu Asn Glu Lys Thr Leu Val Ile Gly	
155 160 165	
GGA GGC AAC TCA GCG GTG GAA TAC GCC ATT GCT TTG TGC AAA ACC ACC	579
Gly Gly Asn Ser Ala Val Glu Tyr Ala Ile Ala Leu Cys Lys Thr Thr	
170 175 180 185	
CCT ACC ACC CTC AAT TAC CGC AAA AAA GAA TTC AGC CGC ATC AAT GAA	627
Pro Thr Thr Leu Asn Tyr Arg Lys Lys Glu Phe Ser Arg Ile Asn Glu	
190 195 200	
GAC AAC GCT AAA AAC TTG CAA GAA GTC CTA AAC AAT AAC ACG CTT AAA	675
Asp Asn Ala Lys Asn Leu Gln Glu Val Leu Asn Asn Asn Thr Leu Lys	
205 210 215	
AGC AAG CTT GGA GTG GAT ATT GAA AGC CTA GAA GAA GAT AAC ACT CAG	723
Ser Lys Leu Gly Val Asp Ile Glu Ser Leu Glu Glu Asp Asn Thr Gln	
220 225 230	
ATT AAG GTT AAC TTC ACC GAT AAC ACG AGC GAA AGT TTT GAT CGT TTG	771
Ile Lys Val Asn Phe Thr Asp Asn Thr Ser Glu Ser Phe Asp Arg Leu	
235 240 245	
CTG TAT GCG ATC GGC GGC TCT ACC CCT TTA GAG TTT TTT AAA CGC TGT	819
Leu Tyr Ala Ile Gly Gly Ser Thr Pro Leu Glu Phe Phe Lys Arg Cys	
250 255 260 265	
TCT TTA GAG CTG GAT CCT AGC ACC AAT ATC CCT GTG GTG AAA GAA AAT	867
Ser Leu Glu Leu Asp Pro Ser Thr Asn Ile Pro Val Val Lys Glu Asn	
270 275 280	
TTA GAG AGC AAC AAT ATC CCT AAT TTG TTC ATC GTG GGC GAT ATT TTA	915
Leu Glu Ser Asn Asn Ile Pro Asn Leu Phe Ile Val Gly Asp Ile Leu	
285 290 295	
TTC AAA TCA GGG GCG AGC ATC GCT ACC GCT TTA AAC CAT GGC TAT GAT	963
Phe Lys Ser Gly Ala Ser Ile Ala Thr Ala Leu Asn His Gly Tyr Asp	
300 305 310	
GTT GCT ATA GAA ATC GCT AAA AGG TTG CAC TCT TAAAGCCGCT CACTCATCAA	1016
Val Ala Ile Glu Ile Ala Lys Arg Leu His Ser	
315 320	
ACGGCTTAGC CTTATACAAA AA	1038

(2) INFORMATION FOR SEQ ID NO:1000:

BNSDOCID: <WO 9843478A1 | >

```

Ile Arg Glu Ile Asn Lys Asp Leu Arg Gly Cys Asp Tyr Ala Thr Asp
40                               45                               50                               55

GTT TTG AGC TTC CCT TTA GAA GCC ATT CCT CAC ACC CCT TTA GGG AGC      244
Val Leu Ser Phe Pro Leu Glu Ala Ile Pro His Thr Pro Leu Gly Ser
                               60                               65                               70

GTG GTG ATT AAT GCG CCA TTA GCT CAA ACT AAC GCT CTG AAA TTA GGA      292
Val Val Ile Asn Ala Pro Leu Ala Gln Thr Asn Ala Leu Lys Leu Gly
                               75                               80                               85

CAT AGC TTA GAA AAT GAG ATC GCT CTT TTA TTC ATT CAT GGG GTG TTG      340
His Ser Leu Glu Asn Glu Ile Ala Leu Leu Phe Ile His Gly Val Leu
                               90                               95                               100

CAT TTG TTG GGC TAT GAC CAT GAA AAA GAT AAG GGC GAA CAA CGC CAA      388
His Leu Leu Gly Tyr Asp His Glu Lys Asp Lys Gly Glu Gln Arg Gln
                               105                               110                               115

AAA GAG AGC GAA CTC ATT AAA GCG TTT AAC TTG CCT TTG AGT TTG ATT      436
Lys Glu Ser Glu Leu Ile Lys Ala Phe Asn Leu Pro Leu Ser Leu Ile
120                               125                               130                               135

GAA CGC ACA CAG GAT TAGGTTTAGA TACTCTACTA ATGCTGACAA ATAAAGCTTT T      492
Glu Arg Thr Gln Asp
                               140

AATTTTAAAG AATGGAA                                                    509

```

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

```

Met Leu Glu Ile Asp Asn Gln Thr Pro Leu Glu Ser Asp Phe Leu Leu
 1                               5                               10                               15
Leu Glu Lys Ile Ala Asn Val Leu Ala Pro Thr Gln Ile Ile Glu Leu
                20                25                30
Val Leu Val Ser Asp Glu Thr Ile Arg Glu Ile Asn Lys Asp Leu Arg
                35                40                45
Gly Cys Asp Tyr Ala Thr Asp Val Leu Ser Phe Pro Leu Glu Ala Ile
                50                55                60
Pro His Thr Pro Leu Gly Ser Val Val Ile Asn Ala Pro Leu Ala Gln
                65                70                75                80
Thr Asn Ala Leu Lys Leu Gly His Ser Leu Glu Asn Glu Ile Ala Leu
                85                90                95
Leu Phe Ile His Gly Val Leu His Leu Leu Gly Tyr Asp His Glu Lys
                100                105                110

```


Thr Glu Ser Ile Met Val Met Pro Tyr Pro Lys Asp Leu Ala Gln Asp
 705 710 715 720
 Glu Lys Leu Glu His Glu Phe Glu Val Ile Lys Asp Cys Ile Val Ser
 725 730 735
 Leu Arg Arg Leu Lys Ile Met Leu Glu Thr Pro Pro Ile Val Leu Lys
 740 745 750
 Glu Ala Ser Val Gly Leu Arg Glu Ala Ile Glu Asn Thr Glu Arg Leu
 755 760 765
 Gln Thr Tyr Ala Gln Lys Leu Ala Arg Leu Glu Lys Val Ser Val Ile
 770 775 780
 Ser Ser Lys Pro Leu Lys Ser Val Ser Asp Val Gly Glu Phe Cys Gln
 785 790 795 800
 Thr Tyr Ala Asn Leu Glu Asn Leu Asp Leu Ser Pro Leu Val Ala Arg
 805 810 815
 Leu Lys Lys Gln Leu Glu Lys Leu Glu Lys Glu Lys Leu Lys Leu Asn
 820 825 830
 Leu His Asn Glu Asn Phe Val Lys Asn Ala Pro Lys Ser Val Leu Glu
 835 840 845
 Lys Ala Lys Glu Ser Leu Lys Thr Leu Leu Glu Lys Glu Ser Lys Ile
 850 855 860
 Lys Gln Glu Leu Asp Leu Leu Glu Gln Pro
 865 870

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 32...451
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GGGCTTTTTT AAACCTCTTC TTATATCTTT A ATG CTA GAA ATA GAC AAC CAA 52
 Met Leu Glu Ile Asp Asn Gln
 1 5
 ACC CCG CTA GAA TCA GAC TTT TTA TTA TTA GAA AAA ATC GCA AAT GTT 100
 Thr Pro Leu Glu Ser Asp Phe Leu Leu Glu Lys Ile Ala Asn Val
 10 15 20
 TTA GCC CCC ACT CAA ATC ATT GAG CTT GTT TTG GTG AGC GAT GAA ACC 148
 Leu Ala Pro Thr Gln Ile Ile Glu Leu Val Leu Val Ser Asp Glu Thr
 25 30 35
 ATT CGA GAA ATC AAC AAG GAT TTA AGG GGT TGC GAT TAC GCT ACC GAT 196

- 1465 -

TTA GAA AAA GAA AGT AAA ATT AAG CAA GAA TTG GAC TTG TTA GAA CAA 2646
 Leu Glu Lys Glu Ser Lys Ile Lys Gln Glu Leu Asp Leu Leu Glu Gln
 860 870

CCA TAATAAAAGG ATAGAAAATG TTTCAAGCGT TAAGCGATGG GTTTAAAAAC GCGCTC 2705
 Pro

AATAAAATCC G 2716

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

Met	Ile	Met	Lys	Gln	Glu	Pro	Thr	Thr	Tyr	Gln	Pro	Glu	Glu	Ile	Glu	1	5	10	15
Lys	Lys	Ile	Tyr	Glu	Ile	Cys	Ser	His	Arg	Gly	Tyr	Phe	Glu	Ile	Asp	20	25	30	
Gly	Asn	Glu	Ala	Ile	Gln	Glu	Lys	Asn	Lys	Arg	Phe	Cys	Leu	Met	Met	35	40	45	
Pro	Pro	Pro	Asn	Val	Thr	Gly	Val	Leu	His	Ile	Gly	His	Ala	Leu	Thr	50	55	60	
Leu	Ser	Leu	Gln	Asp	Ile	Leu	Ala	Arg	Tyr	Lys	Arg	Met	Asp	Gly	Tyr	65	70	75	80
Lys	Thr	Leu	Tyr	Gln	Pro	Gly	Leu	Asp	His	Ala	Gly	Ile	Ala	Thr	Gln	85	90	95	
Asn	Val	Val	Glu	Lys	Gln	Leu	Leu	Ser	Gln	Gly	Ile	Lys	Lys	Glu	Asp	100	105	110	
Leu	Gly	Arg	Glu	Glu	Phe	Ile	Lys	Lys	Val	Trp	Glu	Trp	Lys	Glu	Lys	115	120	125	
Ser	Gly	Gly	Ala	Ile	Leu	Glu	Gln	Met	Lys	Arg	Leu	Gly	Val	Ser	Ala	130	135	140	
Ala	Phe	Ser	Arg	Thr	Arg	Phe	Thr	Met	Asp	Lys	Gly	Leu	Gln	Arg	Ala	145	150	155	160
Val	Lys	Leu	Ala	Phe	Leu	Lys	Trp	Tyr	Glu	Lys	Gly	Leu	Ile	Ile	Gln	165	170	175	
Asp	Asn	Tyr	Met	Val	Asn	Trp	Cys	Thr	Lys	Asp	Gly	Ala	Leu	Ser	Asp	180	185	190	
Ile	Glu	Val	Glu	Tyr	Glu	Glu	Arg	Lys	Gly	Ala	Leu	Tyr	Tyr	Ile	Arg	195	200	205	
Tyr	Tyr	Leu	Glu	Asn	Gln	Lys	Asp	Tyr	Leu	Val	Val	Ala	Thr	Thr	Arg	210	215	220	
Pro	Glu	Thr	Leu	Phe	Gly	Asp	Ser	Ala	Leu	Met	Val	Asn	Pro	Asn	Asp	225	230	235	240
Glu	Arg	Tyr	Lys	His	Leu	Val	Gly	Gln	Lys	Ala	Ile	Leu	Pro	Leu	Ile	245	250	255	
His	Arg	Thr	Ile	Pro	Ile	Ile	Ala	Asp	Glu	His	Val	Glu	Met	Glu	Phe				

GAT AAT TAT CGT TTT AAT GAC GCC ACG ACT TTG TTA TAC CGC TTT TTG Asp Asn Tyr Arg Phe Asn Asp Ala Thr Thr Leu Leu Tyr Arg Phe Leu 635 640 645	1974
TGG GGG GAA TTT TGC GAC TGG TTC ATT GAA TTT TCT AAA GTG GAA AAT Trp Gly Glu Phe Cys Asp Trp Phe Ile Glu Phe Ser Lys Val Glu Asn 650 655 660 665	2022
GAA GCG ATA GAC GAA TTA GGG AGC GTG TTA AAA GAG GCT TTA AAA CTC Glu Ala Ile Asp Glu Leu Gly Ser Val Leu Lys Glu Ala Leu Lys Leu 670 675 680	2070
TTG CAC CCT TTC ATG CCC TTT ATC AGC GAG TCT TTA TAC CAC AAG CTC Leu His Pro Phe Met Pro Phe Ile Ser Glu Ser Leu Tyr His Lys Leu 685 690 695	2118
AGC AAT ACG GAA CTA GAA AAC ACT GAA TCT ATC ATG GTC ATG CCT TAC Ser Asn Thr Glu Leu Glu Asn Thr Glu Ser Ile Met Val Met Pro Tyr 700 705 710	2166
CCT AAA GAT TTG GCG CAA GAT GAA AAA TTA GAG CAT GAA TTT GAA GTG Pro Lys Asp Leu Ala Gln Asp Glu Lys Leu Glu His Glu Phe Glu Val 715 720 725	2214
ATT AAA GAT TGC ATT GTG TCT TTA AGG CGT TTA AAA ATC ATG CTA GAA Ile Lys Asp Cys Ile Val Ser Leu Arg Arg Leu Lys Ile Met Leu Glu 730 735 740 745	2262
ACC CCA CCG ATT GTT CTA AAA GAA GCG AGC GTG GGA TTA AGA GAA GCC Thr Pro Pro Ile Val Leu Lys Glu Ala Ser Val Gly Leu Arg Glu Ala 750 755 760	2310
ATA GAA AAC ACA GAG CGT TTG CAA ACT TAC GCC CAA AAA TTA GCG AGG Ile Glu Asn Thr Glu Arg Leu Gln Thr Tyr Ala Gln Lys Leu Ala Arg 765 770 775	2358
TTG GAA AAA GTC AGC GTG ATT AGT TCT AAG CCT TTA AAA AGC GTG AGC Leu Glu Lys Val Ser Val Ile Ser Ser Lys Pro Leu Lys Ser Val Ser 780 785 790	2406
GAT GTG GGG GAA TTT TGC CAG ACT TAT GCG AAT TTA GAA AAT CTT GAT Asp Val Gly Glu Phe Cys Gln Thr Tyr Ala Asn Leu Glu Asn Leu Asp 795 800 805	2454
TTA AGC CCG CTT GTT GCG CGT TTG AAA AAG CAG TTG GAA AAA TTG GAA Leu Ser Pro Leu Val Ala Arg Leu Lys Lys Gln Leu Glu Lys Leu Glu 810 815 820 825	2502
AAA GAA AAA TTA AAA CTC AAT TTG CAC AAT GAA AAT TTT GTC AAA AAC Lys Glu Lys Leu Lys Leu Asn Leu His Asn Glu Asn Phe Val Lys Asn 830 835 840	2550
GCG CCT AAA AGC GTG CTA GAA AAA GCT AAA GAG AGT TTA AAA ACG CTT Ala Pro Lys Ser Val Leu Glu Lys Ala Lys Glu Ser Leu Lys Thr Leu 845 850 855	2598

CAA TTG TTT TGG GGG CAT CAA ATA CCG GTA TTC ACT TGC GAG AAT AAC	1302
Gln Leu Phe Trp Gly His Gln Ile Pro Val Phe Thr Cys Glu Asn Asn	
410 415 420 425	
CAC CAG TTC GTA AGC TTA GAC ACC CCC TTA AGT TGC CCT ACT TGT AAG	1350
His Gln Phe Val Ser Leu Asp Thr Pro Leu Ser Cys Pro Thr Cys Lys	
430 435 440	
AGC GAA ACA CTA GAG CAA GAT AAG GAT GTG CTA GAC ACA TGG TTT AGT	1398
Ser Glu Thr Leu Glu Gln Asp Lys Asp Val Leu Asp Thr Trp Phe Ser	
445 450 455	
TCA GGG CTA TGG GCG TTT TCC ACT CTA GGG TGG GGG CAA GAA AAA AGC	1446
Ser Gly Leu Trp Ala Phe Ser Thr Leu Gly Trp Gly Gln Glu Lys Ser	
460 465 470	
GGT TTG TTT AAT GAA AGC GAT TTG AAA GAT TTC TAC CCT AAC ACA ACG	1494
Gly Leu Phe Asn Glu Ser Asp Leu Lys Asp Phe Tyr Pro Asn Thr Thr	
475 480 485	
CTC ATT ACT GGG TTT GAC ATC CTC TTT TTT TGG GTG GCT AGG ATG CTT	1542
Leu Ile Thr Gly Phe Asp Ile Leu Phe Phe Trp Val Ala Arg Met Leu	
490 495 500 505	
TTT TGC AGC GAA TCG CTT TTA GGC GAA TTG CCC TTT AAA GAT ATT TAC	1590
Phe Cys Ser Glu Ser Leu Leu Gly Glu Leu Pro Phe Lys Asp Ile Tyr	
510 515 520	
TTG CAC GCC TTA GTG AGA GAT GAA AAG GGT GAA AAA ATG AGC AAA TCT	1638
Leu His Ala Leu Val Arg Asp Glu Lys Gly Glu Lys Met Ser Lys Ser	
525 530 535	
AAG GGT AAT GTG ATC GAT CCT TTA GAG ATG ATA GAA AAA TAC GGC GCG	1686
Lys Gly Asn Val Ile Asp Pro Leu Glu Met Ile Glu Lys Tyr Gly Ala	
540 545 550	
GAT AGC TTG CGT TTC ACT TTA GCC AAT TTG TGC GCT ACG GGT AGG GAC	1734
Asp Ser Leu Arg Phe Thr Leu Ala Asn Leu Cys Ala Thr Gly Arg Asp	
555 560 565	
ATT AAG CTT TCC ACT ACG CAT TTA GAA AAT AAC AAG AAT TTC GCC AAC	1782
Ile Lys Leu Ser Thr Thr His Leu Glu Asn Asn Lys Asn Phe Ala Asn	
570 575 580 585	
AAG CTT TTT AAT GCG GCG AGT TAC TTG AAG CTC AAA CAA GAA TCT TTC	1830
Lys Leu Phe Asn Ala Ala Ser Tyr Leu Lys Leu Lys Gln Glu Ser Phe	
590 595 600	
AAA GAT AAA GAG CGT TTG AAT GAA TAC CAA ACG CCT TTG GGG CGT TAT	1878
Lys Asp Lys Glu Arg Leu Asn Glu Tyr Gln Thr Pro Leu Gly Arg Tyr	
605 610 615	
GCG AAA TCG CGC TTG AAT TCA GCG ACT AAA GAG GCG CGT AAC GCT TTA	1926
Ala Lys Ser Arg Leu Asn Ser Ala Thr Lys Glu Ala Arg Asn Ala Leu	
620 625 630	

AAA GAT GGG GCG TTG AGC GAT ATT GAA GTG GAG TAT GAA GAG CGT AAG	630
Lys Asp Gly Ala Leu Ser Asp Ile Glu Val Glu Tyr Glu Glu Arg Lys	
190 195 200	
GGG GCG TTG TAT TAT ATT AGA TAT TAT TTA GAA AAT CAA AAA GAT TAT	678
Gly Ala Leu Tyr Tyr Ile Arg Tyr Tyr Leu Glu Asn Gln Lys Asp Tyr	
205 210 215	
TTA GTG GTG GCT ACC ACA CGC CCT GAA ACC TTG TTT GGC GAT AGC GCG	726
Leu Val Val Ala Thr Thr Arg Pro Glu Thr Leu Phe Gly Asp Ser Ala	
220 225 230	
CTT ATG GTC AAT CCT AAC GAT GAG AGA TAC AAG CAT TTG GTG GGG CAA	774
Leu Met Val Asn Pro Asn Asp Glu Arg Tyr Lys His Leu Val Gly Gln	
235 240 245	
AAA GCG ATC TTG CCT TTA ATC CAT CGC ACA ATC CCT ATT ATC GCT GAT	822
Lys Ala Ile Leu Pro Leu Ile His Arg Thr Ile Pro Ile Ile Ala Asp	
250 255 260 265	
GAA CAT GTT GAA ATG GAG TTT GGC ACA GGG TGT GTG AAA GTA ACC CCT	870
Glu His Val Glu Met Glu Phe Gly Thr Gly Cys Val Lys Val Thr Pro	
270 275 280	
GGG CAT GAT TTT AAC GAT TAT GAA GTG GGC AAA CGC CAC CAT TTG GAA	918
Gly His Asp Phe Asn Asp Tyr Glu Val Gly Lys Arg His His Leu Glu	
285 290 295	
ACG ATT AAA ATC TTT GAT GAA AAG GGG ATT TTA AAC GCG CAT TGC GGG	966
Thr Ile Lys Ile Phe Asp Glu Lys Gly Ile Leu Asn Ala His Cys Gly	
300 305 310	
GAG TTT GAA AAT TTA GAA CGA TTA GAA GCT AGA GAT AAG GTC GTA GAA	1014
Glu Phe Glu Asn Leu Glu Arg Leu Glu Ala Arg Asp Lys Val Val Glu	
315 320 325	
AGA TTA AAA GAA AAC GCC CTA TTG GAA AAA ATA GAA GAA CAC ACG CAT	1062
Arg Leu Lys Glu Asn Ala Leu Leu Glu Lys Ile Glu Glu His Thr His	
330 335 340 345	
CAA GTG GGG CAT TGC TAT CGT TGT CAT AAT GTG GTA GAA CCT TAT GTG	1110
Gln Val Gly His Cys Tyr Arg Cys His Asn Val Val Glu Pro Tyr Val	
350 355 360	
TCT AAG CAA TGG TTT GTC AAG CCT GAA ATC GCT CAA AGT TCT ATT GAA	1158
Ser Lys Gln Trp Phe Val Lys Pro Glu Ile Ala Gln Ser Ser Ile Glu	
365 370 375	
AAA ATC CAA CAA GGT TTG GCG CGA TTC TAC CCT TCT AAT TGG ATC AAT	1206
Lys Ile Gln Gln Gly Leu Ala Arg Phe Tyr Pro Ser Asn Trp Ile Asn	
380 385 390	
AAT TAC AAC GCT TGG ATG AGG GAA TTA CGC CCT TGG TGT ATC AGC AGG	1254
Asn Tyr Asn Ala Trp Met Arg Glu Leu Arg Pro Trp Cys Ile Ser Arg	
395 400 405	

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 28...2649
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

TAAGGAACGC TCTATTTTAG GATAATA ATG ATA ATG AAA CAA GAA CCC ACC ACC	54
Met Ile Met Lys Gln Glu Pro Thr Thr	
1 5	
TAC CAA CCA GAA GAG ATA GAA AAA AAG ATT TAT GAA ATT TGC TCT CAT	102
Tyr Gln Pro Glu Glu Ile Glu Lys Lys Ile Tyr Glu Ile Cys Ser His	
10 15 20 25	
AGG GGG TAT TTT GAA ATT GAT GGC AAT GAA GCG ATC CAA GAA AAA AAC	150
Arg Gly Tyr Phe Glu Ile Asp Gly Asn Glu Ala Ile Gln Glu Lys Asn	
30 35 40	
AAA CGA TTT TGC TTG ATG ATG CCC CCT CCT AAT GTG ACC GGT GTG TTG	198
Lys Arg Phe Cys Leu Met Met Pro Pro Pro Asn Val Thr Gly Val Leu	
45 50 55	
CAC ATA GGG CAT GCC CTG ACT TTA AGC TTG CAA GAT ATT TTA GCG CGT	246
His Ile Gly His Ala Leu Thr Leu Ser Leu Gln Asp Ile Leu Ala Arg	
60 65 70	
TAC AAA CGC ATG GAT GGG TAT AAG ACT TTG TAT CAG CCC GGG TTG GAT	294
Tyr Lys Arg Met Asp Gly Tyr Lys Thr Leu Tyr Gln Pro Gly Leu Asp	
75 80 85	
CAC GCT GGC ATT GCA ACG CAA AAT GTC GTG GAA AAG CAG CTT TTA AGT	342
His Ala Gly Ile Ala Thr Gln Asn Val Val Glu Lys Gln Leu Leu Ser	
90 95 100 105	
CAA GGG ATT AAA AAA GAA GAT TTA GGG CGT GAA GAG TTC ATT AAA AAA	390
Gln Gly Ile Lys Lys Glu Asp Leu Gly Arg Glu Glu Phe Ile Lys Lys	
110 115 120	
GTG TGG GAA TGG AAA GAA AAG AGC GGG GGA GCG ATT TTA GAG CAA ATG	438
Val Trp Glu Trp Lys Glu Lys Ser Gly Gly Ala Ile Leu Glu Gln Met	
125 130 135	
AAG CGT TTA GGC GTG AGC GCG GCC TTT TCT AGG ACT CGT TTC ACG ATG	486
Lys Arg Leu Gly Val Ser Ala Ala Phe Ser Arg Thr Arg Phe Thr Met	
140 145 150	
GAT AAG GGC TTG CAA AGA GCG GTC AAA TTG GCG TTT TTG AAA TGG TAT	534
Asp Lys Gly Leu Gln Arg Ala Val Lys Leu Ala Phe Leu Lys Trp Tyr	
155 160 165	
GAA AAA GGT CTC ATT ATT CAA GAT AAT TAC ATG GTG AAT TGG TGC ACT	582
Glu Lys Gly Leu Ile Ile Gln Asp Asn Tyr Met Val Asn Trp Cys Thr	
170 175 180 185	

```

      130              135              140
Tyr Ser Lys Gly Gly Lys Val Gly Leu Phe Gly Gly Ala Gly Val Gly
145              150              155              160
Lys Thr Val Ile Ile Met Glu Leu Ile His Asn Val Ala Tyr Lys His
      165              170              175
Asn Gly Tyr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly
      180              185              190
Asn Asp Leu Tyr Phe Glu Met Lys Glu Gly Gly Val Leu Asp Lys Val
      195              200              205
Ala Leu Cys Tyr Gly Gln Met Asn Glu Pro Pro Gly Ala Arg Asn Arg
      210              215              220
Ile Ala Phe Thr Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp Glu Lys
225              230              235              240
Gly Leu Asp Val Leu Met Phe Ile Asp Asn Ile Phe Arg Tyr Ala Gln
      245              250              255
Ser Gly Ala Glu Met Ser Ala Leu Leu Gly Arg Ile Pro Ser Ala Val
      260              265              270
Gly Tyr Gln Pro Thr Leu Ala Gly Glu Met Gly Lys Leu Gln Glu Arg
      275              280              285
Ile Ala Ser Thr Lys Asn Gly Ser Ile Thr Ser Val Gln Ala Val Tyr
      290              295              300
Val Pro Ala Asp Asp Leu Thr Asp Pro Ala Pro Ala Ser Val Phe Ala
305              310              315              320
His Leu Asp Ala Thr Thr Val Leu Asn Arg Lys Ile Ala Glu Lys Gly
      325              330              335
Ile Tyr Pro Ala Val Asp Pro Leu Asp Ser Thr Ser Arg Ile Leu Ser
      340              345              350
Pro Gln Met Ile Gly Glu Lys His Tyr Glu Val Ala Thr Gly Ile Gln
      355              360              365
Gln Val Leu Gln Lys Tyr Lys Asp Leu Gln Asp Ile Ile Ala Ile Leu
      370              375              380
Gly Leu Asp Glu Leu Ser Glu Glu Asp Lys Lys Thr Val Glu Arg Ala
385              390              395              400
Arg Lys Ile Glu Lys Phe Leu Ser Gln Pro Phe Phe Val Ala Glu Val
      405              410              415
Phe Thr Gly Ser Pro Gly Lys Tyr Val Thr Leu Gln Glu Thr Leu Glu
      420              425              430
Gly Phe Gly Gly Ile Leu Glu Gly Lys Tyr Asp His Ile Pro Glu Asn
      435              440              445
Ala Phe Tyr Met Val Gly Ser Ile Gln Glu Val Leu Glu Lys Ala Lys
      450              455              460
Asn Met Lys Asn Ser
465

```

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:


```

TTG CAA GAC ATT ATT GCG ATT TTG GGA TTA GAC GAA TTG AGC GAA GAG      1205
Leu Gln Asp Ile Ile Ala Ile Leu Gly Leu Asp Glu Leu Ser Glu Glu
      380                      385                      390

GAT AAA AAA ACG GTT GAA AGG GCC AGA AAA ATT GAG AAG TTT TTA TCC      1253
Asp Lys Lys Thr Val Glu Arg Ala Arg Lys Ile Glu Lys Phe Leu Ser
      395                      400                      405

CAG CCG TTC TTT GTG GCT GAA GTG TTT ACA GGA AGT CCT GGT AAA TAT      1301
Gln Pro Phe Phe Val Ala Glu Val Phe Thr Gly Ser Pro Gly Lys Tyr
      410                      415                      420

GTA ACC CTT CAA GAG ACT TTA GAG GGC TTT GGA GGG ATT TTA GAG GGC      1349
Val Thr Leu Gln Glu Thr Leu Glu Gly Phe Gly Gly Ile Leu Glu Gly
      425                      430                      435                      440

AAA TAC GAT CAT ATT CCC GAG AAC GCG TTT TAT ATG GTG GGT AGC ATT      1397
Lys Tyr Asp His Ile Pro Glu Asn Ala Phe Tyr Met Val Gly Ser Ile
      445                      450                      455

CAA GAG GTT TTA GAA AAA GCT AAA AAC ATG AAA AAT TCC TAAGGGTTTT GT      1448
Gln Glu Val Leu Glu Lys Ala Lys Asn Met Lys Asn Ser
      460                      465

GATGGCTTTG TTGAAAATTA                                          1468

```

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

```

Met Lys Ala Met Glu Gly Lys Ile Ile Gln Val Leu Gly Pro Val Val
  1           5           10           15
Asp Val Glu Phe Glu Ser Tyr Leu Pro Ala Ile Phe Glu Ala Leu Asp
      20           25           30
Ile Asn Phe Glu Val Asn Gly Val Gln Lys Ser Leu Val Leu Glu Val
      35           40           45
Ala Ala His Leu Gly Gly Asn Arg Val Arg Ala Ile Ala Met Asp Met
      50           55           60
Thr Glu Gly Leu Val Arg Asn Gln Val Ile Lys Ala Arg Gly Lys Met
      65           70           75           80
Ile Glu Val Pro Val Gly Glu Glu Val Leu Gly Arg Ile Phe Asn Val
      85           90           95
Val Gly Glu Ser Ile Asp Asn Leu Glu Pro Leu Lys Pro Ser Leu Thr
      100          105          110
Trp Pro Ile His Arg Lys Ala Pro Ser Phe Glu Gln Gln Ser Thr Lys
      115          120          125
Thr Glu Met Phe Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Ala Pro

```

TTG TTT GGT GGG GCT GGC GTA GGC AAA ACG GTG ATC ATT ATG GAG CTT	533
Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Ile Ile Met Glu Leu	
155 160 165	
ATC CAT AAT GTG GCT TAT AAG CAT AAC GGG TAT TCG GTG TTT GCA GGT	581
Ile His Asn Val Ala Tyr Lys His Asn Gly Tyr Ser Val Phe Ala Gly	
170 175 180	
GTG GGG GAG CGC ACC AGA GAG GGG AAT GAT CTG TAT TTT GAA ATG AAA	629
Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Leu Tyr Phe Glu Met Lys	
185 190 195 200	
GAA GGG GGC GTT TTA GAC AAA GTC GCA CTG TGT TAT GGG CAA ATG AAT	677
Glu Gly Gly Val Leu Asp Lys Val Ala Leu Cys Tyr Gly Gln Met Asn	
205 210 215	
GAG CCA CCA GGC GCG AGG AAC CGC ATC GCA TTC ACC GGC TTG ACG ATG	725
Glu Pro Pro Gly Ala Arg Asn Arg Ile Ala Phe Thr Gly Leu Thr Met	
220 225 230	
GCG GAG TAT TTT CGT GAT GAA AAG GGC TTA GAT GTG TTG ATG TTT ATT	773
Ala Glu Tyr Phe Arg Asp Glu Lys Gly Leu Asp Val Leu Met Phe Ile	
235 240 245	
GAC AAC ATC TTT AGA TAC GCT CAA AGC GGT GCG GAA ATG AGC GCG CTA	821
Asp Asn Ile Phe Arg Tyr Ala Gln Ser Gly Ala Glu Met Ser Ala Leu	
250 255 260	
TTA GGC CGT ATC CCT TCA GCG GTG GGG TAT CAG CCC ACG CTA GCC GGG	869
Leu Gly Arg Ile Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Gly	
265 270 275 280	
GAA ATG GGG AAA CTT CAA GAG CGT ATC GCT TCC ACT AAA AAT GGC TCT	917
Glu Met Gly Lys Leu Gln Glu Arg Ile Ala Ser Thr Lys Asn Gly Ser	
285 290 295	
ATC ACT TCC GTT CAA GCG GTG TAT GTG CCA GCA GAT GAC TTG ACT GAC	965
Ile Thr Ser Val Gln Ala Val Tyr Val Pro Ala Asp Asp Leu Thr Asp	
300 305 310	
CCA GCC CCT GCT TCG GTG TTT GCG CAT TTG GAT GCG ACT ACG GTG TTG	1013
Pro Ala Pro Ala Ser Val Phe Ala His Leu Asp Ala Thr Thr Val Leu	
315 320 325	
AAT AGA AAG ATC GCT GAA AAA GGG ATT TAT CCG GCG GTG GAT CCT TTG	1061
Asn Arg Lys Ile Ala Glu Lys Gly Ile Tyr Pro Ala Val Asp Pro Leu	
330 335 340	
GAT TCC ACT TCA AGG ATT TTA AGC CCT CAA ATG ATC GGT GAG AAA CAC	1109
Asp Ser Thr Ser Arg Ile Leu Ser Pro Gln Met Ile Gly Glu Lys His	
345 350 355 360	
TAT GAA GTC GCT ACC GGT ATC CAG CAG GTT TTA CAA AAA TAC AAG GAT	1157
Tyr Glu Val Ala Thr Gly Ile Gln Gln Val Leu Gln Lys Tyr Lys Asp	
365 370 375	

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 30...1436
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

AAAATAAAAA TTATATTAAT CAAGGAGCG ATG AAA GCG ATG GAA GGT AAA ATC	53
Met Lys Ala Met Glu Gly Lys Ile	
1 5	
ATT CAG GTT TTA GGC CCT GTG GTA GAT GTG GAG TTT GAA TCC TAT CTG	101
Ile Gln Val Leu Gly Pro Val Val Asp Val Glu Phe Glu Ser Tyr Leu	
10 15 20	
CCG GCG ATT TTT GAA GCG TTA GAC ATT AAT TTT GAA GTC AAT GGT GTT	149
Pro Ala Ile Phe Glu Ala Leu Asp Ile Asn Phe Glu Val Asn Gly Val	
25 30 35 40	
CAA AAG TCT TTA GTT TTA GAG GTG GCA GCC CAT TTG GGC GGT AAT CGG	197
Gln Lys Ser Leu Val Leu Glu Val Ala Ala His Leu Gly Gly Asn Arg	
45 50 55	
GTG CGA GCG ATT GCT ATG GAT ATG ACA GAA GGC TTA GTG CGT AAC CAA	245
Val Arg Ala Ile Ala Met Asp Met Thr Glu Gly Leu Val Arg Asn Gln	
60 65 70	
GTG ATC AAG GCT CGC GGC AAA ATG ATT GAA GTG CCT GTG GGC GAA GAA	293
Val Ile Lys Ala Arg Gly Lys Met Ile Glu Val Pro Val Gly Glu Glu	
75 80 85	
GTA TTA GGG CGT ATT TTT AAT GTT GTG GGC GAG AGC ATT GAC AAT TTA	341
Val Leu Gly Arg Ile Phe Asn Val Val Gly Glu Ser Ile Asp Asn Leu	
90 95 100	
GAG CCG CTT AAG CCG TCC TTA ACT TGG CCC ATT CAC AGA AAA GCC CCT	389
Glu Pro Leu Lys Pro Ser Leu Thr Trp Pro Ile His Arg Lys Ala Pro	
105 110 115 120	
AGT TTT GAG CAG CAA AGC ACT AAA ACA GAA ATG TTT GAA ACT GGT ATT	437
Ser Phe Glu Gln Gln Ser Thr Lys Thr Glu Met Phe Glu Thr Gly Ile	
125 130 135	
AAA GTC ATT GAC TTA CTC GCG CCT TAT TCT AAG GGC GGT AAA GTA GGC	485
Lys Val Ile Asp Leu Leu Ala Pro Tyr Ser Lys Gly Gly Lys Val Gly	
140 145 150	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

```

Met Asp Phe Cys Ser Gly Ile Gly Gly Gly Arg Leu Gly Leu Glu Gln
 1             5             10             15
Cys His Leu Lys Cys Val Gly His Ala Glu Ile Asn His Glu Ala Leu
      20             25             30
Arg Thr Tyr Glu Leu Phe Phe Lys Asp Thr His Asn Phe Gly Asp Leu
      35             40             45
Met Arg Ile Asn Pro Asn Asp Leu Pro Asp Phe Asp Ala Leu Ile Ser
      50             55             60
Gly Phe Pro Cys Gln Ala Phe Ser Ile Asn Gly Lys Arg Lys Gly Leu
      65             70             75             80
Glu Asp Glu Arg Gly Thr Ile Ile Tyr Gly Leu Ile Arg Ile Leu Lys
      85             90             95
Val Lys Gln Pro Glu Cys Phe Leu Leu Glu Asn Val Lys Gly Leu Ile
      100            105            110
Asn His Asn Lys Lys Ala Thr Phe Asn Ile Ile Ile Lys Ala Leu Gln
      115            120            125
Glu Val Gly Tyr Thr Thr Tyr Tyr Lys Ile Leu Asn Ser Ala Asp Phe
      130            135            140
Gln Leu Ala Gln Asn Arg Glu Arg Leu Tyr Ile Val Gly Phe Arg Lys
      145            150            155            160
Asp Leu Lys His Pro Phe Asn Phe Pro Leu Gly Leu Ala Asn Asp Tyr
      165            170            175
Tyr Phe Lys Asp Phe Leu Asp Ala Asp Asn Glu Cys Tyr Leu Asp Val
      180            185            190
Ser Asn Ala Ala Phe Gln Arg Tyr Leu His Asn Arg Tyr Asn His Asn
      195            200            205
Arg Val Ser Leu Glu Asp Leu Leu Thr Leu Glu Asn Ala Val Leu Asp
      210            215            220
Thr Arg Gln Ser Asp Leu Arg Leu Tyr Ser Asn Val Phe Pro Thr Leu
      225            230            235            240
Arg Thr Ser Arg His Gly Leu Phe Tyr Thr Gln Lys Gly Lys Ile Lys
      245            250            255
Arg Leu Asn Ala Ile Glu Ser Leu Leu Leu Gln Gly Phe Pro Arg Asp
      260            265            270
Leu Ile Ala Lys Ile Lys Asp Asn Pro Asn Phe Lys Ala Ser His Leu
      275            280            285
Leu Ser Gln Ala Gly Asn Ala Met Ser Val Asn Val Ile Ala Ala Ile
      290            295            300
Ala Lys Gln Met Leu Lys Ala Ile
      305            310

```

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1468 base pairs

Val	Lys	Gly	Leu	Ile	Asn	His	Asn	Lys	Lys	Ala	Thr	Phe	Asn	Ile	Ile	
		110					115					120				
ATC	AAA	GCC	CTA	CAA	GAA	GTG	GGT	TAT	ACA	ACT	TAT	TAT	AAA	ATT	TTA	435
Ile	Lys	Ala	Leu	Gln	Glu	Val	Gly	Tyr	Thr	Thr	Tyr	Tyr	Lys	Ile	Leu	
		125					130				135					
AAC	AGC	GCT	GAT	TTT	CAA	TTA	GCC	CAA	AAT	AGA	GAA	CGC	CTT	TAT	ATC	483
Asn	Ser	Ala	Asp	Phe	Gln	Leu	Ala	Gln	Asn	Arg	Glu	Arg	Leu	Tyr	Ile	
140					145					150					155	
GTA	GGG	TTT	AGG	AAG	GAT	TTA	AAA	CAC	CCA	TTT	AAT	TTC	CCT	TTA	GGT	531
Val	Gly	Phe	Arg	Lys	Asp	Leu	Lys	His	Pro	Phe	Asn	Phe	Pro	Leu	Gly	
				160					165					170		
TTA	GCC	AAT	GAT	TAT	TAT	TTC	AAG	GAT	TTT	TTA	GAC	GCT	GAT	AAT	GAA	579
Leu	Ala	Asn	Asp	Tyr	Tyr	Phe	Lys	Asp	Phe	Leu	Asp	Ala	Asp	Asn	Glu	
			175					180					185			
TGT	TAT	TTG	GAT	GTG	AGT	AAC	GCT	GCA	TTT	CAA	AGA	TAC	TTG	CAC	AAC	627
Cys	Tyr	Leu	Asp	Val	Ser	Asn	Ala	Ala	Phe	Gln	Arg	Tyr	Leu	His	Asn	
		190					195					200				
CGA	TAC	AAC	CAT	AAC	CGG	GTT	TCT	TTA	GAG	GAT	CTC	TTA	ACT	TTA	GAA	675
Arg	Tyr	Asn	His	Asn	Arg	Val	Ser	Leu	Glu	Asp	Leu	Leu	Thr	Leu	Glu	
	205					210					215					
AAC	GCT	GTT	TTA	GAC	ACA	AGA	CAA	TCT	GAT	TTA	AGG	TTG	TAT	TCT	AAT	723
Asn	Ala	Val	Leu	Asp	Thr	Arg	Gln	Ser	Asp	Leu	Arg	Leu	Tyr	Ser	Asn	
220					225				230						235	
GTT	TTT	CCT	ACT	TTA	AGG	ACT	TCT	CGG	CAT	GGC	CTG	TTT	TAT	ACC	CAA	771
Val	Phe	Pro	Thr	Leu	Arg	Thr	Ser	Arg	His	Gly	Leu	Phe	Tyr	Thr	Gln	
				240				245						250		
AAA	GGC	AAA	ATC	AAA	AGA	TTA	AAC	GCT	ATT	GAA	AGC	TTG	CTT	TTG	CAA	819
Lys	Gly	Lys	Ile	Lys	Arg	Leu	Asn	Ala	Ile	Glu	Ser	Leu	Leu	Leu	Gln	
			255				260					265				
GGA	TTT	CCT	AGG	GAT	TTG	ATC	GCT	AAG	ATT	AAA	GAT	AAT	CCT	AAC	TTT	867
Gly	Phe	Pro	Arg	Asp	Leu	Ile	Ala	Lys	Ile	Lys	Asp	Asn	Pro	Asn	Phe	
		270					275					280				
AAA	GCA	AGC	CAT	TTG	CTA	TCC	CAA	GCG	GGG	AAT	GCG	ATG	AGC	GTG	AAT	915
Lys	Ala	Ser	His	Leu	Leu	Ser	Gln	Ala	Gly	Asn	Ala	Met	Ser	Val	Asn	
	285					290					295					
GTG	ATT	GCT	GCA	ATC	GCT	AAA	CAA	ATG	TTA	AAG	GCG	ATT	TAATAAGGGA	GC		966
Val	Ile	Ala	Ala	Ile	Ala	Lys	Gln	Met	Leu	Lys	Ala	Ile				
300					305				310							
TTTAAGGGGA	GAATGATTTC	AAAATACCCC	CTATCCCCTT	AA												1008

(2) INFORMATION FOR SEQ ID NO:992:

```

Val Ser Gly Met Leu Glu Ile Gly Ala Phe Lys Glu Ala Phe Lys Lys
145                      150                      155                      160
Val Leu Gly Lys Lys Leu Thr Gln Glu Val Ile Asp Ala Asn Met Leu
                      165                      170                      175
Ala Ile Gln Arg Ala Tyr Glu Glu Val Gln
                      180                      185

```

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...954
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

```

TTGGGGATTT TAACTTTT ATG GAT TTT TGC TCT GGC ATT GGT GGA GGC CGT      51
                Met Asp Phe Cys Ser Gly Ile Gly Gly Gly Arg
                  1                      5                      10

TTG GGC TTG GAG CAA TGC CAT TTA AAA TGC GTA GGG CAT GCA GAA ATC      99
Leu Gly Leu Glu Gln Cys His Leu Lys Cys Val Gly His Ala Glu Ile
                  15                      20                      25

AAT CAT GAA GCC CTT AGG ACT TAT GAA TTA TTT TTT AAA GAT ACC CAT      147
Asn His Glu Ala Leu Arg Thr Tyr Glu Leu Phe Phe Lys Asp Thr His
                  30                      35                      40

AAT TTT GGG GAT TTG ATG CGA ATC AAC CCT AAT GAT TTA CCC GAT TTT      195
Asn Phe Gly Asp Leu Met Arg Ile Asn Pro Asn Asp Leu Pro Asp Phe
                  45                      50                      55

GAT GCA CTC ATT AGC GGG TTT CCT TGT CAA GCT TTT TCT ATC AAT GGC      243
Asp Ala Leu Ile Ser Gly Phe Pro Cys Gln Ala Phe Ser Ile Asn Gly
                  60                      65                      70                      75

AAA AGG AAG GGG CTT GAA GAT GAA AGA GGG ACG ATT ATT TAC GGG CTT      291
Lys Arg Lys Gly Leu Glu Asp Glu Arg Gly Thr Ile Ile Tyr Gly Leu
                  80                      85                      90

ATT CGC ATT TTA AAA GTT AAA CAG CCT GAA TGT TTC TTG CTT GAA AAT      339
Ile Arg Ile Leu Lys Val Lys Gln Pro Glu Cys Phe Leu Leu Glu Asn
                  95                      100                      105

GTT AAG GGC TTG ATC AAT CAT AAT AAA AAG GCA ACT TTT AAT ATT ATT      387

```

```

Lys Glu Glu Leu Phe Glu Lys Lys Pro Glu Leu Lys Thr Arg Lys Val
      105                      110                      115

TTT TTA GTG GAT TGT TTA AAA ATC TCT ATG GAA ACC TTA AAA CGC CCC      441
Phe Leu Val Asp Cys Leu Lys Ile Ser Met Glu Thr Leu Lys Arg Pro
      120                      125                      130

ATC CCT AAC ACG CCC ATG TTA GGG GCG TTA ATG AAA GTG TCT GGC ATG      489
Ile Pro Asn Thr Pro Met Leu Gly Ala Leu Met Lys Val Ser Gly Met
      135                      140                      145

CTT GAA ATT GGG GCT TTT AAA GAA GCT TTT AAG AAA GTT TTA GGC AAA      537
Leu Glu Ile Gly Ala Phe Lys Glu Ala Phe Lys Lys Val Leu Gly Lys
      150                      155                      160

AAA CTC ACG CAA GAA GTC ATT GAC GCT AAC ATG CTC GCT ATC CAA AGA      585
Lys Leu Thr Gln Glu Val Ile Asp Ala Asn Met Leu Ala Ile Gln Arg
      165                      170                      175                      180

GCT TAT GAA GAA GTT CAA TAACATTAAG GAACAAAGAT GAAAGATTGG AACGAATT      641
Ala Tyr Glu Glu Val Gln
      185

TGAAATGGG                                                                650

```

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

```

Met Phe Gln Ile Arg Trp His Ala Arg Ala Gly Gln Gly Ala Ile Thr
  1           5           10           15
Gly Ala Lys Gly Leu Ala Asp Val Ile Ser Lys Thr Gly Lys Glu Val
      20           25           30
Gln Ala Phe Ala Ser Tyr Gly Ser Ala Lys Arg Gly Ala Ala Met Met
      35           40           45
Ala Tyr Asn Arg Val Asp Asp Glu Pro Ile Leu Asn His Glu Arg Phe
      50           55           60
Met Gln Pro Asp Tyr Val Leu Val Ile Asp Pro Gly Leu Val Phe Ile
      65           70           75           80
Glu Asn Ile Phe Ala Asn Glu Lys Glu Asp Thr Thr Tyr Ile Ile Thr
      85           90           95
Ser Tyr Leu Asn Lys Glu Glu Leu Phe Glu Lys Lys Pro Glu Leu Lys
      100          105          110
Thr Arg Lys Val Phe Leu Val Asp Cys Leu Lys Ile Ser Met Glu Thr
      115          120          125
Leu Lys Arg Pro Ile Pro Asn Thr Pro Met Leu Gly Ala Leu Met Lys
      130          135          140

```

```

Arg Lys Arg Leu Phe Arg Val Phe Val Lys His Cys Ile Leu Ile Pro
385                      390                      395                      400
Leu Lys Ser Leu Val Gly Lys Thr Leu Arg Leu Leu Lys Leu His Ala
                      405                      410                      415
Leu Ala Lys Lys Ile Leu Ile Gln Leu Lys Leu Leu Lys Lys Ser
                      420                      425                      430

```

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...603
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

```

GCTGAATTCA ATTTATTTTA TACGATATTA AGGAGACATA TTACC ATG TTT CAA ATT      57
                               Met Phe Gln Ile
                               1

AGA TGG CAT GCA CGA GCG GGT CAA GGT GCA ATC ACT GGC GCT AAA GGG      105
Arg Trp His Ala Arg Ala Gly Gln Gly Ala Ile Thr Gly Ala Lys Gly
  5                      10                      15                      20

TTG GCT GAT GTG ATT TCA AAA ACA GGC AAA GAA GTG CAA GCG TTC GCT      153
Leu Ala Asp Val Ile Ser Lys Thr Gly Lys Glu Val Gln Ala Phe Ala
          25                      30                      35

TCT TAT GGT TCA GCT AAA AGG GGG GCT GCT ATG ATG GCT TAT AAC CGC      201
Ser Tyr Gly Ser Ala Lys Arg Gly Ala Ala Met Met Ala Tyr Asn Arg
          40                      45                      50

GTT GAT GAT GAA CCT ATC TTA AAC CAT GAA CGC TTC ATG CAG CCT GAT      249
Val Asp Asp Glu Pro Ile Leu Asn His Glu Arg Phe Met Gln Pro Asp
          55                      60                      65

TAT GTG CTG GTG ATT GAC CCT GGT TTG GTT TTC ATT GAA AAC ATC TTC      297
Tyr Val Leu Val Ile Asp Pro Gly Leu Val Phe Ile Glu Asn Ile Phe
          70                      75                      80

GCC AAT GAA AAA GAA GAC ACG ACT TAT ATT ATC ACT AGC TAC CTT AAC      345
Ala Asn Glu Lys Glu Asp Thr Thr Tyr Ile Ile Thr Ser Tyr Leu Asn
          85                      90                      95                      100

AAA GAA GAA TTG TTT GAA AAA AAA CCT GAA TTA AAA ACC CGT AAG GTG      393

```


(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

```

Met Thr Ser Ala Ser Ser His Ser Phe Lys Glu Gln Asp Phe His Ile
 1          5          10          15
Pro Ile Ala Phe Ala Phe Asp Lys Asn Tyr Leu Ile Pro Ala Gly Ala
 20          25          30
Cys Leu Tyr Ser Leu Leu Glu Ser Ile Ala Lys Ala Asn Lys Lys Ile
 35          40          45
Arg Tyr Thr Leu His Ala Leu Val Val Gly Leu Asn Glu Glu Asp Lys
 50          55          60
Ala Lys Leu Asn Gln Ile Thr Glu Pro Phe Lys Glu Phe Ala Ala Leu
 65          70          75          80
Glu Val Arg Asp Ile Glu Ser Phe Leu Asp Thr Ile Pro Asn Pro Phe
 85          90          95
Asp Glu Asp Phe Thr Lys Arg Phe Ser Lys Met Val Leu Val Lys Tyr
100          105          110
Phe Leu Ala Asp Leu Phe Pro Lys Tyr Ser Lys Met Val Trp Ser Asp
115          120          125
Val Asp Val Ile Phe Cys Asn Glu Phe Ser Ala Asp Phe Leu Asn Leu
130          135          140
Glu Glu Asn Asp Glu Asn Tyr Phe Tyr Gly Val Leu Glu Val Glu Lys
145          150          155          160
His His Met Met Glu Gly Phe Leu Phe Cys Asn Leu Asp Tyr Gln Arg
165          170          175
Lys Lys Asn Phe Thr Leu Arg Met His Glu Leu Leu Arg Gly Asn Glu
180          185          190
Ala Lys Gly Glu Leu Asp Phe Thr Lys Trp Cys Trp Pro Asn Met Lys
195          200          205
Ala Leu Gly Ile Glu Tyr Cys Val Phe Pro Tyr Tyr Tyr Thr Ile Lys
210          215          220
Asp Phe Ser Asn Ala Tyr Leu Asn Glu Asn Tyr Lys Lys Thr Ile Leu
225          230          235          240
Glu Ala Arg Glu Asn Pro Thr Ile Ile His Tyr Asp Ala Trp Trp Gly
245          250          255
Ala Val Lys Pro Trp Asp Tyr Pro Phe Gly Leu Lys Ala Asp Leu Trp
260          265          270
Leu Asn Ala Leu Ala Lys Thr Pro Phe Met Ser Asp Trp Ile Asp Ser
275          280          285
Ile Ala Arg Val Glu Ile Gly Ser Glu Lys Trp His Arg Tyr His Ser
290          295          300
Ile Val Ala Tyr His Tyr Phe Pro Leu Trp Lys Thr Glu Glu Gln
305          310          315          320
Ile Ala His Asp Ala Leu Lys Thr Phe Leu Asp His Tyr Phe Ser Cys
325          330          335
Ile His Ala Ala Ile Lys Gln Glu Asn Leu Gly Met Phe Leu Asn His
340          345          350
Tyr Phe Ser His Ala His Ala Glu Ile Lys Glu Asn Ser Leu Glu Met
355          360          365
Phe Leu Asn His Tyr Phe Ser His Val Tyr Arg Leu Pro Lys Lys Ala
370          375          380

```

CAC TAT GAC GCT TGG TGG GGA GCG GTG AAG CCT TGG GAC TAT CCT TTT	819
His Tyr Asp Ala Trp Trp Gly Ala Val Lys Pro Trp Asp Tyr Pro Phe	
250 255 260 265	
GGT TTA AAA GCG GAT TTA TGG CTG AAC GCT TTG GCT AAA ACC CCT TTT	867
Gly Leu Lys Ala Asp Leu Trp Leu Asn Ala Leu Ala Lys Thr Pro Phe	
270 275 280	
ATG AGC GAT TGG ATT GAT TCG ATC GCT AGG GTG GAA ATA GGC AGC GAA	915
Met Ser Asp Trp Ile Asp Ser Ile Ala Arg Val Glu Ile Gly Ser Glu	
285 290 295	
AAA TGG CAT CGT TAC CAC AGC ATC GTT GCC TAT CAC TAC TAC TTT CCC	963
Lys Trp His Arg Tyr His Ser Ile Val Ala Tyr His Tyr Tyr Phe Pro	
300 305 310	
CTA TGG AAG ACT GAA GAG CAG ATC GCC CAT GAC GCA CTC AAG ACC TTT	1011
Leu Trp Lys Thr Glu Glu Gln Ile Ala His Asp Ala Leu Lys Thr Phe	
315 320 325	
TTA GAC CAT TAT TTT TCG TGC ATC CAT GCC GCA ATC AAG CAA GAA AAT	1059
Leu Asp His Tyr Phe Ser Cys Ile His Ala Ala Ile Lys Gln Glu Asn	
330 335 340 345	
CTC GGA ATG TTC TTG AAC CAC TAC TTC TCG CAT GCC CAT GCA GAG ATC	1107
Leu Gly Met Phe Leu Asn His Tyr Phe Ser His Ala His Ala Glu Ile	
350 355 360	
AAA GAA AAC TCC CTT GAA ATG TTC TTG AAC CAC TAC TTC TCG CAT GTT	1155
Lys Glu Asn Ser Leu Glu Met Phe Leu Asn His Tyr Phe Ser His Val	
365 370 375	
TAT AGG CTC CCT AAA AAA GCA CGG AAG AGA CTC TTT AGG GTG TTT GTC	1203
Tyr Arg Leu Pro Lys Lys Ala Arg Lys Arg Leu Phe Arg Val Phe Val	
380 385 390	
AAA CAC TGC ATC CTC ATA CCA CTC AAG AGC CTT GTG GGT AAG ACT CTA	1251
Lys His Cys Ile Leu Ile Pro Leu Lys Ser Leu Val Gly Lys Thr Leu	
395 400 405	
CGA CTC TTA AAA CTC CAT GCG CTA GCT AAA AAA ATC CTA ATC CAA CTC	1299
Arg Leu Leu Lys Leu His Ala Leu Ala Lys Lys Ile Leu Ile Gln Leu	
410 415 420 425	
AAG CTC TTA AAA AAG AGC TAGAGCCAAA ACTTTTAATC AAACGATTTT TTCATATC	1355
Lys Leu Leu Lys Lys Ser	
430	
AATCACATAG CGGAATTTTCG CTT	1378

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

TAC	CTC	ATT	CCT	GCG	GGC	GCG	TGT	CTT	TAT	TCC	TTG	CTA	GAA	AGC	ATC	147
Tyr	Leu	Ile	Pro	Ala	Gly	Ala	Cys	Leu	Tyr	Ser	Leu	Leu	Glu	Ser	Ile	
				30				35					40			
GCT	AAA	GCC	AAT	AAA	AAA	ATC	CGT	TAC	ACC	CTA	CAC	GCT	TTA	GTG	GTA	195
Ala	Lys	Ala	Asn	Lys	Lys	Ile	Arg	Tyr	Thr	Leu	His	Ala	Leu	Val	Val	
			45				50					55				
GGC	TTG	AAT	GAA	GAA	GAT	AAA	GCA	AAG	CTT	AAT	CAA	ATC	ACA	GAG	CCT	243
Gly	Leu	Asn	Glu	Glu	Asp	Lys	Ala	Lys	Leu	Asn	Gln	Ile	Thr	Glu	Pro	
		60					65				70					
TTT	AAA	GAA	TTT	GCC	GCT	TTG	GAA	GTG	AGA	GAT	ATT	GAG	TCT	TTT	TTA	291
Phe	Lys	Glu	Phe	Ala	Ala	Leu	Glu	Val	Arg	Asp	Ile	Glu	Ser	Phe	Leu	
	75					80				85						
GAC	ACT	ATC	CCT	AAC	CCT	TTT	GAT	GAG	GAT	TTC	ACT	AAG	CGT	TTT	TCT	339
Asp	Thr	Ile	Pro	Asn	Pro	Phe	Asp	Glu	Asp	Phe	Thr	Lys	Arg	Phe	Ser	
90				95						100					105	
AAA	ATG	GTG	TTA	GTG	AAG	TAT	TTT	TTG	GCG	GAT	TTG	TTC	CCC	AAA	TAT	387
Lys	Met	Val	Leu	Val	Lys	Tyr	Phe	Leu	Ala	Asp	Leu	Phe	Pro	Lys	Tyr	
				110					115					120		
TCC	AAA	ATG	GTG	TGG	AGC	GAT	GTG	GAT	GTC	ATC	TTT	TGC	AAT	GAA	TTT	435
Ser	Lys	Met	Val	Trp	Ser	Asp	Val	Asp	Val	Ile	Phe	Cys	Asn	Glu	Phe	
			125					130					135			
AGC	GCT	GAT	TTC	TTA	AAC	CTT	GAA	GAA	AAT	GAT	GAG	AAT	TAT	TTT	TAT	483
Ser	Ala	Asp	Phe	Leu	Asn	Leu	Glu	Glu	Asn	Asp	Glu	Asn	Tyr	Phe	Tyr	
		140					145				150					
GGA	GTT	TTA	GAA	GTT	GAA	AAG	CAC	CAC	ATG	ATG	GAA	GGG	TTT	TTG	TTT	531
Gly	Val	Leu	Glu	Val	Glu	Lys	His	His	Met	Met	Glu	Gly	Phe	Leu	Phe	
	155					160					165					
TGC	AAT	TTA	GAT	TAC	CAG	CGC	AAG	AAA	AAT	TTC	ACC	TTA	AGA	ATG	CAT	579
Cys	Asn	Leu	Asp	Tyr	Gln	Arg	Lys	Lys	Asn	Phe	Thr	Leu	Arg	Met	His	
170					175					180					185	
GAG	CTT	TTA	AGG	GGG	AAT	GAG	GCT	AAA	GGG	GAG	TTG	GAT	TTC	ACG	AAA	627
Glu	Leu	Leu	Arg	Gly	Asn	Glu	Ala	Lys	Gly	Glu	Leu	Asp	Phe	Thr	Lys	
			190						195					200		
TGG	TGT	TGG	CCT	AAC	ATG	AAA	GCT	TTA	GGG	ATT	GAA	TAT	TGC	GTT	TTC	675
Trp	Cys	Trp	Pro	Asn	Met	Lys	Ala	Leu	Gly	Ile	Glu	Tyr	Cys	Val	Phe	
			205					210					215			
CCT	TAT	TAT	TAC	ACC	ATT	AAA	GAT	TTT	TCT	AAC	GCG	TAT	TTA	AAC	GAG	723
Pro	Tyr	Tyr	Tyr	Thr	Ile	Lys	Asp	Phe	Ser	Asn	Ala	Tyr	Leu	Asn	Glu	
		220					225					230				
AAT	TAC	AAG	AAA	ACC	ATT	TTA	GAG	GCA	CGA	GAA	AAC	CCT	ACC	ATT	ATC	771
Asn	Tyr	Lys	Lys	Thr	Ile	Leu	Glu	Ala	Arg	Glu	Asn	Pro	Thr	Ile	Ile	
	235					240					245					

130	135	140
Ser Val Asp Lys Asn Ala Pro Leu Glu Lys Val Ala Pro Leu Leu Cys		
145	150	155
Ala Gly Ile Thr Thr Tyr Ser Pro Leu Lys Phe Ser Lys Val Thr Lys		
	165	170
Gly Thr Lys Val Gly Val Ala Gly Phe Gly Gly Leu Gly Ser Met Ala		
	180	185
Val Lys Tyr Ala Val Ala Met Gly Ala Glu Val Ser Val Phe Ala Arg		
	195	200
Asn Glu His Lys Lys Gln Asp Ala Leu Ser Met Gly Val Lys His Phe		
	210	215
Tyr Thr Asp Pro Lys Gln Cys Lys Glu Glu Leu Asp Phe Ile Ile Ser		
225	230	235
Thr Ile Pro Thr His Tyr Asp Leu Lys Asp Tyr Leu Lys Leu Leu Thr		
	245	250
Tyr Asn Gly Asp Leu Ala Leu Val Gly Leu Pro Pro Val Glu Ile Ala		
	260	265
Pro Ala Leu Ser Val Phe Asp Phe Ile His Leu Gly Asn Arg Lys Val		
	275	280
Tyr Gly Ser Leu Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Met Asp		
	290	295
Phe Ser Ile Lys His Asn Ile Tyr Pro Glu Ile Asp Leu Ile Leu Gly		
305	310	315
Lys Asp Ile Asp Thr Ala Tyr His Asn Leu Thr His Gly Lys Ala Lys		
	325	330
Phe Arg Tyr Val Ile Asp Met Lys Lys Ser Phe Asp		
	340	345

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1317
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

TTAAAAAAGG GTGTTTAATT TTTT ATG ACT TCA GCT TCA AGC CAT TCT TTT	51
Met Thr Ser Ala Ser Ser His Ser Phe	
1 5	
AAA GAA CAA GAT TTT CAT ATT CCT ATC GCT TTT GCT TTT GAT AAG AAT	99
Lys Glu Gln Asp Phe His Ile Pro Ile Ala Phe Ala Phe Asp Lys Asn	
10 15 20 25	

```

GGC GAT CTA GCC CTT GTG GGA CTC CCC CCT GTA GAA ATC GCT CCA GCG      872
Gly Asp Leu Ala Leu Val Gly Leu Pro Pro Val Glu Ile Ala Pro Ala
    260                      265                      270

CTT AGC GTT TTT GAT TTT ATC CAT TTA GGC AAT CGC AAG GTT TAT GGC      920
Leu Ser Val Phe Asp Phe Ile His Leu Gly Asn Arg Lys Val Tyr Gly
    275                      280                      285                      290

TCA TTG ATT GGG GGC ATT AAA GAA ACC CAA GAA ATG ATG GAT TTT TCT      968
Ser Leu Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Met Asp Phe Ser
                295                      300                      305

ATC AAA CAC AAT ATT TAC CCT GAA ATA GAT TTG ATC TTA GGC AAG GAT      1016
Ile Lys His Asn Ile Tyr Pro Glu Ile Asp Leu Ile Leu Gly Lys Asp
                310                      315                      320

ATT GAC ACC GCT TAT CAT AAT CTA ACC CAT GGG AAA GCG AAA TTC CGC      1064
Ile Asp Thr Ala Tyr His Asn Leu Thr His Gly Lys Ala Lys Phe Arg
                325                      330                      335

TAT GTG ATT GAT ATG AAA AAA TCG TTT GAT TAAAAGTTTT GGCTCTAGCT CTT  1117
Tyr Val Ile Asp Met Lys Lys Ser Phe Asp
    340                      345

TTTTAAGAGC TTGAGTTGG                                              1136

```

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

```

Met Arg Val Gln Ser Lys Gly Phe Ala Ile Phe Ser Lys Asp Gly His
 1          5          10          15
Phe Lys Pro His Asp Phe Ser Arg His Ala Val Gly Pro Lys Asp Val
          20          25          30
Leu Ile Asp Ile Leu Tyr Ala Gly Ile Cys His Ser Asp Ile His Ser
          35          40          45
Ala Tyr Ser Glu Trp Lys Glu Gly Ile Tyr Pro Met Val Pro Gly His
          50          55          60
Glu Ile Ala Gly Ala Ile Lys Glu Val Gly Lys Glu Val Lys Lys Phe
          65          70          75          80
Lys Val Gly Asp Val Val Gly Val Gly Cys Phe Val Asn Ser Cys Lys
          85          90          95
Ala Cys Lys Pro Cys Lys Glu His Gln Glu Gln Phe Cys Ala Lys Val
          100          105          110
Val Phe Thr Tyr Asp Cys Leu Asp Tyr Phe His Asp Asn Glu Pro His
          115          120          125
Met Gly Gly Tyr Ser Asn Asn Ile Val Val Asp Glu Asn Tyr Val Ile

```

GAC ATT CTT TAT GCA GGG ATT TGT CAT AGC GAT ATT CAT AGC GCT TAT	200
Asp Ile Leu Tyr Ala Gly Ile Cys His Ser Asp Ile His Ser Ala Tyr	
35 40 45 50	
AGC GAA TGG AAA GAA GGC ATT TAC CCT ATG GTT CCT GGG CAT GAA ATT	248
Ser Glu Trp Lys Glu Gly Ile Tyr Pro Met Val Pro Gly His Glu Ile	
55 60 65	
GCT GGG GCC ATC AAA GAA GTG GGT AAG GAA GTT AAG AAA TTT AAG GTT	296
Ala Gly Ala Ile Lys Glu Val Gly Lys Glu Val Lys Lys Phe Lys Val	
70 75 80	
GGC GAT GTG GTG GGC GTG GGC TGT TTT GTC AAT TCA TGC AAA GCG TGT	344
Gly Asp Val Val Gly Val Gly Cys Phe Val Asn Ser Cys Lys Ala Cys	
85 90 95	
AAG CCC TGT AAA GAA CAC CAA GAG CAA TTT TGC GCC AAA GTG GTA TTC	392
Lys Pro Cys Lys Glu His Gln Glu Gln Phe Cys Ala Lys Val Val Phe	
100 105 110	
ACT TAC GAT TGT TTG GAT TAT TTC CAT GAC AAC GAA CCC CAC ATG GGC	440
Thr Tyr Asp Cys Leu Asp Tyr Phe His Asp Asn Glu Pro His Met Gly	
115 120 125 130	
GGA TAC TCT AAT AAT ATT GTA GTG GAT GAA AAC TAT GTG ATT AGC GTG	488
Gly Tyr Ser Asn Asn Ile Val Val Asp Glu Asn Tyr Val Ile Ser Val	
135 140 145	
GAT AAA AAC GCT CCT TTA GAA AAA GTA GCC CCC TTG CTT TGT GCG GGC	536
Asp Lys Asn Ala Pro Leu Glu Lys Val Ala Pro Leu Leu Cys Ala Gly	
150 155 160	
ATC ACC ACT TAT TCG CCC TTA AAA TTT TCT AAG GTT ACT AAA GGC ACA	584
Ile Thr Thr Tyr Ser Pro Leu Lys Phe Ser Lys Val Thr Lys Gly Thr	
165 170 175	
AAA GTT GGC GTC GCT GGG TTT GGC GGG CTA GGA AGC ATG GCG GTT AAA	632
Lys Val Gly Val Ala Gly Phe Gly Gly Leu Gly Ser Met Ala Val Lys	
180 185 190	
TAC GCT GTG GCT ATG GGG GCT GAA GTG AGC GTT TTT GCA AGA AAC GAA	680
Tyr Ala Val Ala Met Gly Ala Glu Val Ser Val Phe Ala Arg Asn Glu	
195 200 205 210	
CAC AAA AAG CAA GAC GCT TTG AGC ATG GGG GTT AAA CAT TTC TAC ACT	728
His Lys Lys Gln Asp Ala Leu Ser Met Gly Val Lys His Phe Tyr Thr	
215 220 225	
GAC CCC AAA CAA TGC AAA GAG GAA TTG GAC TTT ATC ATT TCA ACC ATT	776
Asp Pro Lys Gln Cys Lys Glu Glu Leu Asp Phe Ile Ile Ser Thr Ile	
230 235 240	
CCT ACC CAT TAT GAT TTA AAA GAC TAC CTC AAG CTC TTA ACT TAT AAT	824
Pro Thr His Tyr Asp Leu Lys Asp Tyr Leu Lys Leu Leu Thr Tyr Asn	
245 250 255	

```

Ile Ala Gln Met Gly Arg Ala Ser Gly Leu His Leu Ile Val Ala Thr
      675                      680                      685
Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys Thr Asn Leu
      690                      695                      700
Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys Ile Asp Ser Lys Val
      705                      710                      715                      720
Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu Gly Arg Gly Asp Met
      725                      730                      735
Leu Phe Thr Pro Pro Gly Ala Asn Gly Leu Val Arg Leu His Ala Pro
      740                      745                      750
Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val Asp Phe Ile Lys Ala
      755                      760                      765
Gln Lys Glu Val Gln Tyr Asp Lys Asp Phe Leu Leu Glu Glu Ser Arg
      770                      775                      780
Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp Asp Ile Leu Glu Arg
      785                      790                      795                      800
Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr Ser Thr Ser Phe Leu
      805                      810                      815
Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr Ile Thr Asp
      820                      825                      830
Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala Lys Gly Asn
      835                      840                      845
Arg Glu Ile Leu Gln Asn Phe
      850                      855

```

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1094
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

```

AACCATAAAA ACGATACAAT AGCGGTATTT TAATAAAACA AGGAGTTTTA  ATG AGA      56
                                     Met Arg
                                     1

GTT CAA TCT AAA GGT TTT GCT ATT TTT TCT AAA GAC GGG CAT TTC AAA      104
Val Gln Ser Lys Gly Phe Ala Ile Phe Ser Lys Asp Gly His Phe Lys
      5                      10                      15

CCC CAT GAT TTT AGC CGC CAT GCT GTA GGC CCT AAA GAT GTG TTG ATT      152
Pro His Asp Phe Ser Arg His Ala Val Gly Pro Lys Asp Val Leu Ile
      20                      25                      30

```

225					230					235				240
Pro	Pro	Thr	His	Tyr	Thr	Ile	Tyr	Pro	Lys	Arg	Asn	Arg	Phe	Asp
				245					250				255	
Leu	Thr	Asn	Pro	Thr	Asn	Pro	Pro	Leu	Lys	Glu	Ile	Lys	Gln	Thr
			260					265					270	
Lys	Glu	Arg	Glu	Pro	Thr	Pro	Thr	Lys	Glu	Thr	Leu	Thr	Pro	Thr
		275					280					285		
Pro	Lys	Pro	Ile	Met	Pro	Thr	Leu	Ala	Pro	Ile	Ile	Glu	Asn	Asp
	290					295					300			
Lys	Thr	Glu	Asn	Gln	Lys	Thr	Pro	Asn	His	Pro	Lys	Lys	Glu	Asn
305					310					315				320
Pro	Gln	Glu	Asn	Thr	Gln	Glu	Glu	Met	Ile	Glu	Gly	Arg	Ile	Glu
			325					330					335	
Met	Ile	Lys	Glu	Asn	Leu	Lys	Lys	Glu	Glu	Lys	Glu	Val	Gln	Ala
		340						345				350		
Pro	Asn	Phe	Ser	Pro	Val	Thr	Pro	Thr	Ser	Ala	Lys	Lys	Pro	Met
		355					360					365		
Val	Lys	Glu	Leu	Ser	Glu	Asn	Lys	Glu	Ile	Leu	Asp	Gly	Leu	Tyr
	370					375					380			
Gly	Glu	Val	Gln	Lys	Pro	Lys	Asp	Tyr	Glu	Leu	Pro	Thr	Thr	Gln
385					390					395				400
Leu	Asn	Ala	Val	Cys	Leu	Lys	Asp	Thr	Ser	Leu	Asp	Glu	Asn	Glu
			405					410					415	
Asp	Gln	Lys	Ile	Gln	Asp	Leu	Leu	Ser	Lys	Leu	Arg	Thr	Phe	Lys
		420					425					430		
Asp	Gly	Asp	Ile	Ile	Arg	Thr	Tyr	Ser	Gly	Pro	Ile	Val	Thr	Phe
	435					440					445			
Glu	Phe	Arg	Pro	Ala	Pro	Asn	Val	Lys	Val	Ser	Arg	Ile	Leu	Gly
	450					455				460				
Ser	Asp	Asp	Leu	Ala	Met	Thr	Leu	Cys	Ala	Glu	Ser	Ile	Arg	Gln
465					470					475				480
Ala	Pro	Ile	Lys	Gly	Lys	Asp	Val	Val	Gly	Ile	Glu	Ile	Pro	Asn
			485					490					495	
Gln	Ser	Gln	Ile	Ile	Tyr	Leu	Arg	Glu	Ile	Leu	Glu	Ser	Glu	Phe
		500						505					510	
Gln	Lys	Ser	Ser	Ser	Pro	Leu	Thr	Leu	Ala	Leu	Gly	Lys	Asp	Val
	515						520					525		
Gly	Asn	Pro	Phe	Ile	Thr	Asp	Leu	Lys	Lys	Leu	Pro	His	Leu	Ile
	530					535				540				
Ala	Gly	Thr	Thr	Gly	Ser	Gly	Lys	Ser	Val	Gly	Val	Asn	Ala	Met
545					550					555				560
Leu	Ser	Leu	Leu	Tyr	Lys	Asn	Pro	Pro	Asp	Gln	Leu	Lys	Leu	Val
			565					570					575	
Ile	Asp	Pro	Lys	Met	Val	Glu	Phe	Ser	Ile	Tyr	Ala	Asp	Ile	Pro
		580						585				590		
Leu	Leu	Thr	Pro	Ile	Ile	Thr	Asp	Pro	Lys	Lys	Ala	Ile	Gly	Ala
	595						600					605		
Gln	Ser	Val	Ala	Lys	Glu	Met	Glu	Arg	Arg	Tyr	Ser	Leu	Met	Ser
	610					615					620			
Tyr	Lys	Val	Lys	Thr	Ile	Asp	Ser	Tyr	Asn	Glu	Gln	Ala	Pro	Asn
625					630					635				640
Gly	Val	Glu	Ala	Phe	Pro	Tyr	Leu	Ile	Val	Val	Ile	Asp	Glu	Ala
			645					650					655	
Asp	Leu	Met	Met	Thr	Gly	Gly	Lys	Glu	Ala	Glu	Phe	Pro	Ile	Ala
		660						665				670		

TCT ACG AGT TTT TTA CAA CGC CAA TTA AAA ATC GGC TAC AAC CAA GCC 2498
 Ser Thr Ser Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala
 815 820 825

GCT ACC ATT ACT GAC GAA TTA GAA GCT CAA GGC TTT TTA TCC CCA AGA 2546
 Ala Thr Ile Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg
 830 835 840

AAC GCT AAA GGC AAC AGA GAG ATT TTG CAA AAC TTT TAGGCTTTGT TTTCAT 2598
 Asn Ala Lys Gly Asn Arg Glu Ile Leu Gln Asn Phe
 845 850 855

TGGATATTGG CAAACATTAT TTTTGATTT 2627

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly Val Leu Leu
 1 5 10 15
 Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly Leu Val Gly
 20 25 30
 Arg Phe Gly Val Trp Phe Ala Ala Leu Asn Lys Lys Tyr Phe Gly His
 35 40 45
 Leu Ser Phe Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu Phe Leu Leu
 50 55 60
 Tyr Lys Thr Lys Asn Pro Phe Thr Glu Ile Val Leu Glu Lys Thr Leu
 65 70 75 80
 Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln Ser Ser Leu
 85 90 95
 Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe Leu Arg Pro
 100 105 110
 Phe Ile Gly Asp Phe Gly Leu Tyr Ala Leu Ile Thr Leu Met Val Val
 115 120 125
 Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser Val Phe Tyr
 130 135 140
 Pro Tyr Met Asn Lys Thr Gln Asn Leu Leu Lys Glu Ile Tyr Lys Gln
 145 150 155 160
 Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Pro Lys Lys Glu Gly Phe
 165 170 175
 Glu Asn Thr Pro Ser Asp Ile Gln Lys Lys Glu Thr Lys Asn Asp Lys
 180 185 190
 Glu Lys Glu Asn Arg Lys Glu Asn Pro Ile Asn Glu Asn His Lys Thr
 195 200 205
 Pro Asn Glu Glu Pro Phe Leu Ala Ile Pro Thr Pro Tyr Asn Thr Thr
 210 215 220
 Leu Asn Asp Ser Glu Pro Gln Glu Gly Leu Val Gln Ile Ser Ser His

GCG GAT ATC CCT CAT TTG CTC ACG CCC ATT ATC ACC GAC CCT AAA AAA	1826
Ala Asp Ile Pro His Leu Leu Thr Pro Ile Ile Thr Asp Pro Lys Lys	
590 595 600	
GCT ATT GGG GCT TTG CAA AGC GTG GCT AAA GAA ATG GAA CGC CGG TAT	1874
Ala Ile Gly Ala Leu Gln Ser Val Ala Lys Glu Met Glu Arg Arg Tyr	
605 610 615	
TCT TTA ATG AGC GAA TAC AAG GTT AAA ACC ATT GAT TCT TAT AAT GAA	1922
Ser Leu Met Ser Glu Tyr Lys Val Lys Thr Ile Asp Ser Tyr Asn Glu	
620 625 630 635	
CAA GCC CCA AGT AAC GGC GTT GAA GCG TTC CCC TAT TTG ATT GTG GTG	1970
Gln Ala Pro Ser Asn Gly Val Glu Ala Phe Pro Tyr Leu Ile Val Val	
640 645 650	
ATT GAT GAA TTA GCG GAT TTA ATG ATG ACA GGG GGC AAA GAA GCG GAG	2018
Ile Asp Glu Leu Ala Asp Leu Met Met Thr Gly Gly Lys Glu Ala Glu	
655 660 665	
TTT CCT ATC GCT AGA ATC GCT CAA ATG GGG CGC GCG AGC GGC TTA CAC	2066
Phe Pro Ile Ala Arg Ile Ala Gln Met Gly Arg Ala Ser Gly Leu His	
670 675 680	
CTC ATT GTA GCG ACC CAA CGC CCA AGC GTG GAT GTC GTA ACC GGC TTG	2114
Leu Ile Val Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu	
685 690 695	
ATT AAA ACC AAC TTG CCT TCA AGG GTG AGT TTT AGG GTA GGC ACT AAG	2162
Ile Lys Thr Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys	
700 705 710 715	
ATT GAT TCT AAA GTG ATT TTA GAC ACT GAT GGG GCG CAA AGC TTG TTA	2210
Ile Asp Ser Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu	
720 725 730	
GGA AGA GGC GAT ATG CTC TTT ACC CCC CCA GGA GCG AAC GGG TTA GTG	2258
Gly Arg Gly Asp Met Leu Phe Thr Pro Pro Gly Ala Asn Gly Leu Val	
735 740 745	
CGC TTG CAT GCC CCC TTT GCC ACT GAA GAT GAA ATC AAA AAA ATC GTG	2306
Arg Leu His Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val	
750 755 760	
GAT TTT ATT AAA GCC CAA AAA GAA GTA CAA TAC GAT AAA GAT TTC TTG	2354
Asp Phe Ile Lys Ala Gln Lys Glu Val Gln Tyr Asp Lys Asp Phe Leu	
765 770 775	
CTA GAA GAA TCA CGC ATG CCT TTA GAC ACC CCT AAT TAT CAA GGC GAT	2402
Leu Glu Glu Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp	
780 785 790 795	
GAC ATT TTA GAA AGG GCT AAA GCG GTG ATT TTA GAA AAA AAG ATC ACT	2450
Asp Ile Leu Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr	
800 805 810	

Lys	Lys	Pro	Val	Met	Val	Lys	Glu	Leu	Ser	Glu	Asn	Lys	Glu	Ile	Leu	
365						370					375					
GAC	GGA	TTG	GAT	TAT	GGC	GAA	GTG	CAA	AAA	CCC	AAA	GAT	TAT	GAG	CTT	1202
Asp	Gly	Leu	Asp	Tyr	Gly	Glu	Val	Gln	Lys	Pro	Lys	Asp	Tyr	Glu	Leu	
380					385					390					395	
CCC	ACC	ACG	CAA	TTA	TTG	AAT	GCG	GTT	TGT	TTG	AAA	GAC	ACT	TCT	TTA	1250
Pro	Thr	Thr	Gln	Leu	Leu	Asn	Ala	Val	Cys	Leu	Lys	Asp	Thr	Ser	Leu	
				400					405					410		
GAC	GAA	AAC	GAG	ATT	GAC	CAA	AAA	ATC	CAG	GAT	CTA	TTG	AGC	AAA	CTG	1298
Asp	Glu	Asn	Glu	Ile	Asp	Gln	Lys	Ile	Gln	Asp	Leu	Leu	Ser	Lys	Leu	
			415					420					425			
CGC	ACC	TTT	AAA	ATT	GAT	GGC	GAT	ATT	ATC	CGC	ACT	TAT	TCA	GGC	CCT	1346
Arg	Thr	Phe	Lys	Ile	Asp	Gly	Asp	Ile	Ile	Arg	Thr	Tyr	Ser	Gly	Pro	
		430					435					440				
ATT	GTA	ACC	ACT	TTT	GAA	TTC	CGC	CCA	GCC	CCT	AAC	GTT	AAG	GTG	AGT	1394
Ile	Val	Thr	Thr	Phe	Glu	Phe	Arg	Pro	Ala	Pro	Asn	Val	Lys	Val	Ser	
		445					450				455					
CGT	ATT	TTA	GGC	TTG	AGC	GAT	GAT	TTA	GCG	ATG	ACT	TTA	TGC	GCT	GAA	1442
Arg	Ile	Leu	Gly	Leu	Ser	Asp	Asp	Leu	Ala	Met	Thr	Leu	Cys	Ala	Glu	
460					465					470					475	
TCC	ATC	CGC	ATT	CAA	GCC	CCT	ATT	AAG	GGT	AAA	GAT	GTC	GTT	GGC	ATT	1490
Ser	Ile	Arg	Ile	Gln	Ala	Pro	Ile	Lys	Gly	Lys	Asp	Val	Val	Gly	Ile	
				480					485					490		
GAA	ATC	CCT	AAC	AGC	CAA	AGC	CAA	ATT	ATT	TAT	TTA	AGA	GAA	ATT	CTA	1538
Glu	Ile	Pro	Asn	Ser	Gln	Ser	Gln	Ile	Ile	Tyr	Leu	Arg	Glu	Ile	Leu	
			495					500					505			
GAG	AGC	GAA	TTG	TTT	CAA	AAA	TCC	AGC	TCG	CCC	TTA	ACT	CTA	GCT	TTA	1586
Glu	Ser	Glu	Leu	Phe	Gln	Lys	Ser	Ser	Ser	Pro	Leu	Thr	Leu	Ala	Leu	
		510					515					520				
GGC	AAA	GAC	ATT	GTG	GGT	AAC	CCT	TTC	ATC	ACG	GAT	TTA	AAA	AAG	CTC	1634
Gly	Lys	Asp	Ile	Val	Gly	Asn	Pro	Phe	Ile	Thr	Asp	Leu	Lys	Lys	Leu	
		525				530					535					
CCC	CAT	TTG	CTC	ATC	GCT	GGC	ACG	ACA	GGA	AGC	GGT	AAG	AGC	GTG	GGC	1682
Pro	His	Leu	Leu	Ile	Ala	Gly	Thr	Thr	Gly	Ser	Gly	Lys	Ser	Val	Gly	
540					545					550					555	
GTG	AAT	GCG	ATG	ATT	TTA	TCC	TTA	CTT	TAT	AAA	AAC	CCT	CCC	GAT	CAA	1730
Val	Asn	Ala	Met	Ile	Leu	Ser	Leu	Leu	Tyr	Lys	Asn	Pro	Pro	Asp	Gln	
				560					565					570		
CTC	AAA	TTA	GTG	ATG	ATC	GAT	CCC	AAA	ATG	GTA	GAA	TTT	AGT	ATT	TAT	1778
Leu	Lys	Leu	Val	Met	Ile	Asp	Pro	Lys	Met	Val	Glu	Phe	Ser	Ile	Tyr	
			575					580					585			

140	145	150	155	
GAG ATT TAC AAA CAA TGC TTA CAA GCC TTT AGC CCT AAT TTT AGC CCA				530
Glu Ile Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Pro	160	165	170	
AAA AAA GAG GGT TTT GAA AAC ACC CCA TCA GAT ATT CAA AAA AAA GAA				578
Lys Lys Glu Gly Phe Glu Asn Thr Pro Ser Asp Ile Gln Lys Lys Glu	175	180	185	
ACC AAA AAC GAC AAA GAA AAA GAA AAC CGC AAA GAA AAC CCT ATT AAT				626
Thr Lys Asn Asp Lys Glu Lys Glu Asn Arg Lys Glu Asn Pro Ile Asn	190	195	200	
GAA AAC CAC AAA ACC CCT AAC GAA GAA CCG TTT TTA GCG ATC CCT ACC				674
Glu Asn His Lys Thr Pro Asn Glu Glu Pro Phe Leu Ala Ile Pro Thr	205	210	215	
CCC TAT AAC ACG ACT TTA AAT GAT TCA GAG CCG CAA GAA GGC TTA GTC				722
Pro Tyr Asn Thr Thr Leu Asn Asp Ser Glu Pro Gln Glu Gly Leu Val	220	225	230	235
CAA ATT TCC TCC CAC CCC CCT ACC CAT TAC ACC ATT TAC CCT AAA AGA				770
Gln Ile Ser Ser His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg	240	245	250	
AAC CGA TTT GAT GAT TTG ACT AAC CCC ACT AAC CCC CCT TTA AAA GAA				818
Asn Arg Phe Asp Asp Leu Thr Asn Pro Thr Asn Pro Pro Leu Lys Glu	255	260	265	
ATT AAA CAA GAA ACT AAA GAA AGA GAA CCC ACG CCT ACA AAA GAA ACT				866
Ile Lys Gln Glu Thr Lys Glu Arg Glu Pro Thr Pro Thr Lys Glu Thr	270	275	280	
CTT ACG CCC ACC ACG CCC AAA CCT ATC ATG CCC ACA CTT GCA CCC ATA				914
Leu Thr Pro Thr Thr Pro Lys Pro Ile Met Pro Thr Leu Ala Pro Ile	285	290	295	
ATA GAA AAT GAC AAC AAA ACA GAA AAC CAA AAA ACC CCC AAC CAC CCT				962
Ile Glu Asn Asp Asn Lys Thr Glu Asn Gln Lys Thr Pro Asn His Pro	300	305	310	315
AAA AAA GAA GAA AAC CCA CAA GAA AAC ACG CAA GAA GAA ATG ATA GAA				1010
Lys Lys Glu Glu Asn Pro Gln Glu Asn Thr Gln Glu Glu Met Ile Glu	320	325	330	
GGA AGG ATA GAA GAA ATG ATA AAG GAA AAT CTA AAA AAA GAA GAA AAA				1058
Gly Arg Ile Glu Glu Met Ile Lys Glu Asn Leu Lys Lys Glu Glu Lys	335	340	345	
GAA GTG CAA AAC GCT CCA AAC TTT AGC CCA GTA ACC CCC ACA AGC GCT				1106
Glu Val Gln Asn Ala Pro Asn Phe Ser Pro Val Thr Pro Thr Ser Ala	350	355	360	
AAA AAA CCC GTT ATG GTT AAA GAA TTG AGC GAA AAT AAA GAG ATA TTA				1154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 18...2582
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

AAAGACATGT GCAACCG ATG AAA TCT AAA AAA CTT TAT TTG GCT TTA ATC	50
Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile	
1 5 10	
ATA GGG GTT TTA TTA GCG TTT TTA ACC CTA TCT TCA TGG CTG GGT AAT	98
Ile Gly Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn	
15 20 25	
AGC GGT TTA GTG GGG CGT TTT GGG GTG TGG TTT GCC GCA CTC AAT AAA	146
Ser Gly Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Leu Asn Lys	
30 35 40	
AAA TAT TTT GGG CAT CTT TCA TTC ATT AAT TTA CCC TAT TTA GCA TGG	194
Lys Tyr Phe Gly His Leu Ser Phe Ile Asn Leu Pro Tyr Leu Ala Trp	
45 50 55	
GTT TTA TTC CTT TTA TAC AAG ACT AAA AAC CCT TTT ACA GAA ATC GTT	242
Val Leu Phe Leu Leu Tyr Lys Thr Lys Asn Pro Phe Thr Glu Ile Val	
60 65 70 75	
TTA GAA AAA ACT TTA GGG CAT CTA TTA GGC ATT TTA TCT TTG CTC TTT	290
Leu Glu Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe	
80 85 90	
TTA CAA TCT AGC CTA TTA AAT CAA GGG GAA ATC GGC AAC AGC GCG CGT	338
Leu Gln Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg	
95 100 105	
TTG TTT TTA CGC CCT TTT ATA GGG GAT TTT GGG CTT TAT GCG CTG ATA	386
Leu Phe Leu Arg Pro Phe Ile Gly Asp Phe Gly Leu Tyr Ala Leu Ile	
110 115 120	
ACG CTT ATG GTA GTT ATT TCT TAT TTG ATT CTA TTC AAA CTA CCC CCT	434
Thr Leu Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro	
125 130 135	
AAA AGC GTT TTT TAT CCT TAT ATG AAC AAA ACA CAA AAC CTT TTA AAA	482
Lys Ser Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Asn Leu Leu Lys	

Ile Gln Gln Asp Ile Leu Arg Ala Lys Glu Ile Leu Arg
 270 275 280

AAATGACTCT CAAAAACCTT AAAAATGGAA AAATTT

906

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

Met	Leu	Asn	Phe	Leu	Ser	Ile	Ser	Ser	Glu	Pro	Lys	Ile	Lys	Ser	Leu	1	5	10	15
Ala	Ile	Gly	Lys	Phe	Asp	Gly	Leu	His	Leu	Gly	His	Gln	Ala	Leu	Phe	20	25	30	
Lys	Glu	Leu	Lys	Asp	Pro	Lys	Ala	Leu	Leu	Ile	Ile	Glu	Lys	Lys	His	35	40	45	
Tyr	Thr	Lys	Gly	Tyr	Leu	Thr	Pro	Leu	Lys	Tyr	Arg	Ala	Lys	Leu	Val	50	55	60	
Gly	Met	Pro	Leu	Phe	Phe	Val	Tyr	Leu	Glu	Glu	Ile	Ser	Gln	Leu	Asn	65	70	75	80
Ala	Leu	Asp	Phe	Leu	Asp	Leu	Leu	Lys	Lys	Lys	Phe	Pro	His	Leu	Glu	85	90	95	
Arg	Leu	Val	Val	Gly	Tyr	Asp	Phe	Arg	Phe	Gly	His	Glu	Arg	Gln	Asn	100	105	110	
Asp	Ala	Leu	Phe	Leu	Lys	Glu	Arg	Phe	Glu	Lys	Thr	Ile	Ile	Val	Pro	115	120	125	
Glu	Val	Lys	Val	Gln	Glu	Ile	Ser	Val	His	Ser	Lys	Met	Ile	Lys	Leu	130	135	140	
Ala	Leu	Ser	His	Gly	Asp	Leu	Ser	Leu	Ala	Asn	Lys	Leu	Leu	Gly	Arg	145	150	155	160
Pro	Tyr	Glu	Val	Cys	Gly	Glu	Val	Ile	Ser	Asp	Gln	Gly	Leu	Gly	His	165	170	175	
Lys	Glu	Leu	Ala	Pro	Thr	Leu	Asn	Ile	Lys	Thr	Lys	Asp	Phe	Ile	Leu	180	185	190	
Pro	Ser	Phe	Gly	Val	Tyr	Ala	Ser	Leu	Val	Lys	Ile	Lys	Asp	Pro	Ile	195	200	205	
Tyr	Gln	Lys	Ser	Val	Ser	Phe	Ile	Gly	Asn	Arg	Leu	Ser	Thr	Asp	Gln	210	215	220	
Asn	Phe	Ala	Ile	Glu	Cys	His	Val	Leu	Asp	Thr	Ile	Ile	Glu	Asn	Pro	225	230	235	240
Pro	Gln	Glu	Ile	Ala	Leu	Arg	Trp	Val	Gln	Lys	Ile	Arg	Asp	Asn	Met	245	250	255	
Arg	Phe	Ser	Ser	Leu	Lys	Glu	Leu	Lys	Asn	Gln	Ile	Gln	Gln	Asp	Ile	260	265	270	
Leu	Arg	Ala	Lys	Glu	Ile	Leu	Arg									275	280		

(2) INFORMATION FOR SEQ ID NO:983:

45	50	55	
CGC GCT AAA CTC GTG GGC ATG CCT TTA TTT TTT GTG TAT TTA GAA GAG			243
Arg Ala Lys Leu Val Gly Met Pro Leu Phe Phe Val Tyr Leu Glu Glu			
60	65	70	75
ATT TCA CAA TTA AAC GCC CTA GAT TTT TTA GAT CTT TTA AAA AAG AAA			291
Ile Ser Gln Leu Asn Ala Leu Asp Phe Leu Asp Leu Leu Lys Lys Lys			
80	85	90	
TTT CCC CAT TTA GAA CGC CTG GTC GTG GGC TAT GAT TTC AGG TTT GGG			339
Phe Pro His Leu Glu Arg Leu Val Val Gly Tyr Asp Phe Arg Phe Gly			
95	100	105	
CAT GAG AGG CAA AAT GAC GCT TTA TTT TTA AAA GAG CGT TTT GAA AAA			387
His Glu Arg Gln Asn Asp Ala Leu Phe Leu Lys Glu Arg Phe Glu Lys			
110	115	120	
ACC ATT ATT GTG CCT GAA GTG AAA GTC CAA GAG ATT AGC GTG CAT TCT			435
Thr Ile Ile Val Pro Glu Val Lys Val Gln Glu Ile Ser Val His Ser			
125	130	135	
AAG ATG ATC AAA CTA GCC CTA AGT CAT GGC GAC TTA TCT TTA GCT AAC			483
Lys Met Ile Lys Leu Ala Leu Ser His Gly Asp Leu Ser Leu Ala Asn			
140	145	150	155
AAG CTC TTA GGC AGA CCT TAT GAA GTG TGT GGG GAA GTC ATT AGT GAT			531
Lys Leu Leu Gly Arg Pro Tyr Glu Val Cys Gly Glu Val Ile Ser Asp			
160	165	170	
CAA GGT TTG GGG CAT AAA GAA TTA GCA CCC ACT TTA AAT ATA AAA ACT			579
Gln Gly Leu Gly His Lys Glu Leu Ala Pro Thr Leu Asn Ile Lys Thr			
175	180	185	
AAA GAT TTT ATC CTC CCT AGT TTT GGG GTG TAT GCG AGT TTA GTG AAA			627
Lys Asp Phe Ile Leu Pro Ser Phe Gly Val Tyr Ala Ser Leu Val Lys			
190	195	200	
ATA AAA GAT CCA ATT TAT CAA AAA AGC GTG AGT TTT ATA GGC AAT CGC			675
Ile Lys Asp Pro Ile Tyr Gln Lys Ser Val Ser Phe Ile Gly Asn Arg			
205	210	215	
TTA AGC ACG GAT CAA AAT TTC GCC ATA GAA TGC CAT GTC CTT GAT ACC			723
Leu Ser Thr Asp Gln Asn Phe Ala Ile Glu Cys His Val Leu Asp Thr			
220	225	230	235
ATC ATA GAA AAC CCG CCC CAA GAA ATC GCT TTG CGT TGG GTT CAA AAA			771
Ile Ile Glu Asn Pro Pro Gln Glu Ile Ala Leu Arg Trp Val Gln Lys			
240	245	250	
ATA CGA GAC AAC ATG CGT TTT TCT TCT TTA AAA GAG CTT AAA AAT CAG			819
Ile Arg Asp Asn Met Arg Phe Ser Ser Leu Lys Glu Leu Lys Asn Gln			
255	260	265	
ATC CAA CAA GAC ATC TTA AGA GCC AAA GAG ATT TTG AGA TAATTTGTGT TA			870

```

65          70          75          80
Leu Asp Val Gly Ala Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu
          85          90          95
Lys Gly Ala Lys Arg Val Leu Cys Val Asp Val Gly Lys Met Gln Leu
          100         105         110
Asp Glu Ser Leu Lys Gln Asp Lys Arg Ile Glu Cys Tyr Glu Glu Cys
          115         120         125
Asp Ile Arg Gly Phe Lys Thr Pro Glu Thr Ile Asp Leu Ala Leu Cys
          130         135         140
Asp Val Ser Phe Ile Ser Leu Tyr Tyr Ile Leu Glu Ala Ile Leu Pro
          145         150         155         160
Leu Ser Asp Glu Phe Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly
          165         170         175
Arg Gly Ile Lys Arg Asn Lys Lys Gly Val Val Val Asp Lys Glu Ala
          180         185         190
Ile Leu Asn Ala Leu Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp
          195         200         205
Phe Gln Ile Leu Lys Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly
          210         215         220
Asn Val Glu Phe Phe Ile His Phe Lys Arg Ala
          225         230         235

```

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...858
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

```

TGAAAGGGAA AAACGGGA ATG TTG AAT TTT TTA TCC ATT TCA AGC GAG CCT      51
          Met Leu Asn Phe Leu Ser Ile Ser Ser Glu Pro
          1          5          10

AAA ATT AAA AGC CTA GCT ATC GGT AAA TTT GAC GGC TTG CAT TTA GGG      99
Lys Ile Lys Ser Leu Ala Ile Gly Lys Phe Asp Gly Leu His Leu Gly
          15          20          25

CAT CAA GCC CTT TTT AAA GAG TTA AAA GAT CCC AAA GCC CTT TTA ATC     147
His Gln Ala Leu Phe Lys Glu Leu Lys Asp Pro Lys Ala Leu Leu Ile
          30          35          40

ATA GAA AAA AAA CAT TAC ACT AAA GGC TAT TTA ACC CCC CTA AAA TAC     195
Ile Glu Lys Lys His Tyr Thr Lys Gly Tyr Leu Thr Pro Leu Lys Tyr

```


AAG CGC ATA GAA TGT TAC GAA GAA TGC GAT ATT AGA GGG TTT AAA ACG	438
Lys Arg Ile Glu Cys Tyr Glu Glu Cys Asp Ile Arg Gly Phe Lys Thr	
120 125 130 135	
CCA GAA ACA ATT GAT TTA GCG CTT TGC GAT GTG AGC TTT ATT TCT TTA	486
Pro Glu Thr Ile Asp Leu Ala Leu Cys Asp Val Ser Phe Ile Ser Leu	
140 145 150	
TAT TAT ATT TTA GAA GCG ATT TTG CCT TTA AGC GAT GAA TTT TTA ACA	534
Tyr Tyr Ile Leu Glu Ala Ile Leu Pro Leu Ser Asp Glu Phe Leu Thr	
155 160 165	
CTT TTC AAA CCG CAA TTT GAA GTG GGC AGA GGA ATA AAA CGC AAT AAA	582
Leu Phe Lys Pro Gln Phe Glu Val Gly Arg Gly Ile Lys Arg Asn Lys	
170 175 180	
AAA GGG GTG GTG GTG GAT AAA GAA GCC ATT TTG AAC GCT TTA GAA AAC	630
Lys Gly Val Val Val Asp Lys Glu Ala Ile Leu Asn Ala Leu Glu Asn	
185 190 195	
TTT AAA AAC CAT TTA AAA ACA AAG GAT TTT CAA ATC TTA AAG ATC CAA	678
Phe Lys Asn His Leu Lys Thr Lys Asp Phe Gln Ile Leu Lys Ile Gln	
200 205 210 215	
GAA AGC TTA GTG AAA GGG AAA AAC GGG AAT GTT GAA TTT TTT ATC CAT	726
Glu Ser Leu Val Lys Gly Lys Asn Gly Asn Val Glu Phe Phe Ile His	
220 225 230	
TTC AAG CGA GCC TAAAATTAAA AGCCTAGCTA TCGGTAAATT TGACGGCTTG CATTT	783
Phe Lys Arg Ala	
235	
AGGGCA	789

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

Met Arg Leu Asp Tyr Ala Leu Phe Ser Gln His Leu Val Asn Ser Arg	
1 5 10 15	
Glu Lys Ala Lys Ala Leu Val Leu Lys Asn Gln Val Leu Val Asn Lys	
20 25 30	
Met Val Val Ser Lys Pro Ser Phe Ile Val Lys Glu Asn Asp Lys Ile	
35 40 45	
Glu Leu Ile Ala Glu Lys Leu Phe Val Ser Arg Ala Gly Glu Lys Leu	
50 55 60	
Gly Ala Phe Leu Glu Thr His Phe Val Asp Phe Lys Gly Lys Val Val	

130 135 140
 Leu Ser Glu Val Phe Asn Asn Val Gly Ser Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...738
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

```

TTTCGCTTAT CAAGTCCCC TACCTCAATT TTA ATG CGC TTA GAT TAC GCC TTA      54
                                Met Arg Leu Asp Tyr Ala Leu
                                1              5

TTC AGT CAG CAT TTA GTA AAT AGC AGA GAA AAA GCT AAA GCG TTG GTT      102
Phe Ser Gln His Leu Val Asn Ser Arg Glu Lys Ala Lys Ala Leu Val
    10              15              20

TTA AAA AAT CAG GTT TTA GTC AAT AAA ATG GTG GTT TCC AAA CCC TCT      150
Leu Lys Asn Gln Val Leu Val Asn Lys Met Val Val Ser Lys Pro Ser
    25              30              35

TTT ATA GTG AAA GAG AAC GAT AAA ATT GAA CTC ATC GCT GAA AAA CTT      198
Phe Ile Val Lys Glu Asn Asp Lys Ile Glu Leu Ile Ala Glu Lys Leu
    40              45              50              55

TTC GTT AGC AGG GCT GGG GAA AAA TTA GGG GCT TTT TTA GAA ACC CAT      246
Phe Val Ser Arg Ala Gly Glu Lys Leu Gly Ala Phe Leu Glu Thr His
                60              65              70

TTC GTG GAT TTT AAG GGA AAG GTG GTT TTA GAT GTG GGA GCG AGC AAA      294
Phe Val Asp Phe Lys Gly Lys Val Val Leu Asp Val Gly Ala Ser Lys
                75              80              85

GGG GGC TTT AGT CAA GTG GCT CTT TTA AAA GGG GCT AAA AGA GTG CTT      342
Gly Gly Phe Ser Gln Val Ala Leu Leu Lys Gly Ala Lys Arg Val Leu
    90              95              100

TGC GTG GAT GTG GGG AAA ATG CAA TTA GAT GAA AGT TTG AAA CAA GAC      390
Cys Val Asp Val Gly Lys Met Gln Leu Asp Glu Ser Leu Lys Gln Asp
    105              110              115

```

```

GGT TTG ATT AGA GCG AGT TTG TCC AAT TAC CTT TCA GAG AGC ATA AGA      356
Gly Leu Ile Arg Ala Ser Leu Ser Asn Tyr Leu Ser Glu Ser Ile Arg
              75                      80                      85

GAG GGG CTA ACG ATT GTT GGG TTA GTG GGG GTG GTG ATC TAT CAA AGC      404
Glu Gly Leu Thr Ile Val Gly Leu Val Gly Val Val Ile Tyr Gln Ser
              90                      95                      100

CCT AAA TTA GCG TTA GTG GGG TTA GTC ATC ATG CCG TTA GCT GCT ATT      452
Pro Lys Leu Ala Leu Val Gly Leu Val Ile Met Pro Leu Ala Ala Ile
              105                      110                      115

CCT ATC AGT AAA ATC ATT CGT AAG GTT AAA AAA CTC GCT AAA TCC CAT      500
Pro Ile Ser Lys Ile Ile Arg Lys Val Lys Lys Leu Ala Lys Ser His
              120                      125                      130

CAA GAG AGT AAC GCC AAA ATC ACC GCT CGT TTG AGT GAA GTT TTT AAC      548
Gln Glu Ser Asn Ala Lys Ile Thr Ala Arg Leu Ser Glu Val Phe Asn
              135                      140                      145                      150

AAC GTG GGA AGC GAT TAAAATCTCT AATGGCGAAA AATTAGAGCA TAAGGCTTTT G      604
Asn Val Gly Ser Asp
              155

```

604

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

```

Met Leu Lys Ile Leu Pro Phe Leu Val Ile Leu Ala Tyr Leu Gly Lys
 1              5              10              15
Ser Gly Gly Met Tyr Leu Gly Thr Tyr Phe Thr Asn Phe Ile Gly Leu
              20              25              30
Asp Ile Val Lys Lys Ile Arg Asn Thr Met Leu Glu Ser Leu Leu Lys
              35              40              45
Met Glu Met Asp Phe Phe Asn Arg Thr Lys Lys Gly Glu Leu Ile Ala
              50              55              60
Arg Ile Thr Asn Asp Ile Gly Leu Ile Arg Ala Ser Leu Ser Asn Tyr
              65              70              75              80
Leu Ser Glu Ser Ile Arg Glu Gly Leu Thr Ile Val Gly Leu Val Gly
              85              90              95
Val Val Ile Tyr Gln Ser Pro Lys Leu Ala Leu Val Gly Leu Val Ile
              100              105              110
Met Pro Leu Ala Ala Ile Pro Ile Ser Lys Ile Ile Arg Lys Val Lys
              115              120              125
Lys Leu Ala Lys Ser His Gln Glu Ser Asn Ala Lys Ile Thr Ala Arg

```

```

      195              200              205
Val Glu Lys Met Pro His Gly Ile Glu Ser Val Leu Asp Glu Phe Gly
      210              215              220
Ala Asn Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala
      225              230              235              240
Leu Tyr Lys Asp Val Gln Val Leu Ile Phe Asp Glu Ala Thr Ser Ala
      245              250              255
Leu Asp Asn Asn Thr Glu Glu Ser Val Lys Gln Ser Ile Leu Glu Leu
      260              265              270
Lys Gln Asn Arg Leu Ile Ile Leu Ile Ser His Asn Pro Ser Thr Leu
      275              280              285
Lys Leu Ala Thr Lys His Val Lys Leu Glu His Gly Arg Leu Thr Glu
      290              295              300
Cys
      305

```

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 99...563
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

```

TTTTATTTTC TTCTTTAGTG GTGGCTTTAA GCACGGCTTG GGGGACTTAT TTAGTCAAGC      60
CCACTTTAGA TGAAATTTT ATCAATAAAG ACACTCAC ATG CTC AAA ATC CTG CCT      116
                               Met Leu Lys Ile Leu Pro
                               1              5

TTT TTA GTG ATT TTG GCG TAT TTG GGT AAG AGT GGG GGC ATG TAT TTA      164
Phe Leu Val Ile Leu Ala Tyr Leu Gly Lys Ser Gly Gly Met Tyr Leu
      10              15              20

GGC ACT TAT TTC ACC AAC TTC ATT GGG CTT GAT ATT GTC AAA AAA ATA      212
Gly Thr Tyr Phe Thr Asn Phe Ile Gly Leu Asp Ile Val Lys Lys Ile
      25              30              35

CGC AAC ACT ATG CTA GAA AGC CTT CTT AAA ATG GAA ATG GAT TTT TTT      260
Arg Asn Thr Met Leu Glu Ser Leu Leu Lys Met Glu Met Asp Phe Phe
      40              45              50

AAC AGG ACG AAA AAG GGC GAA TTG ATC GCA AGG ATC ACC AAT GAT ATA      308
Asn Arg Thr Lys Lys Gly Glu Leu Ile Ala Arg Ile Thr Asn Asp Ile
      55              60              65              70

```

```

GCC ACT TCC GCT TTA GAC AAT AAC ACA GAA GAG AGC GTT AAA CAA AGC      878
Ala Thr Ser Ala Leu Asp Asn Asn Thr Glu Glu Ser Val Lys Gln Ser
      255                      260                      265

ATT TTA GAA TTG AAA CAA AAC CGC TTG ATC ATT CTT ATT TCG CAC AAC      926
Ile Leu Glu Leu Lys Gln Asn Arg Leu Ile Ile Leu Ile Ser His Asn
      270                      275                      280

CCA AGC ACG CTA AAA TTA GCC ACT AAG CAT GTG AAA TTA GAG CAT GGG      974
Pro Ser Thr Leu Lys Leu Ala Thr Lys His Val Lys Leu Glu His Gly
      285                      290                      295                      300

CGT TTG ACA GAA TGC TAAGGGTTTT AAGCGTTGGT GTTGCTTTTA TTTTACTAGG G 1030
Arg Leu Thr Glu Cys
      305

TGTC                                                                1034

```

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

```

Met Glu Phe Leu Gly Ser Ile Ala Ile Ala Leu Val Ile Tyr Leu Gly
 1           5           10           15
Gly Asn Glu Val Ile Arg Gly His Ile Ser Val Gly Ala Phe Phe Ser
      20           25           30
Phe Ile Thr Ala Leu Phe Met Leu Tyr Thr Pro Ile Lys Arg Leu Thr
      35           40           45
Arg Ile Val Ser Asn Phe Gln Glu Ala Leu Val Ala Ser Asp Arg Ile
      50           55           60
His Glu Ile Leu Glu Arg Glu Pro Ala Ile Val Asp Gly Glu Leu Thr
      65           70           75           80
Leu Asn Asn Ala Ile His Thr Ile Glu Phe Lys Lys Val Trp Leu Ala
      85           90           95
Tyr Thr Leu Asp Asn Gln Glu Arg Tyr Val Leu Asn Asp Ile Ser Leu
      100          105          110
Lys Phe Gln Gln Asn Glu Ile Ile Ala Leu Lys Gly Glu Ser Gly Ser
      115          120          125
Gly Lys Ser Ser Leu Val Asn Leu Ile Leu Arg Leu Tyr Glu Pro Ser
      130          135          140
Lys Gly Glu Ile Phe Ile Asn Asp Gln Lys Ile Glu Ser Ile Thr Gln
      145          150          155          160
Lys Ser Leu Arg Glu Lys Ile Ser Val Val Thr Gln Arg Val Phe Ile
      165          170          175
Phe Asn Gly Ser Val Ala Glu Asn Val Ala Tyr Gly Leu Glu Ile Asp
      180          185          190
Glu Val Lys Ile Lys Glu Cys Leu Lys Lys Ala Gln Ala Leu Asp Phe

```

GCG TTT TTT TCT TTC ATT ACG GCC CTT TTT ATG CTC TAT ACG CCG ATT	206
Ala Phe Phe Ser Phe Ile Thr Ala Leu Phe Met Leu Tyr Thr Pro Ile	
30 35 40	
AAA CGC TTA ACT AGG ATT GTT TCT AAT TTT CAA GAA GCC TTA GTC GCT	254
Lys Arg Leu Thr Arg Ile Val Ser Asn Phe Gln Glu Ala Leu Val Ala	
45 50 55 60	
AGC GAC AGG ATC CAT GAG ATT TTA GAA AGA GAG CCG GCT ATT GTT GAT	302
Ser Asp Arg Ile His Glu Ile Leu Glu Arg Glu Pro Ala Ile Val Asp	
65 70 75	
GGG GAA TTG ACG CTA AAT AAC GCC ATA CAC ACC ATA GAA TTT AAA AAG	350
Gly Glu Leu Thr Leu Asn Asn Ala Ile His Thr Ile Glu Phe Lys Lys	
80 85 90	
GTA TGG CTG GCT TAT ACG CTA GAC AAT CAA GAG CGT TAT GTT TTA AAC	398
Val Trp Leu Ala Tyr Thr Leu Asp Asn Gln Glu Arg Tyr Val Leu Asn	
95 100 105	
GAT ATT AGT TTG AAG TTC CAA CAA AAT GAA ATC ATC GCT TTA AAG GGC	446
Asp Ile Ser Leu Lys Phe Gln Gln Asn Glu Ile Ile Ala Leu Lys Gly	
110 115 120	
GAA AGC GGG AGC GGT AAA AGC TCA TTA GTG AAT CTG ATC TTA CGC CTT	494
Glu Ser Gly Ser Gly Lys Ser Ser Leu Val Asn Leu Ile Leu Arg Leu	
125 130 135 140	
TAT GAG CCA AGC AAA GGC GAA ATT TTC ATC AAC GAT CAA AAA ATA GAG	542
Tyr Glu Pro Ser Lys Gly Glu Ile Phe Ile Asn Asp Gln Lys Ile Glu	
145 150 155	
AGC ATC ACT CAA AAA TCC TTA AGA GAA AAG ATT AGC GTT GTC ACT CAA	590
Ser Ile Thr Gln Lys Ser Leu Arg Glu Lys Ile Ser Val Val Thr Gln	
160 165 170	
AGG GTG TTT ATT TTT AAC GGG AGC GTG GCT GAA AAT GTG GCG TAT GGT	638
Arg Val Phe Ile Phe Asn Gly Ser Val Ala Glu Asn Val Ala Tyr Gly	
175 180 185	
TTA GAA ATT GAT GAG GTA AAA ATC AAA GAA TGC CTA AAA AAA GCT CAA	686
Leu Glu Ile Asp Glu Val Lys Ile Lys Glu Cys Leu Lys Lys Ala Gln	
190 195 200	
GCC TTA GAT TTT GTT GAA AAA ATG CCT CAT GGG ATA GAG AGC GTT TTA	734
Ala Leu Asp Phe Val Glu Lys Met Pro His Gly Ile Glu Ser Val Leu	
205 210 215 220	
GAT GAA TTT GGC GCT AAT CTT AGC GGC GGC CAA CGC CAA AGA ATC GCC	782
Asp Glu Phe Gly Ala Asn Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala	
225 230 235	
ATT GCA AGA GCT TTG TAT AAA GAC GTT CAA GTT TTA ATC TTT GAT GAA	830
Ile Ala Arg Ala Leu Tyr Lys Asp Val Gln Val Leu Ile Phe Asp Glu	
240 245 250	

```

Lys Ile Phe Lys Lys Ser His Ser Asn Glu Ser Leu Ser Gln Gln Gln
      115                      120                      125
Asn Glu Glu Ile Glu Arg Leu Leu Thr Ser Arg Gly Leu Leu Asn Arg
      130                      135                      140
Phe Phe Lys Pro Leu Phe Asn Phe Val Ser Lys Ser Trp His Ile Tyr
145      150                      155                      160
Pro Ile Gly Phe Leu Phe Gly Leu Gly Phe Asp Thr Ala Ser Glu Ile
      165                      170                      175
Ala Leu Leu Ala Leu Ser Ser Ser Ala Ile Lys Val Ser Met Val Gly
      180                      185                      190
Met Leu Ser Leu Pro Ile Leu Phe Ala Ala Gly Met Ser Leu Phe Asp
      195                      200                      205
Thr Leu Asp Gly Ala Phe Met Leu Lys Ala Tyr Asp Trp Ala Phe Lys
      210                      215                      220
Thr Pro Leu Arg Lys Ile Tyr Tyr Asn Ile Ser Ile Thr Ala Leu Ser
225      230                      235                      240
Val Phe Ile Ala Leu Phe Ile Gly Leu Ile Glu Leu Phe Gln Val Val
      245                      250                      255
Ser Glu Lys Leu His Leu Lys Phe Glu Asn Arg Leu Leu Arg Ala Leu
      260                      265                      270
Gln Ser Leu Glu Phe Thr Asp Leu Gly Tyr Tyr Leu Val Gly Leu Phe
      275                      280                      285
Val Ile Ala Phe Leu Gly Ser Phe Phe Leu Trp Lys Ile Lys Phe Ser
      290                      295                      300
Lys Leu Glu Ser
305

```

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 75...989
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

```

TTGTGAAAGA AAATGAAGCG TTTTAAATAA TCGGTATCAA AAACATCGCC GTGGCTGAAA      60
TTTCTTCGCC TTTA ATG GAG TTT TTA GGT TCA ATC GCT ATA GCG CTA GTG      110
      Met Glu Phe Leu Gly Ser Ile Ala Ile Ala Leu Val
      1                      5                      10

ATT TAT TTA GGG GGG AAT GAA GTG ATT AGA GGC CAT ATT AGC GTG GGG      158
Ile Tyr Leu Gly Gly Asn Glu Val Ile Arg Gly His Ile Ser Val Gly
      15                      20                      25

```

```

GGG GCG TTC ATG CTC AAG GCG TAT GAC TGG GCG TTC AAA ACC CCT TTA      729
Gly Ala Phe Met Leu Lys Ala Tyr Asp Trp Ala Phe Lys Thr Pro Leu
      215                      220                      225

AGA AAA ATC TAT TAC AAT ATC TCT ATC ACG GCC TTA AGC GTG TTT ATC      777
Arg Lys Ile Tyr Tyr Asn Ile Ser Ile Thr Ala Leu Ser Val Phe Ile
      230                      235                      240

GCG CTC TTT ATT GGC TTG ATT GAG CTT TTT CAA GTC GTT AGC GAG AAA      825
Ala Leu Phe Ile Gly Leu Ile Glu Leu Phe Gln Val Val Ser Glu Lys
      245                      250                      255

CTC CAT TTA AAA TTT GAA AAC CGC CTT TTA AGA GCC TTA CAA AGC CTG      873
Leu His Leu Lys Phe Glu Asn Arg Leu Leu Arg Ala Leu Gln Ser Leu
      260                      265                      270                      275

GAA TTT ACA GAC TTG GGC TAT TAC TTG GTG GGC TTA TTT GTA ATA GCG      921
Glu Phe Thr Asp Leu Gly Tyr Tyr Leu Val Gly Leu Phe Val Ile Ala
      280                      285                      290

TTT CTA GGA TCG TTC TTT TTA TGG AAA ATC AAA TTT TCT AAA CTA GAG      969
Phe Leu Gly Ser Phe Phe Leu Trp Lys Ile Lys Phe Ser Lys Leu Glu
      295                      300                      305

AGC TGAATTCTAA GCCCTCAAAT TATCGCTTAA TAAATCTTTA AGGCTTTGAT TTG      1025
Ser

```

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

```

Met Ala Asn Asn Ala Ser Phe Tyr Ala Ala Ala Ser Met Ala Tyr Met
 1          5          10          15
Leu Gly Ala Lys His Ala Phe Asp Ala Asp His Ile Ala Cys Ile Asp
      20          25          30
Asn Thr Ile Arg Lys Leu Thr Gln Gln Gly Lys Asn Ala Tyr Gly Val
      35          40          45
Gly Phe Tyr Phe Ser Met Gly His Ser Ser Val Val Ile Leu Met Thr
      50          55          60
Ile Ile Ser Ala Phe Ala Ile Ala Trp Ala Lys Glu His Thr Pro Met
      65          70          75          80
Leu Glu Glu Ile Gly Gly Val Val Gly Thr Leu Val Ser Gly Leu Phe
      85          90          95
Leu Leu Ile Ile Gly Leu Leu Asn Ala Ile Ile Leu Leu Asp Leu Leu
      100          105          110

```


Met Ala Asn
1

AAC GCT TCG TTT TAT GCG GCG GCG TCT ATG GCC TAC ATG CTA GGG GCA	105
Asn Ala Ser Phe Tyr Ala Ala Ala Ser Met Ala Tyr Met Leu Gly Ala	
5 10 15	
AAG CAT GCG TTT GAT GCG GAT CAC ATC GCT TGC ATA GAT AAC ACC ATT	153
Lys His Ala Phe Asp Ala Asp His Ile Ala Cys Ile Asp Asn Thr Ile	
20 25 30 35	
AGA AAG CTC ACC CAA CAA GGC AAA AAC GCC TAT GGT GTG GGG TTT TAC	201
Arg Lys Leu Thr Gln Gln Gly Lys Asn Ala Tyr Gly Val Gly Phe Tyr	
40 45 50	
TTT TCT ATG GGG CAT TCA AGC GTG GTG ATT TTA ATG ACC ATC ATC AGC	249
Phe Ser Met Gly His Ser Ser Val Val Ile Leu Met Thr Ile Ile Ser	
55 60 65	
GCG TTT GCG ATC GCT TGG GCT AAA GAA CAC ACG CCG ATG CTA GAA GAA	297
Ala Phe Ala Ile Ala Trp Ala Lys Glu His Thr Pro Met Leu Glu Glu	
70 75 80	
ATA GGG GGG GTA GTG GGG ACT TTA GTT TCT GGG CTT TTT TTG CTC ATT	345
Ile Gly Gly Val Val Gly Thr Leu Val Ser Gly Leu Phe Leu Leu Ile	
85 90 95	
ATA GGG CTA TTG AAT GCG ATT ATT CTC TTG GAT TTA TTA AAA ATA TTC	393
Ile Gly Leu Leu Asn Ala Ile Ile Leu Leu Asp Leu Leu Lys Ile Phe	
100 105 110 115	
AAA AAA TCG CAC TCT AAT GAA AGC CTA AGC CAG CAA CAA AAT GAA GAG	441
Lys Lys Ser His Ser Asn Glu Ser Leu Ser Gln Gln Gln Asn Glu Glu	
120 125 130	
ATC GAG CGG CTC TTA ACG AGT AGG GGC TTG CTC AAC CGC TTT TTT AAA	489
Ile Glu Arg Leu Leu Thr Ser Arg Gly Leu Leu Asn Arg Phe Phe Lys	
135 140 145	
CCC TTG TTT AAT TTT GTC TCC AAG TCG TGG CAT ATT TAT CCT ATC GGT	537
Pro Leu Phe Asn Phe Val Ser Lys Ser Trp His Ile Tyr Pro Ile Gly	
150 155 160	
TTT CTT TTT GGG CTG GGT TTT GAT ACC GCT AGT GAA ATC GCG CTT TTG	585
Phe Leu Phe Gly Leu Gly Phe Asp Thr Ala Ser Glu Ile Ala Leu Leu	
165 170 175	
GCC CTC TCT AGC AGC GCG ATT AAA GTG AGT ATG GTG GGC ATG CTC TCT	633
Ala Leu Ser Ser Ser Ala Ile Lys Val Ser Met Val Gly Met Leu Ser	
180 185 190 195	
TTA CCC ATT CTT TTT GCC GCT GGC ATG AGT TTG TTT GAC ACT TTA GAT	681
Leu Pro Ile Leu Phe Ala Ala Gly Met Ser Leu Phe Asp Thr Leu Asp	
200 205 210	

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

```

Met Asp Ile Leu Lys Thr Leu Gln Lys His Leu Gly Asp Val Glu Thr
 1           5           10           15
Ser Asp Phe Thr Thr Asn Ala Ile Glu Lys Ser Gln Gln Ile Ala Lys
          20           25           30
Phe Ser Arg Asp Met Lys Asn Ile Asn Glu Ser Val Gly Ala Leu Gln
          35           40           45
Val Leu Gln Ile Ala Cys Lys Lys Leu Phe Asn Lys Ser Met Gly Leu
          50           55           60
Glu Asp Lys Asp Ala Leu Gln Ala Ser Ile Ile Lys Gln Glu Leu Arg
65           70           75           80
Glu Ile Val Glu Asn Cys Gln Phe Leu Ala Ser Pro Leu Phe Asp Thr
          85           90           95
Gln Leu Asn Ile Ala Ile Asn Asp Glu Ile Phe Ser Met Ile Val Val
          100          105          110
Asn Pro Leu Asp Leu Leu Glu Asn Val Gly Glu Phe Gln Ala Tyr Leu
          115          120          125
Glu Glu Lys Leu Asn Glu Ile Lys Glu Leu Leu Gly Tyr Leu Ser Glu
          130          135          140
Ser Leu Ser Asn Pro Lys Ala Phe Met Pro Ser Phe Ser Asn Gln Ser
145          150          155          160
Leu Lys Asp Leu Leu Ser Asp Asn Leu Arg Ala
          165          170

```

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...972
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

TTTTTAGCGA TTGTGTTCTT GCATGCATTG GGTTCAGCGT TGCTCTTT ATG GCC AAT

57

(B) LOCATION: 25...537

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

TCAATTCTAT TTAAAAGGTT TTTT ATG GAT ATT TTA AAA ACT CTT CAA AAA	51
Met Asp Ile Leu Lys Thr Leu Gln Lys	
1 5	
CAT TTG GGC GAT GTT GAA ACA AGC GAT TTT ACA ACC AAT GCG ATA GAA	99
His Leu Gly Asp Val Glu Thr Ser Asp Phe Thr Thr Asn Ala Ile Glu	
10 15 20 25	
AAA TCC CAA CAA ATC GCT AAA TTC AGT AGG GAC ATG AAA AAT ATA AAC	147
Lys Ser Gln Gln Ile Ala Lys Phe Ser Arg Asp Met Lys Asn Ile Asn	
30 35 40	
GAG AGC GTT GGA GCG TTA CAA GTC TTG CAA ATC GCT TGC AAA AAG CTT	195
Glu Ser Val Gly Ala Leu Gln Val Leu Gln Ile Ala Cys Lys Lys Leu	
45 50 55	
TTC AAT AAG AGC ATG GGT TTA GAA GAT AAA GAC GCT TTG CAA GCT TCT	243
Phe Asn Lys Ser Met Gly Leu Glu Asp Lys Asp Ala Leu Gln Ala Ser	
60 65 70	
ATC ATC AAA CAG GAA TTG CGA GAA ATT GTA GAA AAT TGC CAG TTT TTA	291
Ile Ile Lys Gln Glu Leu Arg Glu Ile Val Glu Asn Cys Gln Phe Leu	
75 80 85	
GCC TCC CCT TTG TTT GAC ACT CAG CTC AAC ATT GCA ATC AAT GAT GAA	339
Ala Ser Pro Leu Phe Asp Thr Gln Leu Asn Ile Ala Ile Asn Asp Glu	
90 95 100 105	
ATT TTT TCC ATG ATT GTG GTT AAT CCG TTG GAT TTA TTG GAA AAT GTG	387
Ile Phe Ser Met Ile Val Val Asn Pro Leu Asp Leu Leu Glu Asn Val	
110 115 120	
GGC GAG TTT CAA GCT TAT TTG GAA GAA AAA TTA AAC GAA ATT AAG GAA	435
Gly Glu Phe Gln Ala Tyr Leu Glu Glu Lys Leu Asn Glu Ile Lys Glu	
125 130 135	
TTA TTA GGT TAT TTG AGT GAA AGC CTT TCA AAC CCT AAA GCC TTC ATG	483
Leu Leu Gly Tyr Leu Ser Glu Ser Leu Ser Asn Pro Lys Ala Phe Met	
140 145 150	
CCA AGT TTT TCA AAT CAA AGC CTT AAA GAT TTA TTA AGC GAT AAT TTG	531
Pro Ser Phe Ser Asn Gln Ser Leu Lys Asp Leu Leu Ser Asp Asn Leu	
155 160 165	
AGG GCT TAGAATTCAG CTCTCTAGTT TAGAAAATTT GATTTTCC	575
Arg Ala	
170	

```

Phe Lys Asp Ala Lys Ser Leu Glu Lys Ala Arg Leu Val Asn Thr Ile
      20              25              30
Val Phe Asp Lys Thr Gly Thr Leu Thr Asn Gly Lys Pro Val Val Lys
      35              40              45
Ser Val His Ser Lys Ile Glu Leu Leu Glu Leu Leu Ser Leu Ala Leu
      50              55              60
Ser Ile Glu Lys Ser Ser Glu His Val Ile Ala Lys Gly Ile Val Glu
      65              70              75              80
Tyr Ala Lys Glu His Asn Ala Pro Leu Lys Glu Met Ser Gly Val Lys
      85              90              95
Val Lys Thr Gly Phe Gly Ile Ser Ala Lys Thr Asp Tyr Gln Gly Thr
      100             105             110
Lys Glu Ile Ile Lys Val Gly Asn Ser Glu Phe Phe Asn Pro Ile Asn
      115             120             125
Thr Leu Glu Ile Lys Glu Asn Gly Ile Leu Val Phe Val Gly Arg Ala
      130             135             140
Ile Ser Glu Lys Glu Asp Glu Leu Leu Gly Ala Phe Val Leu Glu Asp
      145             150             155             160
Leu Pro Lys Lys Gly Val Lys Glu His Ile Ala Gln Ile Lys Asn Leu
      165             170             175
Gly Ile Asn Thr Phe Leu Leu Ser Gly Asp Asn Arg Glu Asn Val Gln
      180             185             190
Lys Cys Ala Phe Glu Leu Gly Ile Asp Gly Tyr Ile Ser Asn Ala Lys
      195             200             205
Pro Gln Asp Lys Leu Asn Lys Ile Lys Glu Leu Lys Glu Lys Gly Gln
      210             215             220
Ile Val Met Met Val Gly Asp Gly Leu Asn Asp Ala Pro Ser Leu Ala
      225             230             235             240
Met Ser Asp Val Ala Val Val Met Ala Lys Gly Ser Asp Val Ser Val
      245             250             255
Gln Ala Ala Asp Ile Val Ser Phe Asn Asn Asp Ile Lys Ser Val Tyr
      260             265             270
Ser Ala Ile Lys Leu Ser Gln Ala Thr Ile Lys Asn Ile Lys Glu Asn
      275             280             285
Leu Phe Trp Ala Phe Cys Tyr Asn Ser Val Phe Ile Pro Leu Ala Cys
      290             295             300
Gly Val Leu Tyr Lys Ala Asn Leu Met Leu Ser Pro Ala Ile Ala Gly
      305             310             315             320
Leu Ala Met Ser Leu Ser Ser Val Ser Val Val Leu Asn Ser Gln Arg
      325             330             335
Leu Arg Asn Phe Lys Ile Lys Asp His
      340             345

```

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

195	200	205	
CCA CAA GAC AAG CTC AAT AAG ATC AAA GAG CTT AAG GAA AAA GGG CAG			730
Pro Gln Asp Lys Leu Asn Lys Ile Lys Glu Leu Lys Glu Lys Gly Gln			
210	215	220	
ATC GTT ATG ATG GTG GGC GAT GGC TTG AAT GAC GCT CCT AGT CTT GCT			778
Ile Val Met Met Val Gly Asp Gly Leu Asn Asp Ala Pro Ser Leu Ala			
225	230	235	240
ATG AGC GAT GTG GCG GTG GTG ATG GCT AAA GGG AGC GAT GTG AGC GTG			826
Met Ser Asp Val Ala Val Val Met Ala Lys Gly Ser Asp Val Ser Val			
245	250	255	
CAA GCA GCG GAC ATT GTG AGT TTT AAT AAC GAT ATT AAA TCG GTT TAT			874
Gln Ala Ala Asp Ile Val Ser Phe Asn Asn Asp Ile Lys Ser Val Tyr			
260	265	270	
AGC GCG ATT AAA TTA AGC CAG GCG ACA ATT AAA AAT ATC AAA GAA AAT			922
Ser Ala Ile Lys Leu Ser Gln Ala Thr Ile Lys Asn Ile Lys Glu Asn			
275	280	285	
TTG TTT TGG GCT TTT TGT TAT AAT AGC GTG TTC ATC CCT TTA GCT TGT			970
Leu Phe Trp Ala Phe Cys Tyr Asn Ser Val Phe Ile Pro Leu Ala Cys			
290	295	300	
GGG GTT CTT TAT AAG GCT AAT CTC ATG TTA AGC CCG GCG ATA GCG GGT			1018
Gly Val Leu Tyr Lys Ala Asn Leu Met Leu Ser Pro Ala Ile Ala Gly			
305	310	315	320
TTA GCG ATG AGT TTA AGC TCT GTG AGT GTG GTC TTA AAC TCC CAA AGG			1066
Leu Ala Met Ser Leu Ser Ser Val Ser Val Val Leu Asn Ser Gln Arg			
325	330	335	
CTA AGG AAT TTT AAA ATT AAG GAT CAT TGAATGAAAG CAACTTTTCA AGTGCCAAG			1122
Leu Arg Asn Phe Lys Ile Lys Asp His			
340	345		
CATTACTTGC AACCA			1137

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

Met	Ser	Ile	Leu	Val	Ala	Asn	Gln	Lys	Ala	Ser	Ser	Leu	Gly	Leu	Phe
1				5				10					15		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

```

AAGTGTGTTGT ATCGGTTTTA GTGATTTCTT GCCCTTGCGC TTTAGGATTG CTACGCCT      58

ATG AGC ATT TTA GTA GCG AAC CAG AAA GCG AGT TCT TTA GGG TTA TTT      106
Met Ser Ile Leu Val Ala Asn Gln Lys Ala Ser Ser Leu Gly Leu Phe
  1           5           10           15

TTT AAA GAC GCT AAA AGT TTA GAA AAA GCA AGG CTA GTC AAT ACG ATC      154
Phe Lys Asp Ala Lys Ser Leu Glu Lys Ala Arg Leu Val Asn Thr Ile
          20           25           30

GTT TTT GAT AAA ACC GGC ACG CTC ACT AAC GGC AAG CCT GTC GTT AAA      202
Val Phe Asp Lys Thr Gly Thr Leu Thr Asn Gly Lys Pro Val Val Lys
          35           40           45

AGC GTT CAT TCT AAG ATA GAA TTA TTA GAG TTA TTG AGT TTA GCG CTC      250
Ser Val His Ser Lys Ile Glu Leu Leu Glu Leu Leu Ser Leu Ala Leu
          50           55           60

AGT ATT GAA AAG AGT AGC GAA CAT GTC ATC GCT AAA GGG ATT GTA GAA      298
Ser Ile Glu Lys Ser Ser Glu His Val Ile Ala Lys Gly Ile Val Glu
          65           70           75           80

TAC GCA AAA GAG CAT AAC GCT CCC TTA AAA GAA ATG AGC GGG GTT AAA      346
Tyr Ala Lys Glu His Asn Ala Pro Leu Lys Glu Met Ser Gly Val Lys
          85           90           95

GTG AAA ACG GGT TTT GGC ATT AGT GCT AAA ACA GAT TAT CAA GGC ACT      394
Val Lys Thr Gly Phe Gly Ile Ser Ala Lys Thr Asp Tyr Gln Gly Thr
          100          105          110

AAA GAG ATT ATT AAA GTA GGC AAC AGC GAG TTT TTT AAC CCT ATT AAC      442
Lys Glu Ile Ile Lys Val Gly Asn Ser Glu Phe Phe Asn Pro Ile Asn
          115          120          125

ACG CTA GAA ATT AAA GAA AAC GGG ATT TTA GTG TTT GTT GGT AGA GCG      490
Thr Leu Glu Ile Lys Glu Asn Gly Ile Leu Val Phe Val Gly Arg Ala
          130          135          140

ATC AGT GAA AAA GAA GAC GAG CTT TTA GGG GCG TTT GTT TTA GAA GAT      538
Ile Ser Glu Lys Glu Asp Glu Leu Leu Gly Ala Phe Val Leu Glu Asp
          145          150          155          160

TTG CCC AAA AAA GGC GTG AAA GAG CAT ATC GCT CAA ATC AAA AAT TTA      586
Leu Pro Lys Lys Gly Val Lys Glu His Ile Ala Gln Ile Lys Asn Leu
          165          170          175

GGC ATT AAC ACC TTT CTT TTA AGC GGA GAC AAT AGG GAG AAT GTC CAA      634
Gly Ile Asn Thr Phe Leu Leu Ser Gly Asp Asn Arg Glu Asn Val Gln
          180          185          190

AAA TGC GCG TTT GAA TTA GGG ATT GAT GGT TAT ATC AGC AAC GCT AAA      682
Lys Cys Ala Phe Glu Leu Gly Ile Asp Gly Tyr Ile Ser Asn Ala Lys

```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

```

Met Lys Pro Thr Asn Glu Pro Lys Lys Pro Phe Phe Gln Ser Pro Ile
 1           5           10           15
Ile Leu Ala Val Leu Gly Gly Ile Leu Ile Phe Phe Leu Arg Ser
          20           25           30
Phe Asn Ser Asp Gly Ser Phe Ser Asp Asn Phe Leu Ala Ser Ser Thr
          35           40           45
Lys Asn Val Ser Tyr His Glu Ile Lys Gln Leu Ile Ser Asn Asn Glu
          50           55           60
Val Glu Asn Val Ser Ile Gly Gln Thr Leu Ile Lys Ala Ser His Lys
65           70           75           80
Glu Gly Asn Asn Arg Val Ile Tyr Ile Ala Lys Arg Val Pro Asp Leu
          85           90           95
Thr Leu Val Pro Leu Leu Asp Glu Lys Lys Ile Asn Tyr Ser Gly Phe
          100          105          110
Ser Glu Ser Asn Phe Phe Thr Asp Met Leu Gly Trp Leu Met Pro Ile
          115          120          125
Leu Val Ile Leu Gly Leu Trp Met Phe Met Ala Asn Arg Met Gln Lys
          130          135          140
Asn Met Gly Gly Gly Ile Phe Gly Met Gly Ser Ala Lys Lys Leu Ile
145          150          155          160
Asn Ala Glu Lys Pro Asn Val Arg Phe Asn Asp Met Ala Gly Asn Glu
          165          170          175
Glu Ala Lys Glu Glu Val Val Glu Ile Val Asp Phe Leu Lys Tyr Pro
          180          185          190
Glu Arg Tyr Ala Asn Leu Gly Ala Lys Ile Pro Lys Gly Val Leu Leu
          195          200          205
Val Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Val Ala
          210          215          220
Gly Glu Arg Met Cys Arg Phe Ser Leu Trp Glu Gly Ala Val Ser Leu
225          230          235          240
Lys Cys Leu Trp Ala
          245

```

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 59...1093
- (D) OTHER INFORMATION:

Lys	Gln	Leu	Ile	Ser	Asn	Asn	Glu	Val	Glu	Asn	Val	Ser	Ile	Gly	Gln	
			60					65					70			
ACT	TTG	ATC	AAA	GCC	AGC	CAT	AAA	GAG	GGC	AAC	AAT	CGT	GTG	ATC	TAT	294
Thr	Leu	Ile	Lys	Ala	Ser	His	Lys	Glu	Gly	Asn	Asn	Arg	Val	Ile	Tyr	
		75					80					85				
ATC	GCT	AAA	CGG	GTG	CCT	GAT	TTG	ACC	TTA	GTG	CCT	TTG	TTA	GAC	GAG	342
Ile	Ala	Lys	Arg	Val	Pro	Asp	Leu	Thr	Leu	Val	Pro	Leu	Leu	Asp	Glu	
		90				95					100					
AAA	AAA	ATC	AAT	TAT	TCT	GGT	TTT	AGC	GAG	TCT	AAC	TTT	TTT	ACG	GAC	390
Lys	Lys	Ile	Asn	Tyr	Ser	Gly	Phe	Ser	Glu	Ser	Asn	Phe	Phe	Thr	Asp	
105						110				115					120	
ATG	CTA	GGG	TGG	CTC	ATG	CCT	ATT	TTA	GTG	ATT	TTA	GGG	CTA	TGG	ATG	438
Met	Leu	Gly	Trp	Leu	Met	Pro	Ile	Leu	Val	Ile	Leu	Gly	Leu	Trp	Met	
				125					130					135		
TTT	ATG	GCG	AAC	CGC	ATG	CAA	AAA	AAT	ATG	GGT	GGG	GGT	ATT	TTT	GGC	486
Phe	Met	Ala	Asn	Arg	Met	Gln	Lys	Asn	Met	Gly	Gly	Gly	Ile	Phe	Gly	
			140					145					150			
ATG	GGG	AGC	GCG	AAA	AAA	CTC	ATT	AAC	GCT	GAA	AAA	CCC	AAT	GTG	CGT	534
Met	Gly	Ser	Ala	Lys	Lys	Leu	Ile	Asn	Ala	Glu	Lys	Pro	Asn	Val	Arg	
		155					160					165				
TTT	AAT	GAC	ATG	GCA	GGC	AAT	GAA	GAA	GCC	AAA	GAA	GAA	GTG	GTA	GAA	582
Phe	Asn	Asp	Met	Ala	Gly	Asn	Glu	Glu	Ala	Lys	Glu	Glu	Val	Val	Glu	
		170				175					180					
ATC	GTA	GAT	TTC	TTA	AAA	TAC	CCT	GAA	CGA	TAC	GCC	AAT	TTA	GGG	GCT	630
Ile	Val	Asp	Phe	Leu	Lys	Tyr	Pro	Glu	Arg	Tyr	Ala	Asn	Leu	Gly	Ala	
185					190					195					200	
AAA	ATC	CCT	AAA	GGC	GTG	TTA	TTA	GTA	GGG	CCT	CCA	GGA	ACC	GGT	AAA	678
Lys	Ile	Pro	Lys	Gly	Val	Leu	Leu	Val	Gly	Pro	Pro	Gly	Thr	Gly	Lys	
				205					210					215		
ACC	CTT	TTA	GCC	AAA	GCG	GTA	GCC	GGC	GAA	CGC	ATG	TGC	CGT	TTT	TCT	726
Thr	Leu	Leu	Ala	Lys	Ala	Val	Ala	Gly	Glu	Arg	Met	Cys	Arg	Phe	Ser	
			220					225					230			
CTA	TGG	GAG	GGA	GCA	GTT	TCA	TTG	AAA	TGT	TTG	TGG	GCT	TAGGGGCAAG	CA		777
Leu	Trp	Glu	Gly	Ala	Val	Ser	Leu	Lys	Cys	Leu	Trp	Ala				
		235					240					245				
GGGTTAGGGA	TTTATTTGAA	ACCGCTAAAA	AACAAGC													814

(2) INFORMATION FOR SEQ ID NO:968:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

```

Met Leu Tyr Ala Ser Lys Thr Ser Leu Phe Leu Gln Ile Lys Gly Lys
 1           5           10           15
Phe Met Leu Arg Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu
          20           25           30
Trp Arg Leu Phe Leu Arg Gln Lys Pro Pro Lys Asp Asn His Ser Tyr
          35           40           45
Thr Gln Gln Thr Pro Lys Glu Leu Glu Asp His Met Ile Val Cys Ser
          50           55           60
Lys Cys Gln Thr Tyr Val Ser Ser Lys Asp Ala Ile Tyr Ser Gly Ala
65           70           75           80
Val Ala Tyr Cys Ser Glu Thr Cys Leu Lys Asp Lys Arg
          85           90

```

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 31...765

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

```

TAAAAAACAA CCAATAAATT AAGGATTATA ATG AAA CCA ACG AAC GAA CCT AAA      54
                               Met Lys Pro Thr Asn Glu Pro Lys
                               1           5

AAA CCT TTT TTT CAA AGT CCC ATT ATC CTT GCG GTT CTT GGA GGG ATT      102
Lys Pro Phe Phe Gln Ser Pro Ile Ile Leu Ala Val Leu Gly Gly Ile
 10           15           20

TTA CTC ATC TTT TTT CTA CGC TCT TTC AAT TCT GAT GGC AGT TTT TCG      150
Leu Leu Ile Phe Phe Leu Arg Ser Phe Asn Ser Asp Gly Ser Phe Ser
25           30           35           40

GAC AAT TTC TTA GCT TCT AGC ACT AAA AAT GTG AGC TAC CAT GAA ATC      198
Asp Asn Phe Leu Ala Ser Ser Thr Lys Asn Val Ser Tyr His Glu Ile
          45           50           55

AAA CAG CTC ATC AGC AAT AAT GAA GTG GAA AAT GTG AGT ATC GGT CAA      246

```

(2) INFORMATION FOR SEQ ID NO:965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...324
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

```

TAAAGGCGAG CAGTTAAAAG ATGAAATCGC TTGTAAAGAC ACTGA ATG CTT TAT GCA      57
                                     Met Leu Tyr Ala
                                     1

TCA AAA ACG AGT TTA TTT TTA CAA ATC AAA GGA AAG TTT ATG TTA AGA      105
Ser Lys Thr Ser Leu Phe Leu Gln Ile Lys Gly Lys Phe Met Leu Arg
  5                10                15                20

ATT TTA ATC CCC TTG CTC ATT ATT GTG TGG GTT TTA TGG CGT TTG TTT      153
Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu Trp Arg Leu Phe
                25                30                35

TTG AGG CAA AAA CCC CCT AAA GAC AAC CAC TCT TAC ACG CAA CAA ACC      201
Leu Arg Gln Lys Pro Pro Lys Asp Asn His Ser Tyr Thr Gln Gln Thr
                40                45                50

CCT AAA GAA TTA GAA GAT CAC ATG ATT GTA TGC TCT AAA TGC CAA ACC      249
Pro Lys Glu Leu Glu Asp His Met Ile Val Cys Ser Lys Cys Gln Thr
                55                60                65

TAT GTC TCT AGC AAA GAC GCT ATT TAT AGC GGG GCG GTG GCG TAT TGC      297
Tyr Val Ser Ser Lys Asp Ala Ile Tyr Ser Gly Ala Val Ala Tyr Cys
                70                75                80

AGT GAA ACC TGT TTG AAG GAT AAG AGG TAAATATGCT TATTTTAGGA CACCCTT      351
Ser Glu Thr Cys Leu Lys Asp Lys Arg
  85                90

TAATCCCT                                                                359

```

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

GAA GAC GCT AAA GTG ACT GCA GAA AAT GAG ATT AAA AGC ATT CAG GAT	343
Glu Asp Ala Lys Val Thr Ala Glu Asn Glu Ile Lys Ser Ile Gln Asp	
90 95 100	
TTG ATG CAA GAT TAC CAA AAA AGC TTA GAA ACC AAC ACA ATC CCT AAC	391
Leu Met Gln Asp Tyr Gln Lys Ser Leu Glu Thr Asn Thr Ile Pro Asn	
105 110 115	
CAT TTA AAC GAA GAA GTT TCC AAT GAA GAA GCC TTA AAC AAA GAA GTT	439
His Leu Asn Glu Glu Val Ser Asn Glu Glu Ala Leu Asn Lys Glu Val	
120 125 130	
TCA AGC GAT GAA TCC CCT AAA GAA GTC CAA TTA GCA ACC GAT AAC AAC	487
Ser Ser Asp Glu Ser Pro Lys Glu Val Gln Leu Ala Thr Asp Asn Asn	
135 140 145	
ACC AAA GAA CAC GAC AAA GAA AAA GAG AAT GTT TGAAGATTTA AAACCGCATT	540
Thr Lys Glu His Asp Lys Glu Lys Glu Asn Val	
150 155 160	
TACAGGAATT AAGAAAGCGT TTGATGGT	568

(2) INFORMATION FOR SEQ ID NO:964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

Met Phe Gly Met Gly Phe Phe Glu Ile Leu Val Val Leu Val Val Ala	
1 5 10 15	
Ile Ile Phe Leu Gly Pro Glu Lys Phe Pro Gln Ala Val Val Asp Val	
20 25 30	
Val Lys Phe Phe Arg Ala Val Lys Lys Thr Leu Asn Asp Ala Lys Asp	
35 40 45	
Thr Leu Asp Lys Glu Ile Asn Ile Glu Glu Ile Lys Lys Glu Thr Leu	
50 55 60	
Glu Tyr Gln Lys Leu Phe Glu Asn Lys Val Glu Ser Leu Lys Gly Val	
65 70 75 80	
Lys Ile Glu Glu Leu Glu Asp Ala Lys Val Thr Ala Glu Asn Glu Ile	
85 90 95	
Lys Ser Ile Gln Asp Leu Met Gln Asp Tyr Gln Lys Ser Leu Glu Thr	
100 105 110	
Asn Thr Ile Pro Asn His Leu Asn Glu Glu Val Ser Asn Glu Glu Ala	
115 120 125	
Leu Asn Lys Glu Val Ser Ser Asp Glu Ser Pro Lys Glu Val Gln Leu	
130 135 140	
Ala Thr Asp Asn Asn Thr Lys Glu His Asp Lys Glu Lys Glu Asn Val	
145 150 155 160	

	180		185		190										
Ile	Ala	Gln	Lys	Ile	Thr	Gln	Lys	Ile	Lys	Ile	Pro	Thr	Ile	Gly	Ile
	195		200		205										
Gly	Ser	Gly	Lys	Asp	Cys	Asp	Gly	Gln	Ile	Leu	Val	Trp	Ser	Asp	Met
	210		215		220										
Leu	Gly	Phe	Phe	Asp	Ser	Phe	Lys	Pro	Lys	Phe	Val	Arg	Glu	Tyr	Leu
	225		230		235										240
Lys	Gly	Lys	Glu	Leu	Ile	Gln	Asn	Ala	Ile	Lys	Gln	Tyr	Ala	Asp	Asp
		245			250									255	
Val	Lys	Lys	Gly	Asn	Phe	Pro	Asn	Glu	Leu	Glu	Ser	Tyr	His		
	260		265										270		

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 41...520
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

AATAACGATA AAATTTTAAA GGGTGTA AAAA GTAGATTGTT	ATG TTT GGC ATG GGC	55
	Met Phe Gly Met Gly	
	1 5	
TTT TTT GAA ATC CTT GTG GTG TTG GTT GTA GCG ATT ATT TTT TTA GGC	103	
Phe Phe Glu Ile Leu Val Val Leu Val Val Ala Ile Ile Phe Leu Gly		
	10 15 20	
CCA GAA AAA TTC CCC CAG GCT GTC GTG GAT GTG GTG AAG TTT TTT CGC	151	
Pro Glu Lys Phe Pro Gln Ala Val Val Asp Val Val Lys Phe Phe Arg		
	25 30 35	
GCG GTT AAA AAA ACG CTC AAT GAC GCT AAG GAC ACT TTA GAT AAA GAA	199	
Ala Val Lys Lys Thr Leu Asn Asp Ala Lys Asp Thr Leu Asp Lys Glu		
	40 45 50	
ATC AAT ATT GAA GAA ATC AAA AAA GAA ACC CTA GAG TAT CAA AAG CTC	247	
Ile Asn Ile Glu Glu Ile Lys Lys Glu Thr Leu Glu Tyr Gln Lys Leu		
	55 60 65	
TTT GAA AAC AAA GTG GAG AGT CTT AAG GGC GTT AAG ATT GAA GAA TTA	295	
Phe Glu Asn Lys Val Glu Ser Leu Lys Gly Val Lys Ile Glu Glu Leu		
	70 75 80 85	

```

Pro Thr Ile Gly Ile Gly Ser Gly Lys Asp Cys Asp Gly Gln Ile Leu
 205                      210                      215

GTG TGG AGC GAT ATG TTA GGC TTT TTT GAT AGC TTT AAG CCT AAA TTC      722
Val Trp Ser Asp Met Leu Gly Phe Phe Asp Ser Phe Lys Pro Lys Phe
 220                      225                      230                      235

GTG CGA GAA TAC CTT AAG GGG AAA GAA TTG ATT CAA AAC GCT ATC AAA      770
Val Arg Glu Tyr Leu Lys Gly Lys Glu Leu Ile Gln Asn Ala Ile Lys
                240                      245                      250

CAA TAC GCT GAT GAT GTG AAA AAG GGA AAC TTC CCT AAC GAA TTA GAA      818
Gln Tyr Ala Asp Asp Val Lys Lys Gly Asn Phe Pro Asn Glu Leu Glu
                255                      260                      265

AGT TAT CAT TAATGAAAGA ACGGATAGTC AATTTAGAAA CTTTGGATTT TGAAATT      874
Ser Tyr His
                270

```

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

```

Met Ser Met Gln Thr Ala Pro Ile Lys Lys Ile Thr Leu Asn His Leu
 1          5          10          15
Gln Ala Lys Lys Asn Gln Glu Lys Ile Ile Ala Ile Thr Ala Tyr Asp
          20          25          30
Ala Leu Phe Ala Gln Ile Phe Asp Pro Leu Val Asp Val Ile Leu Val
          35          40          45
Gly Asp Ser Leu Asn Met Ser Phe Phe Asn Gln Asn Asp Thr Leu Ser
          50          55          60
Ala Ser Val Glu Met Met Leu Tyr His Thr Lys Ala Val Cys Ala Gly
          65          70          75          80
Ala Lys Thr Pro Phe Ile Ile Thr Asp Met Pro Phe Gly Ser Tyr Lys
          85          90          95
Asp Glu Lys Thr Ala Leu Lys Asn Ala Ile Arg Val Tyr Lys Glu Thr
          100          105          110
Gln Ala Ser Ala Ile Lys Leu Glu Gly Gly Lys Glu Lys Ala Lys Leu
          115          120          125
Val Lys Thr Leu Thr Asn Glu Gly Val Ile Val Val Gly His Ile Gly
          130          135          140
Leu Met Pro Gln Phe Val Arg Leu Asp Gly Gly Tyr Lys Ile Lys Gly
          145          150          155          160
Lys Asn Glu Glu Gln Gln Lys Lys Leu Leu Glu Asp Ala Leu Ser Leu
          165          170          175
Glu Glu Ala Gly Val Gly Leu Leu Val Leu Glu Gly Ile Thr Thr Pro

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

AACACTTAGG ATTTTTA ATG AGC ATG CAA ACC GCC CCA ATT AAA AAG ATC	50
Met Ser Met Gln Thr Ala Pro Ile Lys Lys Ile	
1 5 10	
ACT CTC AAC CAC CTC CAA GCT AAA AAA AAT CAA GAA AAA ATC ATC GCT	98
Thr Leu Asn His Leu Gln Ala Lys Lys Asn Gln Glu Lys Ile Ile Ala	
15 20 25	
ATT ACC GCT TAT GAT GCG CTG TTC GCT CAA ATA TTT GAT CCG CTA GTG	146
Ile Thr Ala Tyr Asp Ala Leu Phe Ala Gln Ile Phe Asp Pro Leu Val	
30 35 40	
GAT GTG ATT TTA GTG GGC GAT AGT TTG AAT ATG AGT TTT TTC AAT CAA	194
Asp Val Ile Leu Val Gly Asp Ser Leu Asn Met Ser Phe Phe Asn Gln	
45 50 55	
AAC GAC ACT TTA AGC GCG AGT GTG GAA ATG ATG CTC TAT CAC ACC AAA	242
Asn Asp Thr Leu Ser Ala Ser Val Glu Met Met Leu Tyr His Thr Lys	
60 65 70 75	
GCC GTG TGC GCG GGC GCT AAG ACT CCT TTT ATC ATC ACA GAC ATG CCT	290
Ala Val Cys Ala Gly Ala Lys Thr Pro Phe Ile Ile Thr Asp Met Pro	
80 85 90	
TTT GGA AGC TAT AAA GAT GAA AAA ACA GCC CTA AAA AAC GCC ATT AGG	338
Phe Gly Ser Tyr Lys Asp Glu Lys Thr Ala Leu Lys Asn Ala Ile Arg	
95 100 105	
GTT TAT AAA GAA ACC CAA GCG AGC GCA ATC AAA TTA GAG GGG GGG AAA	386
Val Tyr Lys Glu Thr Gln Ala Ser Ala Ile Lys Leu Glu Gly Gly Lys	
110 115 120	
GAA AAA GCG AAA CTG GTT AAA ACG CTC ACT AAT GAG GGC GTT ATT GTG	434
Glu Lys Ala Lys Leu Val Lys Thr Leu Thr Asn Glu Gly Val Ile Val	
125 130 135	
GTA GGG CAT ATT GGC TTG ATG CCC CAA TTC GTG CGC CTT GAT GGA GGT	482
Val Gly His Ile Gly Leu Met Pro Gln Phe Val Arg Leu Asp Gly Gly	
140 145 150 155	
TAT AAG ATT AAG GGC AAA AAT GAA GAA CAA CAA AAA AAG CTT TTA GAA	530
Tyr Lys Ile Lys Gly Lys Asn Glu Glu Gln Gln Lys Lys Leu Leu Glu	
160 165 170	
GAC GCC TTG AGT TTA GAA GAA GCT GGG GTG GGT TTG TTG GTT TTA GAG	578
Asp Ala Leu Ser Leu Glu Glu Ala Gly Val Gly Leu Leu Val Leu Glu	
175 180 185	
GGT ATA ACC ACC CCT ATC GCT CAA AAA ATC ACG CAA AAA ATC AAA ATC	626
Gly Ile Thr Thr Pro Ile Ala Gln Lys Ile Thr Gln Lys Ile Lys Ile	
190 195 200	
CCC ACG ATC GGC ATA GGG AGC GGT AAA GAT TGC GAT GGG CAG ATT TTA	674

```

      20      25      30
Asp Glu Lys Ile Asn His Leu Lys Gln Gln Leu Thr Glu Lys Gly Val
      35      40      45
Ser Pro Lys Glu Met Asp Lys Asp Lys Phe Glu Glu Tyr Ile Asn
      50      55      60
Arg Ser Tyr Pro Lys Ile Ser Ser Lys Lys Lys Glu Lys Leu Leu Lys
      65      70      75      80
Ser Phe Ser Ile Ala Asp Asp Lys Ser Gly Val Phe Leu Gly Gly Gly
      85      90      95
Tyr Ala Tyr Gly Glu Leu Asn Leu Ser Tyr Gln Gly Glu Met Leu Asp
      100      105      110
Arg Tyr Gly Ala Asn Ala Pro Ser Ala Phe Lys Asn Asn Ile Asn Ile
      115      120      125
Asn Ala Pro Val Ser Met Ile Ser Ala Lys Phe Gly Tyr Gln Lys Tyr
      130      135      140
Phe Val Ser Tyr Phe Gly Thr Arg Phe Tyr Gly Asp Leu Leu Leu Gly
      145      150      155      160
Gly Gly Ala Leu Lys Glu Asp Ala Ile Lys Gln Pro Val Gly Ser Phe
      165      170      175
Ile Tyr Val Leu Gly Ala Val Asn Thr Asp Leu Leu Phe Asp Met Pro
      180      185      190
Leu Asp Phe Lys Thr Lys Lys His Phe Leu Gly Val Tyr Ala Gly Phe
      195      200      205
Gly Ile Gly Leu Met Leu Tyr Gln Asp Arg Pro Asn Gln Asn Gly Arg
      210      215      220
Asn Leu Val Val Gly Gly Tyr Ser Ser Pro Asn Phe Leu Trp Lys Ser
      225      230      235      240
Leu Ile Glu Val Asp Tyr Thr Phe Asn Val Gly Val Ser Leu Thr Leu
      245      250      255
Tyr Arg Lys His Arg Leu Glu Ile Gly Thr Lys Leu Pro Ile Ser Tyr
      260      265      270
Leu Arg Met Gly Val Glu Glu Gly Ala Ile Tyr Gln Asn Lys Glu Asp
      275      280      285
Asp Glu Arg Leu Leu Val Ser Ala Asn Asn Gln Phe Lys Arg Ser Ser
      290      295      300
Phe Leu Leu Val Asn Tyr Ala Phe Ile Phe
      305      310

```

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 18...827
- (D) OTHER INFORMATION:

Lys	Gln	Pro	Val	Gly	Ser	Phe	Ile	Tyr	Val	Leu	Gly	Ala	Val	Asn	Thr	
170					175					180					185	
GAT	TTA	TTG	TTT	GAT	ATG	CCT	TTA	GAT	TTT	AAA	ACT	AAA	AAG	CAT	TTT	630
Asp	Leu	Leu	Phe	Asp	Met	Pro	Leu	Asp	Phe	Lys	Thr	Lys	Lys	His	Phe	
				190					195					200		
TTA	GGC	GTT	TAT	GCG	GGT	TTT	GGG	ATA	GGG	CTT	ATG	CTC	TAT	CAA	GAC	678
Leu	Gly	Val	Tyr	Ala	Gly	Phe	Gly	Ile	Gly	Leu	Met	Leu	Tyr	Gln	Asp	
			205				210						215			
AGG	CCT	AAT	CAA	AAC	GGG	AGG	AAT	TTA	GTA	GTG	GGG	GGC	TAT	TCA	AGC	726
Arg	Pro	Asn	Gln	Asn	Gly	Arg	Asn	Leu	Val	Val	Gly	Gly	Tyr	Ser	Ser	
		220					225					230				
CCT	AAT	TTT	TTA	TGG	AAA	TCT	TTG	ATT	GAA	GTG	GAT	TAC	ACT	TTT	AAT	774
Pro	Asn	Phe	Leu	Trp	Lys	Ser	Leu	Ile	Glu	Val	Asp	Tyr	Thr	Phe	Asn	
	235					240					245					
GTG	GGC	GTG	AGT	TTA	ACG	CTT	TAT	AGG	AAA	CAC	CGT	TTA	GAG	ATT	GGC	822
Val	Gly	Val	Ser	Leu	Thr	Leu	Tyr	Arg	Lys	His	Arg	Leu	Glu	Ile	Gly	
250					255					260				265		
ACA	AAA	TTG	CCG	ATT	AGC	TAT	TTG	AGA	ATG	GGA	GTG	GAA	GAG	GGA	GCG	870
Thr	Lys	Leu	Pro	Ile	Ser	Tyr	Leu	Arg	Met	Gly	Val	Glu	Glu	Gly	Ala	
				270					275					280		
ATT	TAT	CAA	AAT	AAA	GAA	GAT	GAT	GAG	CGT	TTG	TTG	GTT	TCG	GCT	AAC	918
Ile	Tyr	Gln	Asn	Lys	Glu	Asp	Asp	Glu	Arg	Leu	Leu	Val	Ser	Ala	Asn	
			285					290					295			
AAC	CAG	TTC	AAG	CGA	TCC	AGT	TTT	TTA	TTA	GTG	AAT	TAT	GCG	TTT	ATT	966
Asn	Gln	Phe	Lys	Arg	Ser	Ser	Phe	Leu	Leu	Val	Asn	Tyr	Ala	Phe	Ile	
		300					305					310				
TTT	TAAGGCTTGA	TCTTGGAGTT	AAGGTTTAAA	ATTTT												1004
Phe																

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

Met	Leu	Lys	Phe	Lys	Tyr	Gly	Leu	Ile	Tyr	Ile	Ala	Leu	Ile	Leu	Gly
1				5				10					15		
Leu	Gln	Ala	Thr	Asp	Tyr	Asp	Asn	Leu	Glu	Glu	Glu	Asn	Gln	Gln	Leu

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 28...969
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

```

TTACAAC TAT TTATTGTAAA GGCTAAA ATG TTG AAA TTT AAA TAT GGT TTG ATT      54
                        Met Leu Lys Phe Lys Tyr Gly Leu Ile
                          1                      5

TAT ATC GCG CTC ATA CTA GGA CTT CAA GCG ACA GAT TAT GAC AAT TTA      102
Tyr Ile Ala Leu Ile Leu Gly Leu Gln Ala Thr Asp Tyr Asp Asn Leu
10                      15                      20                      25

GAA GAA GAA AAC CAA CAA TTA GAT GAA AAA ATA AAC CAT TTA AAG CAA      150
Glu Glu Glu Asn Gln Gln Leu Asp Glu Lys Ile Asn His Leu Lys Gln
                      30                      35                      40

CAG CTC ACC GAA AAA GGG GTT TCG CCC AAA GAG ATG GAT AAG GAT AAG      198
Gln Leu Thr Glu Lys Gly Val Ser Pro Lys Glu Met Asp Lys Asp Lys
                      45                      50                      55

TTT GAA GAA GAA TAC ATC AAT CGA TCT TAT CCT AAA ATT TCT TCC AAG      246
Phe Glu Glu Glu Tyr Ile Asn Arg Ser Tyr Pro Lys Ile Ser Ser Lys
60                      65                      70

AAA AAA GAG AAA TTG CTC AAA TCT TTT TCC ATA GCC GAT GAT AAG AGT      294
Lys Lys Glu Lys Leu Leu Lys Ser Phe Ser Ile Ala Asp Asp Lys Ser
75                      80                      85

GGG GTT TTT TTA GGG GGT GGG TAT GCT TAT GGG GAA CTT AAC TTG TCT      342
Gly Val Phe Leu Gly Gly Gly Tyr Ala Tyr Gly Glu Leu Asn Leu Ser
90                      95                      100                      105

TAT CAA GGG GAA ATG TTA GAC AGA TAC GGC GCG AAT GCC CCT AGC GCG      390
Tyr Gln Gly Glu Met Leu Asp Arg Tyr Gly Ala Asn Ala Pro Ser Ala
                      110                      115                      120

TTT AAA AAC AAT ATC AAT ATT AAC GCT CCT GTT TCT ATG ATT AGC GCT      438
Phe Lys Asn Asn Ile Asn Ile Asn Ala Pro Val Ser Met Ile Ser Ala
                      125                      130                      135

AAA TTT GGG TAT CAA AAA TAC TTT GTG TCT TAT TTT GGG ACA CGA TTT      486
Lys Phe Gly Tyr Gln Lys Tyr Phe Val Ser Tyr Phe Gly Thr Arg Phe
140                      145                      150

TAT GGG GAT TTA TTG CTT GGG GGT GGG GCA TTA AAA GAG GAT GCA ATC      534
Tyr Gly Asp Leu Leu Leu Gly Gly Gly Ala Leu Lys Glu Asp Ala Ile
155                      160                      165

AAG CAG CCT GTA GGC TCG TTT ATT TAT GTT TTA GGG GCT GTC AAT ACC      582

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

```

Met Gly Leu Glu Asp Lys Cys Leu Leu Tyr Glu Ile Lys Ala Asn Asp
 1           5           10           15
Trp Ser Tyr Ala Asn Phe Phe Asn Gly Asn Lys Ala Ser Phe Lys Gln
          20           25           30
Glu Val Cys Val Asp Thr Ile Lys Pro Ser Ile Thr Ile Leu Ser Arg
          35           40           45
Ser Pro Ser Ile Ala Tyr Gly Gly Ser Ala Ile Val Val Phe Glu Ala
          50           55           60
Leu Asp Lys Asn Leu Ser Gln Ala Phe Val Arg Val Lys Lys Lys Asp
65           70           75           80
Phe Glu Ala Phe Arg Leu Leu Glu Phe Lys Gln Arg Asn Val Phe Ile
          85           90           95
Ala Leu Val Pro Trp Ser Tyr Lys Asn Lys Asp Phe Lys Ala Phe Ile
          100          105          110
Val Ala Lys Asp Lys Ala Tyr Asn Phe Asn Thr Ala Pro Leu Leu Phe
          115          120          125
Lys Arg Lys Ile His Arg Leu Arg Glu Lys Asp Ile Asp Leu Ser Ala
          130          135          140
Leu Lys Asp Lys Ile Ala Lys Gln Glu Lys Phe Gln Asn Asp Thr Glu
145          150          155          160
Gln Ala Leu Leu Glu Arg Phe Ser Asn Ala Arg Pro Lys Asp Leu Glu
          165          170          175
Lys Ile Gln Lys Ile Ala Leu Glu Gln Gly Asp Phe Tyr Lys Asp Phe
          180          185          190
Ser His Phe Gln Ala Leu Lys Pro Leu Asn Gly Pro Phe Lys Met Ala
          195          200          205
Ser Asn Phe Leu Glu Asn Arg Arg Ile Leu Lys Asn Asn Gln Val Leu
          210          215          220
Phe Lys Phe Leu His Leu Gly Val Asp Leu Ile Pro Gly Lys Asp Leu
225          230          235          240
Ser Leu Ala Phe Asp Leu Ser Val Lys Arg Val Phe Lys Gly Glu Phe
          245          250          255
Asp Phe Tyr Gly Asn Ser Leu Ile His Cys Tyr Gly Leu Gly Leu Cys
          260          265          270
Val Phe Leu Ala His Leu Lys Asp Asp Lys Ser Val Gly Ser Ser Gly
          275          280          285
Leu Lys Leu Gly Ser Gly Leu His Leu Gly Met Leu Leu Gln Gly Val
          290          295          300
Phe Val Arg Pro Asn Glu Trp Leu Asn Glu Gln Trp Ile Lys Thr Asn
305          310          315          320
Ile Thr Ala Pro Ile Glu Gln Ala Lys Arg Leu Leu Met Lys Gly
          325          330          335

```

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

-(ii) MOLECULE TYPE: Genomic DNA

GAA CAA GCT TTA TTA GAA AGA TTT TCC AAT GCG CGC CCA AAA GAT TTA	588
Glu Gln Ala Leu Leu Glu Arg Phe Ser Asn Ala Arg Pro Lys Asp Leu	
160 165 170 175	
GAA AAA ATC CAA AAG ATC GCT TTA GAG CAA GGG GAT TTT TAT AAG GAT	636
Glu Lys Ile Gln Lys Ile Ala Leu Glu Gln Gly Asp Phe Tyr Lys Asp	
180 185 190	
TTT TCT CAT TTT CAA GCG CTA AAA CCC TTG AAC GGG CCT TTT AAA ATG	684
Phe Ser His Phe Gln Ala Leu Lys Pro Leu Asn Gly Pro Phe Lys Met	
195 200 205	
GCA AGC AAT TTT TTA GAA AAT CGG CGT ATC TTA AAG AAT AAT CAG GTG	732
Ala Ser Asn Phe Leu Glu Asn Arg Arg Ile Leu Lys Asn Asn Gln Val	
210 215 220	
TTG TTT AAA TTC TTG CAT TTA GGG GTG GAT TTG ATA CCT GGC AAG GAT	780
Leu Phe Lys Phe Leu His Leu Gly Val Asp Leu Ile Pro Gly Lys Asp	
225 230 235	
TTA TCT TTA GCG TTT GAT TTG TCT GTG AAG AGG GTT TTT AAG GGG GAG	828
Leu Ser Leu Ala Phe Asp Leu Ser Val Lys Arg Val Phe Lys Gly Glu	
240 245 250 255	
TTC GAT TTT TAT GGT AAT AGT TTA ATC CAT TGC TAT GGG TTA GGT TTG	876
Phe Asp Phe Tyr Gly Asn Ser Leu Ile His Cys Tyr Gly Leu Gly Leu	
260 265 270	
TGC GTT TTT TTA GCC CAT TTA AAA GAT GAT AAA AGC GTG GGG AGT AGT	924
Cys Val Phe Leu Ala His Leu Lys Asp Asp Lys Ser Val Gly Ser Ser	
275 280 285	
GGT TTG AAA TTA GGG AGC GGG TTG CAT TTA GGG ATG CTT TTG CAA GGG	972
Gly Leu Lys Leu Gly Ser Gly Leu His Leu Gly Met Leu Leu Gln Gly	
290 295 300	
GTT TTT GTC CGG CCC AAT GAA TGG CTT AAT GAG CAA TGG ATA AAA ACC	1020
Val Phe Val Arg Pro Asn Glu Trp Leu Asn Glu Gln Trp Ile Lys Thr	
305 310 315	
AAT ATC ACC GCC CCC ATA GAG CAA GCC AAA CGG CTT TTA ATG AAA GGA T	1069
Asn Ile Thr Ala Pro Ile Glu Gln Ala Lys Arg Leu Leu Met Lys Gly	
320 325 330 335	
AGTCATGTTA AAAACGAATC AAAAAAATGT GCATGCGTTT GAAATTGAAA AG	1121

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 64...1068
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

AAAGAAAATC TGGTATTGGA TAAACCCAAG TCTTTAGAAG TGCCTTTGAC TAGGCCCGAA	60
ATC ATG GGG CTA GAA GAC AAG TGC CTT TTA TAT GAA ATT AAA GCT AAT	108
Met Gly Leu Glu Asp Lys Cys Leu Leu Tyr Glu Ile Lys Ala Asn	
1 5 10 15	
GAT TGG AGT TAT GCT AAT TTT TTC AAT GGC AAT AAA GCG TCT TTC AAA	156
Asp Trp Ser Tyr Ala Asn Phe Phe Asn Gly Asn Lys Ala Ser Phe Lys	
20 25 30	
CAA GAA GTG TGT GTT GAT ACG ATA AAA CCC TCA ATC ACT ATT TTA TCT	204
Gln Glu Val Cys Val Asp Thr Ile Lys Pro Ser Ile Thr Ile Leu Ser	
35 40 45	
CGA TCC CCA AGC ATC GCT TAT GGG GGG AGC GCG ATA GTC GTT TTT GAA	252
Arg Ser Pro Ser Ile Ala Tyr Gly Gly Ser Ala Ile Val Val Phe Glu	
50 55 60	
GCT TTG GAT AAG AAT TTG TCT CAA GCG TTT GTG CGC GTC AAA AAA AAG	300
Ala Leu Asp Lys Asn Leu Ser Gln Ala Phe Val Arg Val Lys Lys Lys	
65 70 75	
GAT TTT GAA GCT TTC AGG CTT TTA GAA TTC AAA CAG CGT AAT GTT TTT	348
Asp Phe Glu Ala Phe Arg Leu Leu Glu Phe Lys Gln Arg Asn Val Phe	
80 85 90 95	
ATC GCT CTA GTG CCT TGG TCT TAT AAA AAT AAG GAT TTT AAG GCG TTC	396
Ile Ala Leu Val Pro Trp Ser Tyr Lys Asn Lys Asp Phe Lys Ala Phe	
100 105 110	
ATT GTC GCT AAA GAT AAA GCC TAT AAC TTT AAT ACC GCC CCT TTA TTG	444
Ile Val Ala Lys Asp Lys Ala Tyr Asn Phe Asn Thr Ala Pro Leu Leu	
115 120 125	
TTC AAG CGA AAA ATC CAT CGT TTG AGG GAA AAA GAT ATA GAC TTA AGC	492
Phe Lys Arg Lys Ile His Arg Leu Arg Glu Lys Asp Ile Asp Leu Ser	
130 135 140	
GCC TTA AAA GAT AAG ATT GCA AAG CAA GAA AAA TTT CAA AAC GAC ACT	540
Ala Leu Lys Asp Lys Ile Ala Lys Gln Glu Lys Phe Gln Asn Asp Thr	
145 150 155	

TCT CTA AAA GAG GTT GAA CCG CTT TTG GTA AAT AAA AAT ATT AAA ATA 627
 Ser Leu Lys Glu Val Glu Pro Leu Leu Val Asn Lys Asn Ile Lys Ile
 190 195 200

ATC ACT AAA AAT GAC GAT ATA CTA GAC ATA AAG GAA GTA TTA TGAAACAAA 678
 Ile Thr Lys Asn Asp Asp Ile Leu Asp Ile Lys Glu Val Leu
 205 210 215

CAACCATTA CCACTCTGTG GAATTAGTAG GGATAGGCTT GCACAAG 725

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

Met	Asp	Lys	Asn	Gln	Tyr	His	Arg	Pro	His	Arg	Ala	Ser	Gln	Thr	Ala	1	5	10	15
Phe	Asn	Glu	Arg	Ile	Val	Met	Leu	Lys	Thr	Asn	Gln	Lys	Asn	Val	His	20	25	30	
Ala	Phe	Glu	Ile	Glu	Lys	Gln	Glu	Pro	Glu	Ala	Val	Ile	Gly	Phe	Leu	35	40	45	
Glu	Lys	Asn	His	Ala	Leu	Leu	Gln	Tyr	Phe	Leu	Ile	Ile	Phe	Lys	Tyr	50	55	60	
Asp	Ile	Glu	Ser	Glu	Val	Lys	Ala	Val	Leu	Arg	Lys	His	Gln	Leu	Leu	65	70	75	80
Phe	Leu	Glu	Thr	Asn	Arg	Val	Leu	Asn	Gly	Arg	His	Ile	Lys	Thr	Met	85	90	95	
Pro	Leu	Lys	Asp	Glu	Thr	Asp	His	Pro	Lys	Pro	Asn	His	Ser	Lys	Thr	100	105	110	
Glu	Pro	Lys	Thr	Thr	Ile	Tyr	Glu	Arg	His	Ile	Arg	Ser	Gly	Glu	Glu	115	120	125	
Ile	Tyr	Ser	Thr	Asn	His	Leu	Ile	Phe	Leu	Gly	Asn	Ile	His	Asn	Gly	130	135	140	
Ala	Lys	Ile	Ile	Ser	Glu	Gly	Cys	Val	Ser	Val	Tyr	Gly	Val	Cys	Glu	145	150	155	160
Gly	Ala	Ile	Val	Cys	Phe	Gly	Glu	Cys	Leu	Ile	Leu	Lys	Glu	Val	Lys	165	170	175	
Ser	Ala	Gln	Ile	Val	Phe	Gln	Asn	Lys	Ile	Leu	Ser	Leu	Lys	Glu	Val	180	185	190	
Glu	Pro	Leu	Val	Asn	Lys	Asn	Ile	Lys	Ile	Ile	Thr	Lys	Asn	Asp		195	200	205	
Asp	Ile	Leu	Asp	Ile	Lys	Glu	Val	Leu								210	215		

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 19...669
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

TGAATGGCTT AATGAGCA ATG GAT AAA AAC CAA TAT CAC CGC CCC CAT AGA	51
Met Asp Lys Asn Gln Tyr His Arg Pro His Arg	
1 5 10	
GCA AGC CAA ACG GCT TTT AAT GAA AGG ATA GTC ATG TTA AAA ACG AAT	99
Ala Ser Gln Thr Ala Phe Asn Glu Arg Ile Val Met Leu Lys Thr Asn	
15 20 25	
CAA AAA AAT GTG CAT GCG TTT GAA ATT GAA AAG CAA GAG CCT GAA GCG	147
Gln Lys Asn Val His Ala Phe Glu Ile Glu Lys Gln Glu Pro Glu Ala	
30 35 40	
GTC ATA GGG TTT TTA GAA AAA AAC CAT GCC CTT TTG CAA TAT TTT CTT	195
Val Ile Gly Phe Leu Glu Lys Asn His Ala Leu Leu Gln Tyr Phe Leu	
45 50 55	
ATT ATT TTT AAA TAC GAT ATT GAA TCA GAA GTC AAA GCC GTT TTG CGC	243
Ile Ile Phe Lys Tyr Asp Ile Glu Ser Glu Val Lys Ala Val Leu Arg	
60 65 70 75	
AAA CAC CAG CTT TTG TTT TTA GAA ACG AAT CGC GTT TTA AAC GGA CGC	291
Lys His Gln Leu Leu Phe Leu Glu Thr Asn Arg Val Leu Asn Gly Arg	
80 85 90	
CAT ATC AAA ACC ATG CCT TTA AAA GAC GAA ACC GAT CAT CCA AAA CCC	339
His Ile Lys Thr Met Pro Leu Lys Asp Glu Thr Asp His Pro Lys Pro	
95 100 105	
AAT CAT TCT AAA ACA GAA CCT AAA ACA ACG ATT TAT GAG CGC CAT ATC	387
Asn His Ser Lys Thr Glu Pro Lys Thr Thr Ile Tyr Glu Arg His Ile	
110 115 120	
AGG AGT GGG GAA GAG ATT TAT AGC ACT AAT CAC CTT ATT TTT TTG GGT	435
Arg Ser Gly Glu Glu Ile Tyr Ser Thr Asn His Leu Ile Phe Leu Gly	
125 130 135	
AAT ATC CAT AAT GGA GCC AAG ATT ATT TCA GAG GGC TGT GTG TCT GTT	483
Asn Ile His Asn Gly Ala Lys Ile Ile Ser Glu Gly Cys Val Ser Val	
140 145 150 155	
TAT GGG GTT TGC GAA GGG GCG ATT GTG TGC TTT GGA GAG TGT TTG ATC	531
Tyr Gly Val Cys Glu Gly Ala Ile Val Cys Phe Gly Glu Cys Leu Ile	
160 165 170	
TTA AAA GAA GTC AAG AGC GCT CAA ATC GTT TTT CAA AAC AAA ATT TTG	579
Leu Lys Glu Val Lys Ser Ala Gln Ile Val Phe Gln Asn Lys Ile Leu	
175 180 185	

BNSDOCID: <WO 9843478A1.1_>

AAAATCTAAA AAATGCTTTT TAGCGTTTTT TAGCCAAATA ATAAG

2070

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

Met	Gln	Leu	Asp	Glu	Asp	Leu	Glu	Phe	Ala	Lys	Lys	Ile	Phe	Asn	Pro	1	5	10	15
Asn	Arg	Ala	Phe	Ala	Lys	Gln	Ala	Arg	Ile	Lys	Asn	Met	Cys	Glu	Tyr	20	25	30	
Lys	Asp	Leu	Val	His	Glu	Ala	Asn	Glu	Asp	Tyr	Glu	His	Phe	Trp	Gly	35	40	45	
Asp	Leu	Ala	Lys	Gln	Lys	Leu	Thr	Trp	Phe	Lys	Pro	Phe	Asp	Lys	Val	50	55	60	
Leu	Asn	Ser	Asp	Asn	Ala	Pro	Phe	Phe	Lys	Trp	Phe	Glu	Asn	Gly	Lys	65	70	75	80
Ile	Asn	Val	Ser	Tyr	Asn	Cys	Ile	Asp	Arg	His	Leu	Lys	Asp	Lys	Lys	85	90	95	
Asn	Lys	Val	Ala	Ile	Ile	Phe	Glu	Gly	Glu	Met	Gly	Asp	Tyr	Asn	Val	100	105	110	
Ile	Thr	Tyr	Arg	Lys	Leu	His	Ser	Glu	Val	Asn	Lys	Thr	Ala	Asn	Leu	115	120	125	
Leu	Lys	Asn	Glu	Phe	Asn	Val	Lys	Lys	Gly	Asp	Arg	Val	Ile	Ile	Tyr	130	135	140	
Met	Pro	Met	Ile	Val	Glu	Ser	Val	Tyr	Met	Met	Leu	Ala	Cys	Thr	Arg	145	150	155	160
Ile	Gly	Ala	Ile	His	Ser	Ile	Val	Phe	Ala	Gly	Phe	Ser	Pro	Glu	Ala	165	170	175	
Leu	Arg	Asp	Arg	Ile	Asn	Asp	Ala	Gln	Ala	Lys	Leu	Val	Ile	Thr	Ala	180	185	190	
Asp	Gly	Thr	Phe	Arg	Lys	Gly	Lys	Pro	Tyr	Met	Leu	Lys	Pro	Ala	Leu	195	200	205	
Asp	Lys	Ala	Leu	Glu	Asn	Asn	Ala	Cys	Pro	Ser	Val	Glu	Lys	Ala	Leu	210	215	220	
Ile	Val	Ile	Arg	Asn	Ala	Lys	Glu	Ile	Asp	Tyr	Val	Arg	Gly	Arg	Asp	225	230	235	240
Phe	Val	Tyr	Asn	Glu	Met	Val	Asn	Tyr	Gln	Ser	Asp	Lys	Cys	Glu	Pro	245	250	255	
Glu	Met	Met	Asp	Ser	Glu	Asp	Pro	Leu	Phe	Leu	Leu	Tyr	Thr	Ser	Gly	260	265	270	
Ser	Thr	Gly	Lys	Pro	Lys	Gly	Val	Gln	His	Ser	Ser	Ala	Gly	Tyr	Leu	275	280	285	
Leu	Trp	Ala	Gln	Met	Thr	Met	Glu	Trp	Val	Phe	Asp	Ile	Arg	Asp	Asn	290	295	300	
Asp	Asn	Phe	Trp	Cys	Thr	Ala	Asp	Ile	Gly	Trp	Ile	Thr	Gly	His	Thr	305	310	315	320
Tyr	Val	Val	Tyr	Gly	Pro	Leu	Ala	Cys	Gly	Ala	Thr	Thr	Leu	Ile	Leu				

AGG GCC AGT TGC GCG ACT TTA CCT TTG CCT GGA ATC CAT GCG GAA GTT	1400
Arg Ala Ser Cys Ala Thr Leu Pro Leu Pro Gly Ile His Ala Glu Val	
440 445 450	
TTA AAC GAA GAC GGC ACT AAA ACA AAG CCT GGA GAG CAA GGG TTT TTA	1448
Leu Asn Glu Asp Gly Thr Lys Thr Lys Pro Gly Glu Gln Gly Phe Leu	
455 460 465 470	
TGC ATC ACT AAG CCA TGG CCT TCT ATG ATA AGA AAC ATT TGG GGC GAT	1496
Cys Ile Thr Lys Pro Trp Pro Ser Met Ile Arg Asn Ile Trp Gly Asp	
475 480 485	
GAA AAA CGA TAC ATT GAT AGC TAT TTT TCT CAG ATC AAG TTG AAT GGG	1544
Glu Lys Arg Tyr Ile Asp Ser Tyr Phe Ser Gln Ile Lys Leu Asn Gly	
490 495 500	
GAA TAT GTC TAC CTC TCT GGA GAT GGC GCT ATC GTG GAT GAA AAC GGA	1592
Glu Tyr Val Tyr Leu Ser Gly Asp Gly Ala Ile Val Asp Glu Asn Gly	
505 510 515	
TAC ATT ACT ATT ATT GGG CGC ACA GAT GAT ATT GTG AAT GTG AGT GGG	1640
Tyr Ile Thr Ile Ile Gly Arg Thr Asp Asp Ile Val Asn Val Ser Gly	
520 525 530	
CAT AGG ATT GGC ACG GCT GAA GTG GAG AGC GCT ATT TCC AAG CAT GAA	1688
His Arg Ile Gly Thr Ala Glu Val Glu Ser Ala Ile Ser Lys His Glu	
535 540 545 550	
ATG GTG GCT GAA TGC GCG GTG GTG GGT ATC CCT GAT GCG ATT AAA GGA	1736
Met Val Ala Glu Cys Ala Val Val Gly Ile Pro Asp Ala Ile Lys Gly	
555 560 565	
GAG GGC TTG TTT GCG TTT GTG GTG CTG TGC GAT GGG GCT AAA TGC AAT	1784
Glu Gly Leu Phe Ala Phe Val Val Leu Cys Asp Gly Ala Lys Cys Asn	
570 575 580	
CTT GGC GAG AGT TTA GAA TTG CTA AAA GAA ATG AAC CAT ATC TTA TCC	1832
Leu Gly Glu Ser Leu Glu Leu Leu Lys Glu Met Asn His Ile Leu Ser	
585 590 595	
ATT GAG ATT GGA AAG ATC GCG AAA TTA GAC AAT GTC ATG TAT GTG CCA	1880
Ile Glu Ile Gly Lys Ile Ala Lys Leu Asp Asn Val Met Tyr Val Pro	
600 605 610	
GGT TTG CCT AAA ACC AGG AGC GGG AAA ATC ATG AGA AGG CTT TTG AAA	1928
Gly Leu Pro Lys Thr Arg Ser Gly Lys Ile Met Arg Arg Leu Leu Lys	
615 620 625 630	
TCC ATC GCC AAA AAA GAG CCT ATC ACT CAA GAT TTA AGC ACG CTA GAA	1976
Ser Ile Ala Lys Lys Glu Pro Ile Thr Gln Asp Leu Ser Thr Leu Glu	
635 640 645	
GAT GTG AAT GTG GTT AAA GAA ATA ATG AGC ATC GCT CAA ATG GAG GAG T	2025
Asp Val Asn Val Val Lys Glu Ile Met Ser Ile Ala Gln Met Glu Glu	
650 655 660	

AAC GCC TGC CCT AGC GTG GAA AAA GCG CTC ATT GTG ATA CGA AAC GCC	728
Asn Ala Cys Pro Ser Val Glu Lys Ala Leu Ile Val Ile Arg Asn Ala	
215 220 225 230	
AAA GAG ATT GAC TAT GTG AGA GGG CGC GAT TTT GTC TAT AAT GAA ATG	776
Lys Glu Ile Asp Tyr Val Arg Gly Arg Asp Phe Val Tyr Asn Glu Met	
235 240 245	
GTC AAT TAC CAA TCC GAC AAA TGC GAA CCT GAA ATG ATG GAC TCT GAA	824
Val Asn Tyr Gln Ser Asp Lys Cys Glu Pro Glu Met Met Asp Ser Glu	
250 255 260	
GAT CCT TTA TTC TTG CTC TAT ACA AGC GGA TCA ACC GGA AAG CCT AAA	872
Asp Pro Leu Phe Leu Leu Tyr Thr Ser Gly Ser Thr Gly Lys Pro Lys	
265 270 275	
GGC GTT CAA CAC AGC AGT GCG GGG TAT TTG TTA TGG GCG CAA ATG ACG	920
Gly Val Gln His Ser Ser Ala Gly Tyr Leu Leu Trp Ala Gln Met Thr	
280 285 290	
ATG GAG TGG GTT TTT GAT ATT AGA GAT AAC GAT AAT TTT TGG TGC ACC	968
Met Glu Trp Val Phe Asp Ile Arg Asp Asn Asp Asn Phe Trp Cys Thr	
295 300 305 310	
GCC GAT ATT GGC TGG ATC ACA GGG CAC ACT TAT GTG GTT TAT GGA CCT	1016
Ala Asp Ile Gly Trp Ile Thr Gly His Thr Tyr Val Val Tyr Gly Pro	
315 320 325	
TTA GCT TGT GGG GCG ACG ACT TTG ATA CTA GAA GGC ACG ATG TCT TAT	1064
Leu Ala Cys Gly Ala Thr Thr Leu Ile Leu Glu Gly Thr Met Ser Tyr	
330 335 340	
CCG GAT TAT GGG AGA TGG TGG AGG ATG ATA GAA GAA TAC CGT GTG GAT	1112
Pro Asp Tyr Gly Arg Trp Trp Arg Met Ile Glu Glu Tyr Arg Val Asp	
345 350 355	
AAA TTC TAC ACT TCC CCT ACC GCT ATA AGA ATG TTG CAT GCC AAA GGT	1160
Lys Phe Tyr Thr Ser Pro Thr Ala Ile Arg Met Leu His Ala Lys Gly	
360 365 370	
GAA AAC GAA CCC TCA AAG TAT AAT TTA GAG TCG CTC AAA GTT TTA GGA	1208
Glu Asn Glu Pro Ser Lys Tyr Asn Leu Glu Ser Leu Lys Val Leu Gly	
375 380 385 390	
ACG GTG GGA GAG CCC ATT AAC CCT ACA GCA TGG AAA TGG TTT TAT GAA	1256
Thr Val Gly Glu Pro Ile Asn Pro Thr Ala Trp Lys Trp Phe Tyr Glu	
395 400 405	
AAA ATC GGC AAC TCA AAA TGC AGC ATC GTG GAT ACT TGG TGG CAG ACA	1304
Lys Ile Gly Asn Ser Lys Cys Ser Ile Val Asp Thr Trp Trp Gln Thr	
410 415 420	
GAA ACA GGC GGG CAC ATC ATC AGC CCT TTA CCG GGA GCT ACG CCT ATA	1352
Glu Thr Gly Gly His Ile Ile Ser Pro Leu Pro Gly Ala Thr Pro Ile	
425 430 435	

ATAAAAAATG CGCTTAAAC CATGAAAAAG GAGATGCG ATG CAA TTA GAC GAA GAT	56
Met Gln Leu Asp Glu Asp	
1 5	
TTA GAA TTC GCT AAA AAA ATC TTT AAC CCT AAC AGA GCG TTT GCC AAG	104
Leu Glu Phe Ala Lys Lys Ile Phe Asn Pro Asn Arg Ala Phe Ala Lys	
10 15 20	
CAA GCC AGG ATT AAA AAC ATG TGC GAA TAT AAA GAT TTA GTG CAT GAA	152
Gln Ala Arg Ile Lys Asn Met Cys Glu Tyr Lys Asp Leu Val His Glu	
25 30 35	
GCC AAT GAA GAT TAT GAA CAT TTT TGG GGC GAT TTA GCC AAG CAG AAA	200
Ala Asn Glu Asp Tyr Glu His Phe Trp Gly Asp Leu Ala Lys Gln Lys	
40 45 50	
CTC ACA TGG TTT AAA CCT TTT GAT AAG GTT TTA AAC AGC GAT AAC GCC	248
Leu Thr Trp Phe Lys Pro Phe Asp Lys Val Leu Asn Ser Asp Asn Ala	
55 60 65 70	
CCT TTT TTC AAA TGG TTT GAA AAC GGC AAA ATC AAT GTT TCT TAC AAT	296
Pro Phe Phe Lys Trp Phe Glu Asn Gly Lys Ile Asn Val Ser Tyr Asn	
75 80 85	
TGC ATA GAC AGG CAT TTA AAA GAC AAA AAA AAT AAA GTG GCG ATC ATT	344
Cys Ile Asp Arg His Leu Lys Asp Lys Lys Asn Lys Val Ala Ile Ile	
90 95 100	
TTT GAA GGG GAA ATG GGG GAT TAT AAT GTC ATC ACT TAC AGA AAA CTC	392
Phe Glu Gly Glu Met Gly Asp Tyr Asn Val Ile Thr Tyr Arg Lys Leu	
105 110 115	
CAC TCT GAA GTC AAT AAA ACA GCC AAC CTT TTA AAA AAC GAA TTC AAT	440
His Ser Glu Val Asn Lys Thr Ala Asn Leu Leu Lys Asn Glu Phe Asn	
120 125 130	
GTC AAA AAA GGC GAT AGG GTC ATT ATC TAT ATG CCC ATG ATT GTA GAA	488
Val Lys Lys Gly Asp Arg Val Ile Ile Tyr Met Pro Met Ile Val Glu	
135 140 145 150	
AGC GTT TAT ATG ATG CTC GCA TGC ACT AGG ATT GGA GCG ATC CAT AGC	536
Ser Val Tyr Met Met Leu Ala Cys Thr Arg Ile Gly Ala Ile His Ser	
155 160 165	
ATC GTT TTT GCT GGG TTT AGC CCT GAA GCC TTA AGG GAT AGG ATC AAC	584
Ile Val Phe Ala Gly Phe Ser Pro Glu Ala Leu Arg Asp Arg Ile Asn	
170 175 180	
GAC GCT CAA GCT AAA TTA GTT ATC ACA GCG GAT GGG ACT TTT AGA AAA	632
Asp Ala Gln Ala Lys Leu Val Ile Thr Ala Asp Gly Thr Phe Arg Lys	
185 190 195	
GGC AAA CCT TAC ATG CTC AAG CCA GCC CTT GAC AAG GCT CTA GAA AAT	680
Gly Lys Pro Tyr Met Leu Lys Pro Ala Leu Asp Lys Ala Leu Glu Asn	
200 205 210	

65					70					75					80
Glu	His	Arg	Leu	Gln	Asn	Lys	Asn	Ile	Gln	Ile	Gln	Leu	Leu	Asp	His
				85					90					95	
His	Ile	Ser	Gly	Lys	Glu	Val	Ala	Glu	Ser	Phe	His	Trp	Tyr	Phe	Leu
			100					105					110		
Asp	Ile	Asn	Arg	Cys	Ala	Thr	Lys	Ile	Val	Tyr	Glu	Phe	Leu	Lys	Lys
		115					120					125			
His	Tyr	Ala	Ile	Leu	Glu	Pro	Lys	Asn	Thr	Thr	Trp	Leu	Glu	Pro	Leu
	130					135					140				
Val	Glu	Met	Val	Asn	Ser	Val	Asp	Ile	Trp	Asp	Thr	Gln	Gly	Tyr	Gly
145				150					155						160
Phe	Glu	Leu	Gly	Lys	Val	Cys	Met	Arg	Met	Ile	Asn	Gln	Ser	Ser	Glu
			165					170						175	
Leu	Asn	Arg	Phe	Met	Phe	Asp	Asp	Glu	Asn	Arg	Asn	Tyr	Lys	Leu	Lys
			180					185					190		
Leu	Leu	Glu	Glu	Val	Lys	Asn	Tyr	Leu	Phe	Leu	Glu	Asn	Ala	Pro	Val
	195						200					205			
Ala	Tyr	Asp	Asn	Asp	Leu	Phe	Lys	Leu	Lys	Lys	Ile	Ala	Leu	Gly	Gly
	210					215					220				
Asp	Pro	Asp	Ala	Glu	Thr	Met	Asp	Asn	Ile	Ser	Ser	Asn	Ala	Gln	Thr
225				230				235						240	
His	Leu	Leu	Ser	Leu	Lys	Lys	His	Asp	Cys	Ser	Val	Tyr	Tyr	Gln	Asp
			245					250						255	
Lys	Lys	Gly	Phe	Leu	Ser	Tyr	Ser	Met	Gly	Gly	Ile	Ser	Val	Leu	Ala
			260					265					270		
Asn	Leu	Phe	Leu	Thr	Gln	Asn	Pro	Asp	Phe	Asp	Phe	Tyr	Met	Asp	Val
	275						280					285			
Asn	Ala	Lys	Gly	Asn	Val	Ser	Leu	Arg	Ala	Asn	Gly	Asn	Cys	Asp	Val
	290					295					300				
Cys	Glu	Leu	Ser	Gln	Met	Cys	Phe	Asn	Gly	Gly	Gly	His	Arg	Asn	Ala
305				310					315					320	
Ser	Gly	Gly	Lys	Ile	Asp	Gly	Phe	Arg	Glu	Ser	Phe	Asn	Tyr	Arg	Asp
			325					330						335	
Ile	Lys	Glu	Gln	Ile	Glu	Glu	Ile	Phe	Asn	Asn	Ala				
			340					345							

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...2024
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

TTA GGG GGC GAC CCT GAT GCA GAA ACG ATG GAC AAT ATC TCT TCA AAC	723
Leu Gly Gly Asp Pro Asp Ala Glu Thr Met Asp Asn Ile Ser Ser Asn	
225 230 235	
GCG CAA ACG CAT TTG CTC TCT TTA AAA AAG CAT GAT TGC AGC GTT TAT	771
Ala Gln Thr His Leu Leu Ser Leu Lys Lys His Asp Cys Ser Val Tyr	
240 245 250	
TAC CAG GAT AAA AAA GGG TTT TTA AGT TAT TCT ATG GGG GGC ATT AGC	819
Tyr Gln Asp Lys Lys Gly Phe Leu Ser Tyr Ser Met Gly Gly Ile Ser	
255 260 265	
GTG TTG GCT AAC CTT TTT TTA ACG CAA AAT CCG GAT TTT GAT TTT TAT	867
Val Leu Ala Asn Leu Phe Leu Thr Gln Asn Pro Asp Phe Asp Phe Tyr	
270 275 280 285	
ATG GAT GTG AAC GCT AAA GGG AAT GTG AGC TTA AGG GCG AAT GGG AAT	915
Met Asp Val Asn Ala Lys Gly Asn Val Ser Leu Arg Ala Asn Gly Asn	
290 295 300	
TGC GAT GTG TGC GAA CTC AGT CAA ATG TGT TTT AAT GGG GGT GGG CAT	963
Cys Asp Val Cys Glu Leu Ser Gln Met Cys Phe Asn Gly Gly Gly His	
305 310 315	
AGG AAT GCG AGC GGA GGC AAG ATT GAT GGT TTT AGG GAG AGT TTC AAT	1011
Arg Asn Ala Ser Gly Gly Lys Ile Asp Gly Phe Arg Glu Ser Phe Asn	
320 325 330	
TAT AGG GAT ATT AAA GAA CAA ATT GAA GAA ATC TTC AAC AAC GCT TAAAA	1061
Tyr Arg Asp Ile Lys Glu Gln Ile Glu Glu Ile Phe Asn Asn Ala	
335 340 345	
CTAAGCTGTT TAGAAAAAAC TAACAAAAAC TGAAAAGAGT TTAAAAGCTC	1111

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

Met Met Gln Val Tyr His Leu Ser His Ile Asp Leu Asp Gly Tyr Ala	
1 5 10 15	
Cys Gln Leu Val Ser Lys Gln Phe Phe Lys Asn Ile Gln Cys Tyr Asn	
20 25 30	
Ala Asn Tyr Gly Arg Glu Val Ser Ala Arg Ile Tyr Glu Ile Leu Asn	
35 40 45	
Ala Ile Ala Gln Ser Lys Glu Ser Glu Phe Leu Ile Leu Val Ser Asp	
50 55 60	
Leu Asn Leu Asn Leu Asn Glu Ala Glu Tyr Leu Gln Asp Lys Ile Gln	

	Met	Met	Gln	Val	Tyr	His	Leu	Ser	His	Ile	Asp	Leu	Asp	
	1				5					10				
GGC TAT GCA TGC CAG CTT GTT TCA AAA CAA TTT TTT AAA AAT ATC CAA														99
Gly Tyr Ala Cys Gln Leu Val Ser Lys Gln Phe Phe Lys Asn Ile Gln														
	15				20					25				
TGC TAT AAC GCT AAT TAC GGG CGT GAA GTC TCA GCG AGA ATT TAT GAG														147
Cys Tyr Asn Ala Asn Tyr Gly Arg Glu Val Ser Ala Arg Ile Tyr Glu														
	30				35				40				45	
ATT TTA AAC GCA ATC GCT CAG TCT AAA GAG AGT GAA TTC CTT ATT TTG														195
Ile Leu Asn Ala Ile Ala Gln Ser Lys Glu Ser Glu Phe Leu Ile Leu														
				50				55				60		
GTT AGC GAT TTG AAT CTG AAT TTG AAT GAA GCA GAG TAT TTG CAG GAT														243
Val Ser Asp Leu Asn Leu Asn Leu Asn Glu Ala Glu Tyr Leu Gln Asp														
				65				70				75		
AAG ATC CAA GAA CAC CGC TTG CAA AAT AAA AAC ATT CAA ATC CAG CTT														291
Lys Ile Gln Glu His Arg Leu Gln Asn Lys Asn Ile Gln Ile Gln Leu														
				80				85				90		
TTA GAT CAC CAT ATC AGC GGT AAG GAA GTG GCT GAG AGT TTC CAT TGG														339
Leu Asp His His Ile Ser Gly Lys Glu Val Ala Glu Ser Phe His Trp														
	95						100			105				
TAT TTT TTA GAC ATT AAC CGT TGC GCG ACT AAA ATC GTG TAT GAA TTT														387
Tyr Phe Leu Asp Ile Asn Arg Cys Ala Thr Lys Ile Val Tyr Glu Phe														
	110				115				120				125	
TTG AAA AAG CAT TAC GCT ATT TTA GAG CCA AAA AAC ACA ACA TGG CTA														435
Leu Lys Lys His Tyr Ala Ile Leu Glu Pro Lys Asn Thr Thr Trp Leu														
				130				135					140	
GAG CCT TTA GTG GAA ATG GTC AAT TCT GTG GAT ATT TGG GAC ACG CAA														483
Glu Pro Leu Val Glu Met Val Asn Ser Val Asp Ile Trp Asp Thr Gln														
				145				150					155	
GGT TAT GGC TTT GAA TTA GGC AAG GTG TGC ATG CGC ATG ATT AAC CAA														531
Gly Tyr Gly Phe Glu Leu Gly Lys Val Cys Met Arg Met Ile Asn Gln														
	160						165					170		
AGC TCT GAA TTG AAT CGT TTC ATG TTT GAT GAT GAA AAC CGC AAC TAT														579
Ser Ser Glu Leu Asn Arg Phe Met Phe Asp Asp Glu Asn Arg Asn Tyr														
	175						180					185		
AAA TTA AAG CTT TTA GAA GAA GTT AAA AAC TAT TTG TTT TTA GAA AAT														627
Lys Leu Lys Leu Leu Glu Val Lys Asn Tyr Leu Phe Leu Glu Asn														
	190				195				200				205	
GCC CCT GTA GCC TAT GAT AAC GAT TTG TTC AAA CTC AAA AAA ATC GCT														675
Ala Pro Val Ala Tyr Asp Asn Asp Leu Phe Lys Leu Lys Lys Ile Ala														
				210				215					220	

Glu	Gly	Leu	Val	Gly	Lys	Ala	Pro	Ser	Val	Gly	Leu	Glu	Lys	Glu	Ile
			20					25					30		
Ser	Ser	Ser	Asp	Glu	Ser	Phe	Leu	Lys	Leu	Ile	Ser	Thr	Pro	Tyr	Ala
		35					40					45			
Arg	Val	Val	Ile	Ser	Ala	Ile	Glu	Lys	Glu	Glu	Ser	Ser	Ile	Glu	Leu
	50					55					60				
Leu	Ala	Pro	Val	Val	Leu	Val	Thr	Ser	Leu	Ser	Asp	Leu	Met	Leu	Gly
65					70					75					80
Gly	Glu	Gly	Ala	Ser	Lys	Glu	Glu	Met	Asp	Asn	Asp	Asp	Leu	Asp	Ala
				85					90					95	
Phe	Lys	Glu	Met	Ala	Ser	Asn	Ile	Phe	Gly	Ala	Ile	Ala	Thr	Ser	Leu
			100					105					110		
Lys	Ser	Gln	Glu	Leu	Leu	Pro	Lys	Leu	Asn	Phe	Thr	Thr	Ile	Asn	Ala
		115					120					125			
Glu	Ile	Ala	Lys	Glu	Leu	Pro	Lys	Lys	Glu	Asp	Tyr	Ala	Lys	Ala	Met
	130					135					140				
Val	Phe	Ser	Phe	Lys	Met	Glu	Ala	Ile	Lys	Glu	Ser	Gln	Ile	Ile	Leu
145				150						155					160
Leu	Thr	Thr	Ala	Ala	Phe	Glu	Gly	Gln	Phe	Glu	Lys	Thr	His	Lys	Glu
			165					170					175		
Glu	Lys	Glu	Glu	Thr	Thr	Glu	Gly	Val	Ala	Glu	Glu	Val	Lys	Thr	His
			180				185						190		
Asp	Ala	Ser	Leu	Glu	Asn	Ile	Glu	Ile	Arg	Asn	Ile	Ser	Met	Leu	Leu
	195						200					205			
Asp	Val	Lys	Leu	Asn	Val	Lys	Val	Arg	Ile	Gly	Gln	Lys	Lys	Met	Ile
	210					215					220				
Leu	Lys	Asp	Val	Val	Ser	Met	Asp	Ile	Gly	Ser	Val	Val	Glu	Leu	Asp
225				230						235					240
Gln	Leu	Val	Asn	Asp	Pro	Leu	Glu	Ile	Leu	Val	Asp	Asp	Lys	Val	Ile
			245						250					255	
Ala	Lys	Gly	Glu	Val	Val	Ile	Val	Asp	Gly	Asn	Phe	Gly	Ile	Gln	Ile
			260					265					270		
Thr	Asp	Ile	Gly	Thr	Lys	Lys	Glu	Arg	Leu	Glu	Gln	Leu	Lys	His	
	275						280					285			

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1056
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

TAAAAAAGGA GA ATG ATG CAA GTT TAC CAC CTT TCA CAC ATT GAT TTA GAC

51

TAC GCT AAA GCG ATG GTG TTT TCT TTT AAA ATG GAA GCC ATC AAA GAA	483
Tyr Ala Lys Ala Met Val Phe Ser Phe Lys Met Glu Ala Ile Lys Glu	
140 145 150 155	
AGC CAA ATC ATT TTA TTG ACT ACG GCG GCT TTT GAG GGC CAA TTT GAA	531
Ser Gln Ile Ile Leu Leu Thr Thr Ala Ala Phe Glu Gly Gln Phe Glu	
160 165 170	
AAA ACG CAT AAA GAA GAA AAA GAA GAA ACG ACA GAG GGC GTT GCT GAA	579
Lys Thr His Lys Glu Glu Lys Glu Thr Thr Glu Gly Val Ala Glu	
175 180 185	
GAG GTT AAA ACC CAT GAT GCG TCT TTA GAA AAC ATA GAA ATC CGC AAT	627
Glu Val Lys Thr His Asp Ala Ser Leu Glu Asn Ile Glu Ile Arg Asn	
190 195 200	
ATC AGC ATG CTT TTA GAC GTG AAA TTG AAC GTT AAG GTG CGC ATC GGG	675
Ile Ser Met Leu Leu Asp Val Lys Leu Asn Val Lys Val Arg Ile Gly	
205 210 215	
CAA AAA AAA ATG ATT TTA AAA GAC GTG GTC TCT ATG GAT ATA GGG AGC	723
Gln Lys Lys Met Ile Leu Lys Asp Val Val Ser Met Asp Ile Gly Ser	
220 225 230 235	
GTG GTA GAG CTG GAT CAA TTG GTG AAT GAC CCT TTG GAA ATT CTT GTA	771
Val Val Glu Leu Asp Gln Leu Val Asn Asp Pro Leu Glu Ile Leu Val	
240 245 250	
GAT GAC AAG GTG ATC GCT AAG GGC GAA GTG GTG ATT GTG GAT GGG AAT	819
Asp Asp Lys Val Ile Ala Lys Gly Glu Val Val Ile Val Asp Gly Asn	
255 260 265	
TTT GGC ATT CAA ATC ACG GAT ATT GGC ACT AAA AAA GAA CGC TTA GAA	867
Phe Gly Ile Gln Ile Thr Asp Ile Gly Thr Lys Lys Glu Arg Leu Glu	
270 275 280	
CAA TTG AAA CAT TAAATCTTTT TATCATAAAA AGGAAAGGGA TATG	913
Gln Leu Lys His	
285	

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

Met	Gln	Asp	Phe	Ile	Lys	Ile	Phe	Ile	Gln	Glu	Val	Val	Ser	Thr	Leu
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...879
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

ATAGAAGAAG AGTGAGAA ATG CAA GAT TTT ATT AAG ATT TTT ATT CAA GAG	51
Met Gln Asp Phe Ile Lys Ile Phe Ile Gln Glu	
1 5 10	
GTT GTC TCT ACT TTA GAA GGG TTA GTG GGT AAG GCT CCA AGC GTG GGA	99
Val Val Ser Thr Leu Glu Gly Leu Val Gly Lys Ala Pro Ser Val Gly	
15 20 25	
TTA GAA AAA GAA ATT TCT AGT AGC GAC GAA TCT TTT TTG AAA TTA ATC	147
Leu Glu Lys Glu Ile Ser Ser Ser Asp Glu Ser Phe Leu Lys Leu Ile	
30 35 40	
AGC ACG CCT TAT GCA AGA GTT GTG ATA AGC GCG ATT GAA AAA GAA GAG	195
Ser Thr Pro Tyr Ala Arg Val Val Ile Ser Ala Ile Glu Lys Glu Glu	
45 50 55	
AGC TCT ATT GAA TTA CTG GCT CCG GTA GTT TTA GTT ACC TCT TTA AGC	243
Ser Ser Ile Glu Leu Leu Ala Pro Val Val Leu Val Thr Ser Leu Ser	
60 65 70 75	
GAT TTG ATG CTA GGA GGT GAG GGA GCG AGT AAG GAA GAA ATG GAT AAT	291
Asp Leu Met Leu Gly Gly Glu Gly Ala Ser Lys Glu Glu Met Asp Asn	
80 85 90	
GAC GAT TTA GAC GCT TTT AAA GAA ATG GCT TCT AAT ATT TTT GGC GCG	339
Asp Asp Leu Asp Ala Phe Lys Glu Met Ala Ser Asn Ile Phe Gly Ala	
95 100 105	
ATC GCT ACA AGC TTG AAG TCT CAA GAA TTG CTC CCT AAA CTC AAT TTC	387
Ile Ala Thr Ser Leu Lys Ser Gln Glu Leu Leu Pro Lys Leu Asn Phe	
110 115 120	
ACC ACT ATA AAC GCT GAA ATC GCT AAA GAG CTT CCT AAA AAA GAA GAT	435
Thr Thr Ile Asn Ala Glu Ile Ala Lys Glu Leu Pro Lys Lys Glu Asp	
125 130 135	

115	120	125	
GTC AAT GCG TTA GGC AAG TAT AAA ACC GTT TCT CAA GTC GTG GCG ATT			493
Val Asn Ala Leu Gly Lys Tyr Lys Thr Val Ser Gln Val Val Ala Ile			
130	135	140	
GGT GCT TTA TTG GCT GAT GTA ACT TAC TCT TAT GCG CTT GTG GCT ATA			541
Gly Ala Leu Leu Ala Asp Val Thr Tyr Ser Tyr Ala Leu Val Ala Ile			
145	150	155	160
GCG GTT TTT TTA ACC CTT TAT TCG GGG ATA GAT TAC ACC ATT AAA TAT			589
Ala Val Phe Leu Thr Leu Tyr Ser Gly Ile Asp Tyr Thr Ile Lys Tyr			
165	170	175	
TAT AAA TCT TAATATTTTA AAAGAAGTTT TTAGCGTTCT TT			630
Tyr Lys Ser			

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

Met	Lys	Val	Leu	Lys	Leu	Leu	Pro	Asn	Phe	Leu	Thr	Ile	Leu	Arg	Ile
1				5					10					15	
Val	Leu	Ser	Leu	Phe	Leu	Leu	Phe	Leu	Leu	Leu	Asn	Thr	Arg	Thr	Tyr
			20					25					30		
Phe	Ser	Phe	Leu	Thr	Pro	Phe	Gln	Thr	Asn	Met	Ile	Ser	Ser	Leu	Val
		35				40					45				
Phe	Leu	Phe	Ala	Ala	Leu	Thr	Asp	Leu	Leu	Asp	Gly	Tyr	Ile	Ala	Arg
		50				55					60				
Ser	Tyr	Lys	Ala	Lys	Ser	Arg	Phe	Gly	Glu	Ile	Phe	Asp	Pro	Leu	Ala
65					70					75				80	
Asp	Lys	Ile	Leu	Ile	Leu	Ser	Ala	Phe	Leu	Gly	Leu	Val	Tyr	Leu	Asp
			85						90					95	
Arg	Val	Asn	Ala	Trp	Ile	Pro	Phe	Val	Ile	Leu	Gly	Arg	Glu	Phe	Phe
			100					105					110		
Ile	Ser	Gly	Leu	Arg	Val	Leu	Ala	Asn	Glu	Lys	Lys	Asp	Ile	Pro	
		115					120					125			
Val	Asn	Ala	Leu	Gly	Lys	Tyr	Lys	Thr	Val	Ser	Gln	Val	Val	Ala	Ile
		130				135					140				
Gly	Ala	Leu	Leu	Ala	Asp	Val	Thr	Tyr	Ser	Tyr	Ala	Leu	Val	Ala	Ile
145					150					155					160
Ala	Val	Phe	Leu	Thr	Leu	Tyr	Ser	Gly	Ile	Asp	Tyr	Thr	Ile	Lys	Tyr
				165					170					175	
Tyr	Lys	Ser													

Leu Thr Thr Ala Val Val Leu Met Cys Val Ala Leu Gly Phe Leu Ala
 180 185 190
 Arg Ala Phe Leu Asn Phe Ser Gln Val Phe Leu Lys Ala
 195 200 205

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...598
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

```

GTGTGGCGCT TGGTTTTTTG GCGCGCGCGT TTTTGAATTT TTCACAAGTC TTTTGAAG      60
C ATG AAA GTT TTA AAA CTC CTG CCT AAT TTT TTA ACA ATT TTA CGC ATT      109
  Met Lys Val Leu Lys Leu Leu Pro Asn Phe Leu Thr Ile Leu Arg Ile
    1             5             10             15

GTC TTA TCC TTA TTT TTA TTA TTT TTA TTG TTA AAC ACG CGC ACT TAT      157
Val Leu Ser Leu Phe Leu Leu Phe Leu Leu Leu Asn Thr Arg Thr Tyr
          20             25             30

TTT AGT TTT TTA ACC CCC TTT CAA ACC AAT ATG ATC TCT TCA TTG GTT      205..
Phe Ser Phe Leu Thr Pro Phe Gln Thr Asn Met Ile Ser Ser Leu Val
          35             40             45

TTT TTG TTT GCC GCG CTC ACG GAT TTA TTG GAC GGC TAC ATC GCT AGA      253
Phe Leu Phe Ala Ala Leu Thr Asp Leu Leu Asp Gly Tyr Ile Ala Arg
          50             55             60

AGC TAT AAA GCC AAA TCG CGC TTT GGG GAA ATC TTT GAT CCT TTA GCG      301
Ser Tyr Lys Ala Lys Ser Arg Phe Gly Glu Ile Phe Asp Pro Leu Ala
          65             70             75             80

GAT AAA ATC CTT ATT TTG AGC GCG TTT TTA GGG TTA GTT TAT TTG GAT      349
Asp Lys Ile Leu Ile Leu Ser Ala Phe Leu Gly Leu Val Tyr Leu Asp
          85             90             95

CGT GTG AAT GCG TGG ATC CCG TTT GTG ATT TTA GGG CGT GAA TTT TTT      397
Arg Val Asn Ala Trp Ile Pro Phe Val Ile Leu Gly Arg Glu Phe Phe
          100            105            110

ATT TCA GGG CTT AGA GTC TTA GCC GCT AAT GAG AAA AAG GAT ATT CCT      445
Ile Ser Gly Leu Arg Val Leu Ala Ala Asn Glu Lys Lys Asp Ile Pro

```

```

Ser Ile Phe Tyr Leu His Lys Leu Tyr Arg Glu Leu Ser Leu Tyr Thr
  130                      135                      140

CAA GAA AGG TTT TTT TTA AGC GGG TTT AGG TTG TTG CTT TTT AGT TTC      481
Gln Glu Arg Phe Phe Leu Ser Gly Phe Arg Leu Leu Leu Phe Ser Phe
  145                      150                      155                      160

ATG CTG GCT CTT TTA GGG ATT TTA GTG CAA GCG TTA GTT ATC ATT TTT      529
Met Leu Ala Leu Leu Gly Ile Leu Val Gln Ala Leu Val Ile Ile Phe
                      165                      170                      175

TTA ACG ACC GCT GTG GTT TTA ATG TGT GTG GCG CTT GGT TTT TTG GCG      577
Leu Thr Thr Ala Val Val Leu Met Cys Val Ala Leu Gly Phe Leu Ala
                      180                      185                      190

CGC GCG TTT TTG AAT TTT TCA CAA GTC TTT TTG AAA GCA TGAAAGTTTTT AA      628
Arg Ala Phe Leu Asn Phe Ser Gln Val Phe Leu Lys Ala
                      195                      200                      205

AACTCCTGCC TAATTT      644

```

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

```

Arg Tyr Phe Leu Gln Asn Ile Ile His Ile His Gln Asn Lys Glu Leu
  1                      5                      10                      15
Gln Phe Ile Lys Lys Cys Leu Leu Gly Tyr Phe Phe Ala Pro Leu Cys
                      20                      25                      30
Gly Ala Ile Leu Leu Val Leu Phe Ile Val Ser Ser Gly Ala Lys Ser
                      35                      40                      45
Phe Gln Ile Ser Asn Leu Phe Asn Asn Gln Leu Ala Tyr Ile Val Leu
                      50                      55                      60
Leu Ser Leu Phe Leu Cys Ala Leu Gly Phe Ile Ala Gly Ala Ile Gly
                      65                      70                      75                      80
Phe Tyr Arg Leu Ser Lys Ile Thr Arg His Leu Ser Phe Phe Glu Asn
                      85                      90                      95
Phe Ala Phe Ser Phe Leu Ala Val Ile Leu Cys Ala Ile Leu Ser Tyr
                      100                      105                      110
Leu Val Pro Asn Ala Ser Asn Ala Leu Ser Leu Ile Gly Asn Gly Val
                      115                      120                      125
Ser Ile Phe Tyr Leu His Lys Leu Tyr Arg Glu Leu Ser Leu Tyr Thr
                      130                      135                      140
Gln Glu Arg Phe Phe Leu Ser Gly Phe Arg Leu Leu Leu Phe Ser Phe
                      145                      150                      155                      160
Met Leu Ala Leu Leu Gly Ile Leu Val Gln Ala Leu Val Ile Ile Phe
                      165                      170                      175

```

Val Asp Gly Gly Thr Thr Phe Lys
145 150

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 2...616
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

A AGA TAT TTC TTG CAA AAC ATT ATC CAC ATC CAC CAA AAC AAA GAG TTG	49
Arg Tyr Phe Leu Gln Asn Ile Ile His Ile His Gln Asn Lys Glu Leu	
1 5 10 15	
CAA TTC ATT AAA AAA TGC TTG TTG GGC TAT TTT TTC GCC CCT TTG TGT	97
Gln Phe Ile Lys Lys Cys Leu Leu Gly Tyr Phe Phe Ala Pro Leu Cys	
20 25 30	
GGG GCT ATT CTG TTA GTG CTT TTT ATT GTT TCA AGC GGG GCA AAA TCG	145
Gly Ala Ile Leu Leu Val Leu Phe Ile Val Ser Ser Gly Ala Lys Ser	
35 40 45	
TTT CAA ATT TCT AAT CTC TTT AAC AAT CAA CTA GCC TAT ATC GTT TTG	193
Phe Gln Ile Ser Asn Leu Phe Asn Asn Gln Leu Ala Tyr Ile Val Leu	
50 55 60	
TTG TCT CTT TTT TTG TGC GCG CTT GGG TTT ATT GCC GGA GCG ATT GGT	241
Leu Ser Leu Phe Leu Cys Ala Leu Gly Phe Ile Ala Gly Ala Ile Gly	
65 70 75 80	
TTT TAT AGG CTT TCT AAA ATC ACA CGC CAT CTG AGT TTT TTT GAA AAT	289
Phe Tyr Arg Leu Ser Lys Ile Thr Arg His Leu Ser Phe Phe Glu Asn	
85 90 95	
TTC GCT TTC AGT TTT TTA GCG GTG ATT TTA TGC GCT ATT TTA AGC TAT	337
Phe Ala Phe Ser Phe Leu Ala Val Ile Leu Cys Ala Ile Leu Ser Tyr	
100 105 110	
CTT GTC CCT AAC GCC AGT AAC GCT CTT TCG CTA ATC GGT AAT GGC GTT	385
Leu Val Pro Asn Ala Ser Asn Ala Leu Ser Leu Ile Gly Asn Gly Val	
115 120 125	
TCT ATT TTT TAT TTG CAC AAA CTC TAT AGA GAA TTG AGC CTT TAC ACG	433

Asn	Ala	Val	Glu	Thr	Met	Val	Lys	Tyr	Ala	Ala	Val	Asp	Leu	Gly	Glu		
				65					70					75			
TTT	AAC	ATT	AGA	GTG	AAT	GCG	GTT	AGT	GGC	GGG	CCT	ATT	GAT	ACG	GAC	350	
Phe	Asn	Ile	Arg	Val	Asn	Ala	Val	Ser	Gly	Gly	Pro	Ile	Asp	Thr	Asp		
			80					85					90				
GCT	TTG	AAA	GCC	TTC	CCT	GAT	TAT	GTG	GAG	ATT	AAA	GAA	AAA	GTA	GAA	398	
Ala	Leu	Lys	Ala	Phe	Pro	Asp	Tyr	Val	Glu	Ile	Lys	Glu	Lys	Val	Glu		
		95					100					105					
GAG	CAA	TCG	CCC	CTA	AAA	CGC	ATG	GGC	AAT	CCT	AAC	GAT	CTA	GCC	GGA	446	
Glu	Gln	Ser	Pro	Leu	Lys	Arg	Met	Gly	Asn	Pro	Asn	Asp	Leu	Ala	Gly		
	110					115					120						
GCG	GCT	TAT	TTT	TTA	TGC	GAT	GAG	ACC	CAA	AGC	GGT	TGG	CTT	ACA	GGG	494	
Ala	Ala	Tyr	Phe	Leu	Cys	Asp	Glu	Thr	Gln	Ser	Gly	Trp	Leu	Thr	Gly		
125					130					135					140		
CAA	ACG	ATC	GTT	GTA	GAT	GGC	GGG	ACT	ACT	TTT	AAA	TAAAGATATT	TCTTGC			546	
Gln	Thr	Ile	Val	Val	Asp	Gly	Gly	Thr	Thr	Phe	Lys						
				145					150								

546

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

Met	Arg	Leu	Lys	Pro	Lys	Gly	Leu	Asn	Asn	Ile	Tyr	Thr	Ala	Thr	Val		
1				5				10					15				
Leu	Ala	Phe	Val	Val	Gly	Ala	Gln	Glu	Ala	Ala	Lys	Arg	Met	Gln	Lys		
			20					25					30				
Ile	Gly	Gly	Gly	Ala	Ile	Val	Ser	Leu	Ser	Ser	Thr	Gly	Asn	Leu	Val		
	35						40					45					
Tyr	Met	Pro	Asn	Tyr	Ala	Gly	His	Gly	Asn	Ser	Lys	Asn	Ala	Val	Glu		
	50					55					60						
Thr	Met	Val	Lys	Tyr	Ala	Ala	Val	Asp	Leu	Gly	Glu	Phe	Asn	Ile	Arg		
65					70				75					80			
Val	Asn	Ala	Val	Ser	Gly	Gly	Pro	Ile	Asp	Thr	Asp	Ala	Leu	Lys	Ala		
				85					90					95			
Phe	Pro	Asp	Tyr	Val	Glu	Ile	Lys	Glu	Lys	Val	Glu	Glu	Gln	Ser	Pro		
	100						105						110				
Leu	Lys	Arg	Met	Gly	Asn	Pro	Asn	Asp	Leu	Ala	Gly	Ala	Ala	Tyr	Phe		
	115					120						125					
Leu	Cys	Asp	Glu	Thr	Gln	Ser	Gly	Trp	Leu	Thr	Gly	Gln	Thr	Ile	Val		
	130					135					140						

130		135		140
Phe Ser Leu Lys Asn Ile	Ala Phe Ala Lys His	Lys Asp Asn Leu Pro		
145		150		155
Lys His Leu Asn Ser Lys	Asp Leu Lys Ser Phe	Ile Tyr Thr Leu Ile		160
	165		170	175
Asn Tyr Arg Thr Arg Ser	Ser Tyr Glu Lys Arg	Asn Lys Cys Ile Leu		
	180		185	190
Leu Leu Ile Ile Leu Gly	Gly Leu Arg Lys Ser	Glu Val Phe Asn Leu		
	195		200	205
Glu Leu Arg Asn Ile Val	Leu Glu Lys Glu His	Tyr Ile Leu Leu Ile		
	210		215	220
Lys Gly Lys Asn Asn Lys	Glu Arg Lys Ala Phe	Ile Lys Ile Ala Gln		
225		230		235
Thr Asp Ile Asp Thr Leu	Ala Pro Leu Ile Arg	Ile Leu Leu Glu Ser		240
	245		250	255
Ile Ala Lys Asn Leu Leu	Ser His			
	260			

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 75...530
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

TTGACAGAGT GGATTTTTTT ATTTCTAACG CTATTATTTA TGGGCGTTCT GTCGTGGGGG	60
GATTTGCACC GTTT ATG CGA TTA AAA CCT AAG GGG TTA AAC AAC ATT TAC	110
Met Arg Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr	
1 5 10	
ACA GCC ACC GTG TTA GCG TTC GTC GTA GGG GCT CAA GAA GCG GCA AAA	158
Thr Ala Thr Val Leu Ala Phe Val Val Gly Ala Gln Glu Ala Ala Lys	
15 20 25	
CGC ATG CAA AAA ATA GGC GGT GGG GCG ATC GTG AGC TTA AGT TCT ACC	206
Arg Met Gln Lys Ile Gly Gly Gly Ala Ile Val Ser Leu Ser Ser Thr	
30 35 40	
GGG AAT CTA GTT TAT ATG CCT AAT TAC GCC GGG CAT GGC AAT TCC AAA	254
Gly Asn Leu Val Tyr Met Pro Asn Tyr Ala Gly His Gly Asn Ser Lys	
45 50 55 60	
AAC GCG GTA GAA ACC ATG GTC AAA TAC GCT GCC GTG GAT TTA GGC GAA	302

AGA ACT AGA AGC AGT TAT GAA AAG AGA AAT AAG TGT ATT TTG CTC TTG	633
Arg Thr Arg Ser Ser Tyr Glu Lys Arg Asn Lys Cys Ile Leu Leu Leu	
180 185 190	
ATT ATT TTG GGT GGT TTG AGA AAA TCT GAG GTT TTT AAT TTA GAA TTG	681
Ile Ile Leu Gly Gly Leu Arg Lys Ser Glu Val Phe Asn Leu Glu Leu	
195 200 205 210	
AGA AAT ATT GTT TTA GAG AAA GAG CAT TAT ATC TTG CTT ATA AAA GGC	729
Arg Asn Ile Val Leu Glu Lys Glu His Tyr Ile Leu Leu Ile Lys Gly	
215 220 225	
AAA AAC AAT AAA GAG CGA AAA GCG TTC ATT AAA ATC GCT CAA ACA GAT	777
Lys Asn Asn Lys Glu Arg Lys Ala Phe Ile Lys Ile Ala Gln Thr Asp	
230 235 240	
ATT GAC ACA CTC GCA CCG CTT ATC CGT ATC CTT TTG GAA AGT ATT GCT	825
Ile Asp Thr Leu Ala Pro Leu Ile Arg Ile Leu Leu Glu Ser Ile Ala	
245 250 255	
AAA AAT CTT TTA TCC CAC TAGCGCGAAA AACTCCGTCC TTTAGGGCGG AGATGTAA	881
Lys Asn Leu Leu Ser His	
260	
GCGTTTAG	889

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

Met	Lys	Lys	Ser	Asn	Asp	Asn	Asn	Ala	Leu	Ala	Arg	Ser	Gln	Arg	Glu
1				5				10					15		
Leu	Phe	Val	Gly	Ile	Arg	Asp	Phe	Ile	Val	Phe	Lys	Phe	Lys	Arg	Met
		20					25						30		
Val	Val	Phe	Asn	Gly	Val	Arg	Asp	Phe	Thr	Lys	Met	Arg	Phe	Leu	Ser
		35					40					45			
Ile	Glu	Leu	Glu	Lys	Cys	Glu	Asn	Ile	Lys	Asp	Leu	Glu	Lys	Leu	Cys
	50					55				60					
His	Thr	Ile	Tyr	Asn	Gln	Gly	Thr	Lys	His	Ile	Leu	Met	Met	Arg	Val
65				70						75				80	
Leu	Phe	Leu	Phe	Phe	Asp	Tyr	Phe	Cys	Lys	His	Leu	Lys	Val	Lys	Arg
			85					90					95		
Leu	Arg	Leu	Leu	Asn	Glu	Glu	Met	Leu	Val	Asn	Phe	Leu	Phe	Glu	Leu
			100					105					110		
Ala	Lys	Gln	Arg	Lys	Ile	Asn	Ser	Met	Ala	Lys	Tyr	Val	Met	Tyr	Ile
		115					120					125			
Arg	Gln	Phe	Phe	Asp	Tyr	Leu	Asp	Arg	Thr	Lys	His	Tyr	Glu	Phe	Tyr

(B) LOCATION: 52...843

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

ATTACATTCT TTTTGATTTC TATTGAAAAA TTTAATATTA AGAGGACTTT T ATG AAA	57
Met Lys	
1	
AAA TCA AAT GAC AAT AAC GCA CTC GCC AGA AGT CAA AGG GAG TTG TTT	105
Lys Ser Asn Asp Asn Asn Ala Leu Ala Arg Ser Gln Arg Glu Leu Phe	
5 10 15	
GTA GGG ATT AGG GAT TTT ATT GTT TTT AAA TTT AAG CGT ATG GTT GTT	153
Val Gly Ile Arg Asp Phe Ile Val Phe Lys Phe Lys Arg Met Val Val	
20 25 30	
TTT AAC GGA GTA AGG GAT TTT ACA AAA ATG AGA TTT TTG TCC ATA GAA	201
Phe Asn Gly Val Arg Asp Phe Thr Lys Met Arg Phe Leu Ser Ile Glu	
35 40 45 50	
TTA GAA AAA TGC GAA AAT ATT AAA GAT TTG GAA AAA TTA TGT CAT ACA	249
Leu Glu Lys Cys Glu Asn Ile Lys Asp Leu Glu Lys Leu Cys His Thr	
55 60 65	
ATT TAT AAT CAA GGC ACA AAG CAT ATT TTG ATG ATG CGT GTA TTG TTT	297
Ile Tyr Asn Gln Gly Thr Lys His Ile Leu Met Met Arg Val Leu Phe	
70 75 80	
TTA TTC TTT GAC TAT TTC TGC AAG CAT TTG AAA GTT AAG CGA TTG AGA	345
Leu Phe Phe Asp Tyr Phe Cys Lys His Leu Lys Val Lys Arg Leu Arg	
85 90 95	
CTA CTC AAT GAA GAA ATG CTT GTG AAT TTT TTA TTT GAG TTA GCT AAA	393
Leu Leu Asn Glu Glu Met Leu Val Asn Phe Leu Phe Glu Leu Ala Lys	
100 105 110	
CAA AGA AAA ATT AAT TCA ATG GCA AAA TAT GTG ATG TAT ATT AGG CAA	441
Gln Arg Lys Ile Asn Ser Met Ala Lys Tyr Val Met Tyr Ile Arg Gln	
115 120 125 130	
TTT TTT GAT TAC TTG GAT AGG ACT AAA CAT TAT GAA TTT TAT TTT AGT	489
Phe Phe Asp Tyr Leu Asp Arg Thr Lys His Tyr Glu Phe Tyr Phe Ser	
135 140 145	
CTT AAA AAT ATA GCC TTT GCT AAA CAC AAG GAT AAT TTG CCT AAG CAT	537
Leu Lys Asn Ile Ala Phe Ala Lys His Lys Asp Asn Leu Pro Lys His	
150 155 160	
CTA AAT TCA AAA GAT TTA AAA TCT TTT ATA TAT ACT CTT ATA AAC TAT	585
Leu Asn Ser Lys Asp Leu Lys Ser Phe Ile Tyr Thr Leu Ile Asn Tyr	
165 170 175	

CAA ATC ATC TCT TTT TTA GAC TAC AAA CAA CAG CAT AAT GGC AAA TTG 489
 Gln Ile Ile Ser Phe Leu Asp Tyr Lys Gln Gln His Asn Gly Lys Leu
 135 140 145

TTA GTG AAA GTT TCC CCC ACA ATA TAC GAG TAAACTTGC CATTGTTGTG GGA 542
 Leu Val Lys Val Ser Pro Thr Ile Tyr Glu
 150 155

ATATCAACCA CAAGC 557

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

Met	Lys	Glu	Leu	Leu	Gly	Ile	Glu	Ile	Asp	Glu	Glu	Leu	Asp	Thr	Lys	1	5	10	15
Arg	Leu	Ile	Pro	Thr	Tyr	Ser	Lys	Leu	Tyr	Ser	Leu	Lys	Lys	Tyr	Ser	20	25	30	
Lys	Lys	Phe	Lys	Arg	Leu	Gln	Arg	Lys	Gln	Ser	Arg	Arg	Val	Leu	Lys	35	40	45	
Ser	Lys	Gln	Asn	Lys	Thr	Lys	Leu	Gly	Gly	Asn	Phe	Tyr	Lys	Thr	Gln	50	55	60	
Lys	Lys	Leu	Asn	Gln	Ala	Phe	Asp	Lys	Ser	Ser	His	Gln	Lys	Thr	Asp	65	70	75	80
Arg	Tyr	His	Lys	Ile	Thr	Ser	Glu	Leu	Ser	Lys	Gln	Phe	Glu	Leu	Ile	85	90	95	
Val	Val	Glu	Asp	Leu	Gln	Val	Lys	Asn	Met	Thr	Lys	Arg	Ala	Lys	Leu	100	105	110	
Lys	Asn	Val	Lys	Gln	Lys	Ser	Gly	Leu	Asn	Gln	Ser	Ile	Leu	Asn	Ala	115	120	125	
Ser	Phe	Tyr	Gln	Ile	Ile	Ser	Phe	Leu	Asp	Tyr	Lys	Gln	Gln	His	Asn	130	135	140	
Gly	Lys	Leu	Leu	Val	Lys	Val	Ser	Pro	Thr	Ile	Tyr	Glu				145	150	155	

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...519
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

```

ATAACAACC ATGACAACT AACGGACTTT AAGCAATACC AAACAGAC ATG AAA GAA      57
                                     Met Lys Glu
                                     1

TTA CTA GGG ATA GAA ATA GAT GAA GAG CTG GAT ACT AAA CGA CTT ATC      105
Leu Leu Gly Ile Glu Ile Asp Glu Glu Leu Asp Thr Lys Arg Leu Ile
   5                               10                               15

CCT ACT TAT TCC AAA TTG TAT TCT TTA AAA AAA TAC TCT AAA AAA TTT      153
Pro Thr Tyr Ser Lys Leu Tyr Ser Leu Lys Lys Tyr Ser Lys Lys Phe
  20                               25                               30                               35

AAA AGA TTA CAA AGA AAA CAA AGC CGT AGG GTG TTA AAG TCT AAA CAA      201
Lys Arg Leu Gln Arg Lys Gln Ser Arg Arg Val Leu Lys Ser Lys Gln
                               40                               45                               50

AAC AAA ACC AAA TTA GGA GGT AAT TTT TAC AAA ACC CAA AAG AAA TTA      249
Asn Lys Thr Lys Leu Gly Gly Asn Phe Tyr Lys Thr Gln Lys Lys Leu
                               55                               60                               65

AAC CAA GCC TTT GAC AAG TCT AGT CAT CAA AAA ACA GAC AGA TAC CAT      297
Asn Gln Ala Phe Asp Lys Ser Ser His Gln Lys Thr Asp Arg Tyr His
                               70                               75                               80

AAA ATC ACA AGC GAA CTT TCA AAG CAA TTT GAA TTG ATA GTA GTT GAA      345
Lys Ile Thr Ser Glu Leu Ser Lys Gln Phe Glu Leu Ile Val Val Glu
   85                               90                               95

GAT TTG CAA GTA AAA AAC ATG ACT AAA AGA GCT AAA CTC AAA AAT GTT      393
Asp Leu Gln Val Lys Asn Met Thr Lys Arg Ala Lys Leu Lys Asn Val
 100                               105                               110                               115

AAA CAA AAG AGT GGG CTT AAT CAA TCT ATT TTA AAC GCT TCA TTC TAT      441
Lys Gln Lys Ser Gly Leu Asn Gln Ser Ile Leu Asn Ala Ser Phe Tyr
                               120                               125                               130

```

TGG GTA GTG CAA CTT CTC AAA TAGAAAGTTT GAAAAAAGA GAAAATGCCC TATT 874
Trp Val Val Gln Leu Leu Lys
270

TGATCATTTA 884

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

[illegible]

GAA AAG TTT GCT AAA AAT TTA ACC CAA CTG ACA CAA GAA GAA TTC ATG	195
Glu Lys Phe Ala Lys Asn Leu Thr Gln Leu Thr Gln Glu Glu Phe Met	
45 50 55	
CGT TTA AGA GAG CCA CAA AAA CAA GTG GTC ATC AAA AAC ATA GGC AAT	243
Arg Leu Arg Glu Pro Gln Lys Gln Val Val Ile Lys Asn Ile Gly Asn	
60 65 70	
ATG ACA CGC CTG CAT TCA AAA AGA GCG ATG GAT TAT ATC GCT AAA CAT	291
Met Thr Arg Leu His Ser Lys Arg Ala Met Asp Tyr Ile Ala Lys His	
75 80 85 90	
GGT GAG CTA GTG AGA GAT GAA TTT TTT AAT GAA GTT AAT TAT AAT GAC	339
Gly Glu Leu Val Arg Asp Glu Phe Phe Asn Glu Val Asn Tyr Asn Asp	
95 100 105	
ATA GCA GAG CAA TGG AAT GAG CAA TTT GAA AAA TTA TTA GAA AAT AAG	387
Ile Ala Glu Gln Trp Asn Glu Gln Phe Glu Lys Leu Leu Glu Asn Lys	
110 115 120	
AGC CGT GTT AAA AAT TGC GCT TTA CAT CTA GTG TTT AGC ATT GAT GAA	435
Ser Arg Val Lys Asn Cys Ala Leu His Leu Val Phe Ser Ile Asp Glu	
125 130 135	
AAT TGT AAT GAA AAA AAT TTA AAA GCT TTG GAA TTA AGC GTG TAT CAA	483
Asn Cys Asn Glu Lys Asn Leu Lys Ala Leu Glu Leu Ser Val Tyr Gln	
140 145 150	
ACA CTC ACT AAC ACG CTA GGT TAT GAT TAT CCT TTT ATA ATG AAA CTC	531
Thr Leu Thr Asn Thr Leu Gly Tyr Asp Tyr Pro Phe Ile Met Lys Leu	
155 160 165 170	
CAT ACA CAC CAA AAC AAT CCG CAT GCG CAT GTG ATT ATC AAC AAA ACT	579
His Thr His Gln Asn Asn Pro His Ala His Val Ile Ile Asn Lys Thr	
175 180 185	
AAC AAA ATT ACC AAT AAG CAA CTA TGC TTT AAT TCT AAA GAC AGC TGT	627
Asn Lys Ile Thr Asn Lys Gln Leu Cys Phe Asn Ser Lys Asp Ser Cys	
190 195 200	
AAA GAG TTT TAC CAC ACA CTA AGA GAA ACA TTT AAA GAT TAT TTA TTT	675
Lys Glu Phe Tyr His Thr Leu Arg Glu Thr Phe Lys Asp Tyr Leu Phe	
205 210 215	
GCT AAC TCA AAA GGC GAA TTG CAA TAT TCT AAC ACG CCT AAT ATT TAT	723
Ala Asn Ser Lys Gly Glu Leu Gln Tyr Ser Asn Thr Pro Asn Ile Tyr	
220 225 230	
AAG GCG ATT AAA GAC ATA GAA ACA GAG CTA GAT GCA CTA GAA AAC AGG	771
Lys Ala Ile Lys Asp Ile Glu Thr Glu Leu Asp Ala Leu Glu Asn Arg	
235 240 245 250	
CTA GAA ACA ATA AGA GTT TTA GGC ATG AAA ACT ATT TTT ATA AAG TTT	819
Leu Glu Thr Ile Arg Val Leu Gly Met Lys Thr Ile Phe Ile Lys Phe	
255 260 265	

(2) INFORMATION FOR SEO ID NO:937:

(A) LENGTH: 884 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 22...840
(D) OTHER INFORMATION:

GGAGAATAAA	ATTACAATAA	A	ATG	GCG	TTA	GAA	AAA	AGT	TAT	AGT	AAA	AAC	51			
			Met	Ala	Leu	Glu	Lys	Ser	Tyr	Ser	Lys	Asn				
			1				5					10				
TTT	GAA	AGC	GAT	GAG	CTT	TTT	GAT	TAT	GAG	ATC	ATC	AAG	CCC	AAA	AAG	99
Phe	Glu	Ser	Asp	Glu	Leu	Phe	Asp	Tyr	Glu	Ile	Ile	Lys	Pro	Lys	Lys	
			15						20					25		
ACG	CTT	AAG	ATA	CAA	TAC	ACT	TAT	GCT	AAA	CGC	TAC	TAT	AAA	GAA	GTA	147
Thr	Leu	Lys	Ile	Gln	Tyr	Thr	Tyr	Ala	Lys	Arg	Tyr	Tyr	Lys	Glu	Val	
			30					35					40			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

```

Met Lys Arg Ser His Leu Glu Asn Ala Leu Asn Tyr Ala Leu Glu Asn
 1           5           10           15
Ser Glu Thr Ala Tyr Asn Glu Met Phe Leu Glu Cys Asp Lys Gln Phe
      20           25           30
Ile Leu Glu Ser Trp Leu Asn Asp Phe Asp Leu Thr Lys Asp Tyr Asn
      35           40           45
Glu Thr Met His Leu Val Phe Ser Ile Lys Asp Lys Pro Asp Glu Glu
      50           55           60
Thr Met Gln Gly Leu Leu His Ser Thr Trp Glu Ser Leu Lys Ile Arg
      65           70           75           80
Leu Pro Glu Tyr Lys Phe Ala Leu Val Pro His Ala His Gln Asp His
      85           90           95
Ala His Ile His Cys Phe Ile Asn Lys Thr Asn Gln Leu Thr Arg Arg
      100          105          110
Arg Leu Arg Phe Lys Gly His Glu Asp Cys Lys Glu Phe Phe Asn Glu
      115          120          125
Leu Arg Ser Glu Phe Ala Tyr Arg Leu Asn Asp His Leu Leu Ser Glu
      130          135          140
Glu Tyr Leu Tyr Val Asn Glu Pro Lys Leu Lys Glu Leu Asp Asn Ile
      145          150          155          160
Lys Gln Gln Leu Gln Asp Leu Glu Lys Glu Glu Lys Ala Leu Glu Gln
      165          170          175
Ile Lys Ser Pro Gln Asp Glu Trp Asp Leu Asn Lys Ala Leu Gln Ser
      180          185          190
Glu Tyr Leu Gln Glu Leu Lys Tyr Lys Asn Lys Ala Lys Ala Leu Asp
      195          200          205
Ile Gln Asn Asn His Ser Thr Pro Leu Lys Gln Lys Ile Ser Glu Phe
      210          215          220
Lys Ile Ala Leu Phe Asn His Lys Asp Thr Ser Asp Asp Glu Lys Glu
      225          230          235          240
Gln Leu Asp Ile Asp Arg Ile Asp Lys Arg Lys Pro Val Ser Glu His
      245          250          255
Leu Lys Asn Thr Asn Lys His Glu Leu Tyr Glu Leu Leu Gly Phe Tyr
      260          265          270
Gln Lys Glu Leu Asp Lys Lys Gln Asn His Ser Ala Phe Lys Asn Phe
      275          280          285
Ala Ile Leu Asn Gly Leu Asp Arg Asp Phe Glu Arg Glu Thr Asn Gly
      290          295          300
Tyr Ser Val Leu Lys Lys Lys Glu Met Leu Leu Asn Lys Leu Glu His
      305          310          315          320
Leu Asp Lys Arg Leu Leu Asp Lys Asn Ser His Leu Leu Leu Ala Gln
      325          330          335
Leu Arg Asn Glu Val Lys Thr Lys Gln Asn Ile Gln Tyr Asn Thr Leu
      340          345          350
Thr Asn Pro Ile Leu Leu Ala Lys Ala Leu Glu Leu Ser Lys Asp Lys
      355          360          365
Arg Pro Thr Leu Lys Thr Phe Lys Asn Ala Tyr Phe Ser Ala Arg Lys
      370          375          380
Tyr Gln Phe Met Leu Glu Ser Phe Lys Thr Lys Gln Asn Asp Pro Thr
      385          390          395          400
Tyr Lys Leu Asn Asp Asn Thr Tyr Glu Leu Val Ser Lys Gln Leu Gln
      405          410          415
Asp Tyr Gln Asn Thr Met Leu Leu Leu Ala Lys Glu Arg Leu Leu Phe

```

Leu Phe Leu Glu Gln Asp Leu Lys Gln Lys Glu Glu Glu Phe Glu Arg	
435 440 445	
GCC AAA GAA CAT TAT GTG AAA TCT TCA AAA CAT TAT AGA GAA ACT TCA	1452
Ala Lys Glu His Tyr Val Lys Ser Ser Lys His Tyr Arg Glu Thr Ser	
450 455 460	
TTG TCT CCA AAA GAA AAA CAA GGC TTT CTC AAA CAA ATT AAA CAA TTT	1500
Leu Ser Pro Lys Glu Lys Gln Gly Phe Leu Lys Gln Ile Lys Gln Phe	
465 470 475	
TCT AAA ATT TCT AAG GAT ATT CTC TAT ACT TGT AAT GAG ATC ATA GGA	1548
Ser Lys Ile Ser Lys Asp Ile Leu Tyr Thr Cys Asn Glu Ile Ile Gly	
480 485 490	
GCT AAT AGG TTT TTA ACC CAC TAT GAC AAC CTA AAC CTT GAA AAA GTC	1596
Ala Asn Arg Phe Leu Thr His Tyr Asp Asn Leu Asn Leu Glu Lys Val	
495 500 505 510	
CTA GAA CAC GCT AAA GAT ACT AAG CTA GAG CAA AAA GAA ATT CAA GCT	1644
Leu Glu His Ala Lys Asp Thr Lys Leu Glu Gln Lys Glu Ile Gln Ala	
515 520 525	
ATC ACA AAA GAG CCT AAT AAC GAT GAG CCT TGG ATT GAG TTT GGT AAA	1692
Ile Thr Lys Glu Pro Asn Asn Asp Glu Pro Trp Ile Glu Phe Gly Lys	
530 535 540	
AAA GAA CAA GCT AGA GCT AAA GCA CAC TAT CAA GCT ATG CTA GAA AAA	1740
Lys Glu Gln Ala Arg Ala Lys Ala His Tyr Gln Ala Met Leu Glu Lys	
545 550 555	
GAA AAA GCT AAA GAA TTA GCT AAA CAA CAA GCT AAC ACC TTG CAC TCT	1788
Glu Lys Ala Lys Glu Leu Ala Lys Gln Gln Ala Asn Thr Leu His Ser	
560 565 570	
AAT GAG CTT GAT GAT GAC CCT AAA GCT CAT GCT GGA TTA AAA CAA AAT	1836
Asn Glu Leu Asp Asp Asp Pro Lys Ala His Ala Gly Leu Lys Gln Asn	
575 580 585 590	
GAC AAC ACA AAC TTT AAA GGG CGT AAT AGA TAATGCTCTC AAGCGATGAT TGC	1889
Asp Asn Thr Asn Phe Lys Gly Arg Asn Arg	
595 600	
CTTTAATGTT CTTAATAAAG AATATACCCT TTGAAAGGGG TTTAT	1934

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

210	215	220	
GAA TTT AAA ATC GCT CTG TTT AAT CAC AAA GAC ACA AGC GAT GAT GAA			780
Glu Phe Lys Ile Ala Leu Phe Asn His Lys Asp Thr Ser Asp Asp Glu			
225	230	235	
AAA GAA CAG CTA GAT ATT GAC AGG ATA GAT AAG AGA AAA CCA GTA AGC			828
Lys Glu Gln Leu Asp Ile Asp Arg Ile Asp Lys Arg Lys Pro Val Ser			
240	245	250	
GAA CAC TTA AAA AAC ACT AAC AAA CAC GAG CTA TAC GAA CTC TTA GGC			876
Glu His Leu Lys Asn Thr Asn Lys His Glu Leu Tyr Glu Leu Leu Gly			
255	260	265	270
TTT TAT CAA AAA GAA TTA GAT AAA AAA CAA AAC CAT TCA GCC TTT AAG			924
Phe Tyr Gln Lys Glu Leu Asp Lys Lys Gln Asn His Ser Ala Phe Lys			
275	280	285	
AAT TTT GCT ATT CTC AAT GGT TTA GAC AGA GAC TTT GAA AGA GAG ACT			972
Asn Phe Ala Ile Leu Asn Gly Leu Asp Arg Asp Phe Glu Arg Glu Thr			
290	295	300	
AAT GGC TAT TCT GTT TTA AAG AAA AAA GAA ATG CTT TTA AAT AAG CTT			1020
Asn Gly Tyr Ser Val Leu Lys Lys Lys Glu Met Leu Leu Asn Lys Leu			
305	310	315	
GAA CAC CTA GAC AAA CGC CTT TTA GAT AAA AAC TCA CAC TTA CTA TTA			1068
Glu His Leu Asp Lys Arg Leu Leu Asp Lys Asn Ser His Leu Leu Leu			
320	325	330	
GCC CAG CTA AGA AAT GAA GTT AAA ACC AAG CAA AAC ATC CAA TAC AAC			1116
Ala Gln Leu Arg Asn Glu Val Lys Thr Lys Gln Asn Ile Gln Tyr Asn			
335	340	345	350
ACT CTA ACT AAT CCT ATT CTT TTA GCC AAA GCC TTA GAA CTT TCT AAA			1164
Thr Leu Thr Asn Pro Ile Leu Leu Ala Lys Ala Leu Glu Leu Ser Lys			
355	360	365	
GAT AAA CGC CCC ACT CTC AAA ACT TTT AAA AAC GCT TAT TTT AGT GCT			1212
Asp Lys Arg Pro Thr Leu Lys Thr Phe Lys Asn Ala Tyr Phe Ser Ala			
370	375	380	
AGA AAA TAT CAA TTC ATG CTA GAG AGC TTT AAA ACT AAG CAA AAT GAC			1260
Arg Lys Tyr Gln Phe Met Leu Glu Ser Phe Lys Thr Lys Gln Asn Asp			
385	390	395	
CCC ACT TAC AAG CTT AAT GAT AAC ACT TAT GAG CTA GTG AGT AAG CAA			1308
Pro Thr Tyr Lys Leu Asn Asp Asn Thr Tyr Glu Leu Val Ser Lys Gln			
400	405	410	
CTA CAA GAC TAT CAA AAC ACC ATG CTT TTA TTA GCC AAA GAG AGA TTA			1356
Leu Gln Asp Tyr Gln Asn Thr Met Leu Leu Leu Ala Lys Glu Arg Leu			
415	420	425	430
CTT TTT TTA GAA CAA GAT TTA AAA CAA AAA GAA GAA GAG TTT GAA AGA			1404

AAACATAGGG CAAATCTAGT TGGCACAAAA ACAGCTAGTC CTGTGCTTAT TAAAAACATA	60
GGGCAA ATG AAA CGC TCC CAC TTA GAA AAT GCC CTA AAT TAT GCT TTA	108
Met Lys Arg Ser His Leu Glu Asn Ala Leu Asn Tyr Ala Leu	
1 5 10	
GAA AAT AGC GAA ACA GCT TAC AAT GAA ATG TTT TTA GAA TGC GAT AAG	156
Glu Asn Ser Glu Thr Ala Tyr Asn Glu Met Phe Leu Glu Cys Asp Lys	
15 20 25 30	
CAA TTC ATC TTA GAG AGT TGG CTC AAT GAC TTT GAT TTG ACT AAA GAT	204
Gln Phe Ile Leu Glu Ser Trp Leu Asn Asp Phe Asp Leu Thr Lys Asp	
35 40 45	
TAT AAC GAG ACT ATG CAC TTA GTT TTT TCT ATC AAA GAT AAG CCA GAT	252
Tyr Asn Glu Thr Met His Leu Val Phe Ser Ile Lys Asp Lys Pro Asp	
50 55 60	
GAA GAG ACA ATG CAA GGG CTT TTA CAT TCT ACT TGG GAG AGC TTA AAA	300
Glu Glu Thr Met Gln Gly Leu Leu His Ser Thr Trp Glu Ser Leu Lys	
65 70 75	
ATA AGA TTG CCT GAA TAC AAG TTT GCC CTT GTG CCA CAC GCT CAT CAA	348
Ile Arg Leu Pro Glu Tyr Lys Phe Ala Leu Val Pro His Ala His Gln	
80 85 90	
GAC CAT GCC CAT ATC CAT TGT TTT ATC AAT AAG ACT AAT CAG CTC ACA	396
Asp His Ala His Ile His Cys Phe Ile Asn Lys Thr Asn Gln Leu Thr	
95 100 105 110	
CGA AGA AGA CTG CGT TTT AAG GGG CAT GAA GAT TGT AAA GAA TTT TTT	444
Arg Arg Arg Leu Arg Phe Lys Gly His Glu Asp Cys Lys Glu Phe Phe	
115 120 125	
AAT GAA TTA AGA AGT GAG TTT GCT TAT AGG TTG AAT GAC CAC TTA TTG	492
Asn Glu Leu Arg Ser Glu Phe Ala Tyr Arg Leu Asn Asp His Leu Leu	
130 135 140	
AGC GAA GAA TAC TTG TAT GTC AAT GAG CCA AAA CTT AAA GAG CTA GAC	540
Ser Glu Glu Tyr Leu Tyr Val Asn Glu Pro Lys Leu Lys Glu Leu Asp	
145 150 155	
AAT ATC AAA CAA CAA TTA CAA GAC TTG GAA AAA GAA GAA AAA GCC TTA	588
Asn Ile Lys Gln Gln Leu Gln Asp Leu Glu Lys Glu Glu Lys Ala Leu	
160 165 170	
GAA CAA ATC AAA TCC CCA CAA GAT GAG TGG GAC TTA AAC AAG GCT TTA	636
Glu Gln Ile Lys Ser Pro Gln Asp Glu Trp Asp Leu Asn Lys Ala Leu	
175 180 185 190	
CAA AGC GAG TAT TTA CAA GAA CTC AAA TAT AAA AAC AAA GCA AAA GCC	684
Gln Ser Glu Tyr Leu Gln Glu Leu Lys Tyr Lys Asn Lys Ala Lys Ala	
195 200 205	
CTA GAC ATT CAA AAT AAC CAC AGC ACC CCT TTA AAA CAA AAG ATT TCT	732
Leu Asp Ile Gln Asn Asn His Ser Thr Pro Leu Lys Gln Lys Ile Ser	

Gly Thr Ile Gln Thr Glu Ala Leu Glu Gln Glu Ile Glu Trp Phe Ser
 50 55 60

CAA GAC TAT CAC ATT CCT ATG GAG AAT ATT TTA CAT GTC CTT TCT ATC 299
 Gln Asp Tyr His Ile Pro Met Glu Asn Ile Leu His Val Leu Ser Ile
 65 70 75

AAT CCC TAT CAA TGAAAAGAGC CTTAGTTTTC TCAAAAACAA CTTTCAAGCT 351
 Asn Pro Tyr Gln
 80

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

Met Ser Phe Ala Pro Met Leu Leu Ala Thr Ile Asn Asn Ser Ile Gly
 1 5 10 15
 Asn Lys Asp Lys His Val Ser Leu Glu Tyr Leu Ile Gly Leu Phe Met
 20 25 30
 Asp Lys Lys Thr Thr Asn Leu Ser Asn Thr Asp Lys Tyr Ile Ile Gly
 35 40 45
 Thr Ile Gln Thr Glu Ala Leu Glu Gln Glu Ile Glu Trp Phe Ser Gln
 50 55 60
 Asp Tyr His Ile Pro Met Glu Asn Ile Leu His Val Leu Ser Ile Asn
 65 70 75 80
 Pro Tyr Gln

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...1866
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

```

65          70          75          80
Thr Asp Pro Thr Ala Asn His Asn Lys Gln Gly Ile His Tyr Cys Thr
          85          90          95
Glu Asn Lys Lys Thr Gly Lys Cys Asp Pro Ile Asp Asn Val Phe Arg
          100          105          110
Thr Thr Arg Leu Asp Asn Glu Leu Glu Gln Glu Ile Gln Thr Leu Thr
          115          120          125
Leu Asp Leu Thr Lys Ala Pro Asn Lys Asp Ala Gln Ser Gln Ala Tyr
          130          135          140
Ala Asn Phe Asn Gln Arg Ile Lys Leu Leu Thr Leu Lys Tyr Leu Lys
145          150          155          160
Glu Ile Thr Asn Gln Met Leu Phe Leu Asn Gln Thr Met Ala Met Gln
          165          170          175
Ser Glu Ile Met Ala Asp Asp Tyr Phe Arg Gln Asn Asn Asp Gly Phe
          180          185          190
Gly Lys Glu Glu Asn His Ile Asp Lys Gln Leu Thr Gln Lys Arg Ile
          195          200          205
Asn Glu Arg Glu Arg Ala Arg Ile Tyr Phe Gln Asn Pro Asn Val Lys
          210          215          220
Phe Asp Gln Phe Gly Phe Pro Ile Phe Ser Ile Trp Asp
225          230          235

```

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 63...311
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

```

TCAAACCAAA ACCAACACAA AATTTGCTAA ACTACAATCA AATCAATTTA GGGAGGATAA      60
AA ATG TCA TTT GCC CCT ATG TTA TTA GCT ACA ATC AAT AAC TCT ATT      107
Met Ser Phe Ala Pro Met Leu Leu Ala Thr Ile Asn Asn Ser Ile
   1             5             10             15

GGC AAT AAA GAT AAG CAT GTG AGT TTA GAG TAT CTT ATA GGG CTT TTT      155
Gly Asn Lys Asp Lys His Val Ser Leu Glu Tyr Leu Ile Gly Leu Phe
          20             25             30

ATG GAT AAA AAA ACA ACT AAT CTA AGC AAT ACT GAC AAG TAT ATT ATA      203
Met Asp Lys Lys Thr Thr Asn Leu Ser Asn Thr Asp Lys Tyr Ile Ile
          35             40             45

GGC ACA ATT CAA ACA GAG GCA CTA GAG CAA GAA ATA GAA TGG TTT TCA      251

```

CGC TTA GAT AAC GAA TTA GAA CAA GAA ATC CAA ACG CTC ACA CTT GAT	441
Arg Leu Asp Asn Glu Leu Glu Gln Glu Ile Gln Thr Leu Thr Leu Asp	
115 120 125 130	
TTA ACC AAA GCC CCC AAT AAA GAC GCT CAA AGC CAA GCC TAC GCA AAT	489
Leu Thr Lys Ala Pro Asn Lys Asp Ala Gln Ser Gln Ala Tyr Ala Asn	
135 140 145	
TTC AAT CAA AGG ATT AAA TTA CTT ACT CTA AAA TAT TTA AAA GAA ATT	537
Phe Asn Gln Arg Ile Lys Leu Leu Thr Leu Lys Tyr Leu Lys Glu Ile	
150 155 160	
ACC AAT CAA ATG CTC TTT TTA AAT CAA ACA ATG GCA ATG CAA AGC GAG	585
Thr Asn Gln Met Leu Phe Leu Asn Gln Thr Met Ala Met Gln Ser Glu	
165 170 175	
ATT ATG GCA GAT GAT TAT TTT AGG CAA AAT AAT GAT GGC TTT GGG AAA	633
Ile Met Ala Asp Asp Tyr Phe Arg Gln Asn Asn Asp Gly Phe Gly Lys	
180 185 190	
GAA GAA AAC CAT ATA GAC AAA CAA TTA ACG CAA AAA AGA ATA AAC GAA	681
Glu Glu Asn His Ile Asp Lys Gln Leu Thr Gln Lys Arg Ile Asn Glu	
195 200 205 210	
AGA GAA AGA GCC AGA ATA TAC TTT CAA AAC CCT AAT GTT AAA TTT GAC	729
Arg Glu Arg Ala Arg Ile Tyr Phe Gln Asn Pro Asn Val Lys Phe Asp	
215 220 225	
CAA TTT GGT TTT CCC ATT TTT AGT ATA TGG GAT TAAGGGTTTA GTGATGAGAG	782
Gln Phe Gly Phe Pro Ile Phe Ser Ile Trp Asp	
230 235	
ATAGAATAAG TATTTTTTTT CCAAACCTATT CCTATTTTAG TGGTAGTGTT G	833

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

Met Gln Ser Leu Ala Gly Gly Leu Ser Gly Arg Ala Trp Gly Glu Met	
1 5 10 15	
Leu Cys Lys Met Val Asn Asp Ser Asn Tyr Glu Ser Glu Gln Ala Leu	
20 25 30	
Leu Ala Thr Gly Asn Ser Ser Glu Gln Lys Arg Arg Phe Leu Leu	
35 40 45	
Arg Val Lys Lys Lys Val Asn Asp Asn Arg Gln Leu Lys Lys Lys Leu	
50 55 60	
Asp Pro Phe Leu Lys Arg Leu Asp Val Leu Gln Thr Glu Phe Gly Val	

Pro Lys 260 265 270

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...762
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

TAGCGGTTGG	GTAATTC	ACT	CCAATCTCTA	AGTGGCAGTG	GCTATGAAAA	C	ATG	CAA	57
							Met	Gln	
							1		
TCA	CTT	GCT	GGG	GGA	TTG	AGT	GGT	AGA	105
Ser	Leu	Ala	Gly	Gly	Leu	Ser	Gly	Arg	
	5				10			Trp	
								Gly	
								Glu	
								Met	
								Leu	
								Cys	
AAA	ATG	GTA	AAC	GAT	AGT	AAT	TAT	GAA	153
Lys	Met	Val	Asn	Asp	Ser	Asn	Tyr	Glu	
	20					25		Ser	
								Glu	
								Gln	
								Ala	
								Leu	
								Leu	
								Ala	
ACA	GGC	AAT	AGC	TCA	GAA	GAG	CAA	AAA	201
Thr	Gly	Asn	Ser	Ser	Glu	Glu	Gln	Lys	
	35				40			Arg	
								Arg	
								Phe	
								Leu	
								Leu	
								Arg	
								Val	
AAG	AAA	AAG	GTT	AAT	GAT	AAT	AGG	CAG	249
Lys	Lys	Lys	Val	Asn	Asp	Asn	Arg	Gln	
				55				Leu	
								Lys	
								Lys	
								Lys	
								Leu	
								Asp	
								Pro	
TTT	CTA	AAA	AGA	CTT	GAT	GTC	CTA	CAA	297
Phe	Leu	Lys	Arg	Leu	Asp	Val	Leu	Gln	
				70				Thr	
								Glu	
								Phe	
								Gly	
								Val	
								Thr	
								Asp	
CCT	ACA	GCT	AAC	CAT	AAT	AAG	CAA	GGG	345
Pro	Thr	Ala	Asn	His	Asn	Lys	Gln	Gly	
								Ile	
								His	
								Tyr	
								Cys	
								Thr	
								Glu	
								Asn	
AAA	AAG	ACA	GGT	AAA	TGC	GAC	CCT	ATT	393
Lys	Lys	Thr	Gly	Lys	Cys	Asp	Pro	Ile	
	100					105		Asp	
								Asn	
								Val	
								Phe	
								Arg	
								Thr	
								Thr	

CTC ATT GAA CGC ATC AAA AAC GCC CTA GAC GCT AAC CAC ATT GAA ATC 824
 Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp Ala Asn His Ile Glu Ile
 245 250 255

CCT TTC AAC AAG CTA GAT ATT GCT ATT AAA AAT CAA GAC TCT CCT AAA T 873
 Pro Phe Asn Lys Leu Asp Ile Ala Ile Lys Asn Gln Asp Ser Pro Lys
 260 265 270

GATTGGTGTG AGATGTATTG ATTGTAG 900

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

Met	Asp	Glu	Ile	Lys	Thr	Leu	Leu	Val	Asp	Phe	Phe	Pro	Gln	Ala	Lys	1	5	10	15
His	Phe	Gly	Ile	Ile	Leu	Ile	Lys	Ala	Ile	Val	Val	Phe	Cys	Ile	Gly	20	25	30	
Phe	Tyr	Phe	Ser	Phe	Phe	Leu	Gln	Lys	Lys	Thr	Met	Lys	Phe	Leu	Ser	35	40	45	
Lys	Lys	Asp	Glu	Ile	Leu	Ala	Asn	Phe	Val	Ala	Gln	Val	Thr	Phe	Ile	50	55	60	
Leu	Ile	Leu	Ile	Ile	Thr	Thr	Ile	Ile	Ala	Leu	Ser	Thr	Leu	Gly	Val	65	70	75	80
Gln	Thr	Thr	Ser	Ile	Ile	Thr	Val	Leu	Gly	Thr	Val	Gly	Ile	Ala	Val	85	90	95	
Ala	Leu	Ala	Leu	Lys	Asp	Tyr	Leu	Ser	Ser	Ile	Ala	Gly	Gly	Ile	Ile	100	105	110	
Leu	Ile	Ile	Leu	His	Pro	Phe	Lys	Lys	Gly	Asp	Ile	Ile	Glu	Ile	Ser	115	120	125	
Gly	Leu	Glu	Gly	Lys	Val	Glu	Ala	Leu	Asn	Phe	Phe	Asn	Thr	Ser	Leu	130	135	140	
Arg	Leu	His	Asp	Gly	Arg	Leu	Ala	Val	Leu	Pro	Asn	Arg	Ser	Val	Ala	145	150	155	160
Asn	Ser	Asn	Ile	Ile	Asn	Ser	Asn	Asn	Thr	Ala	Cys	Arg	Arg	Ile	Glu	165	170	175	
Trp	Val	Cys	Gly	Val	Gly	Tyr	Gly	Ser	Asp	Ile	Glu	Leu	Val	His	Lys	180	185	190	
Thr	Ile	Lys	Asp	Val	Ile	Asp	Ala	Met	Glu	Lys	Ile	Asp	Lys	Asn	Met	195	200	205	
Pro	Thr	Phe	Ile	Gly	Ile	Thr	Asp	Phe	Gly	Gln	Ser	Ser	Leu	Asn	Phe	210	215	220	
Thr	Ile	Arg	Val	Trp	Ala	Lys	Ile	Glu	Asp	Gly	Ile	Phe	Asn	Val	Arg	225	230	235	240
Ser	Glu	Leu	Ile	Glu	Arg	Ile	Lys	Asn	Ala	Leu	Asp	Ala	Asn	His	Ile	245	250	255	
Glu	Ile	Pro	Phe	Asn	Lys	Leu	Asp	Ile	Ala	Ile	Lys	Asn	Gln	Asp	Ser				

Gly	Ile	Ile	Leu	Ile	Lys	Ala	Ile	Val	Val	Phe	Cys	Ile	Gly	Phe	Tyr		
20						25					30						
TTT	TCA	TTT	TTC	TTA	CAA	AAA	AAA	ACC	ATG	AAA	TTT	TTA	TCC	AAA	AAG	200	
Phe	Ser	Phe	Phe	Leu	Gln	Lys	Lys	Thr	Met	Lys	Phe	Leu	Ser	Lys	Lys		
35					40				45					50			
GAT	GAG	ATT	TTA	GCG	AAT	TTT	GTC	GCA	CAG	GTT	ACT	TTT	ATC	TTA	ATC	248	
Asp	Glu	Ile	Leu	Ala	Asn	Phe	Val	Ala	Gln	Val	Thr	Phe	Ile	Leu	Ile		
				55				60						65			
CTT	ATC	ATC	ACC	ACA	ATC	ATT	GCG	CTC	AGC	ACG	CTA	GGC	GTG	CAA	ACC	296	
Leu	Ile	Ile	Thr	Thr	Ile	Ile	Ala	Leu	Ser	Thr	Leu	Gly	Val	Gln	Thr		
			70					75					80				
ACC	TCT	ATT	ATC	ACT	GTT	TTA	GGA	ACG	GTA	GGG	ATT	GCT	GTG	GCG	TTG	344	
Thr	Ser	Ile	Ile	Thr	Val	Leu	Gly	Thr	Val	Gly	Ile	Ala	Val	Ala	Leu		
		85					90					95					
GCT	TTA	AAA	GAT	TAT	CTT	TCA	AGC	ATT	GCT	GGA	GGG	ATA	ATC	CTT	ATT	392	
Ala	Leu	Lys	Asp	Tyr	Leu	Ser	Ser	Ile	Ala	Gly	Gly	Ile	Ile	Leu	Ile		
	100					105					110						
ATC	TTG	CAC	CCT	TTC	AAA	AAA	GGA	GAC	ATC	ATT	GAA	ATC	TCT	GGC	CTA	440	
Ile	Leu	His	Pro	Phe	Lys	Lys	Gly	Asp	Ile	Ile	Glu	Ile	Ser	Gly	Leu		
115					120				125					130			
GAG	GGC	AAA	GTA	GAA	GCG	CTT	AAT	TTT	TTT	AAC	ACT	TCT	TTA	CGC	TTG	488	
Glu	Gly	Lys	Val	Glu	Ala	Leu	Asn	Phe	Phe	Asn	Thr	Ser	Leu	Arg	Leu		
				135				140						145			
CAT	GAC	GGA	CGC	TTG	GCG	GTT	TTA	CCC	AAT	AGA	AGT	GTC	GCT	AAT	TCT	536	
His	Asp	Gly	Arg	Leu	Ala	Val	Leu	Pro	Asn	Arg	Ser	Val	Ala	Asn	Ser		
			150					155					160				
AAT	ATT	ATC	AAT	AGC	AAT	AAC	ACG	GCG	TGT	CGG	CGC	ATT	GAA	TGG	GTT	584	
Asn	Ile	Ile	Asn	Ser	Asn	Asn	Thr	Ala	Cys	Arg	Arg	Ile	Glu	Trp	Val		
		165					170					175					
TGT	GGG	GTA	GGG	TAT	GGG	AGC	GAT	ATT	GAA	CTG	GTG	CAT	AAG	ACT	ATA	632	
Cys	Gly	Val	Gly	Tyr	Gly	Ser	Asp	Ile	Glu	Leu	Val	His	Lys	Thr	Ile		
	180					185					190						
AAA	GAT	GTT	ATT	GAT	GCA	ATG	GAA	AAA	ATT	GAT	AAA	AAC	ATG	CCC	ACT	680	
Lys	Asp	Val	Ile	Asp	Ala	Met	Glu	Lys	Ile	Asp	Lys	Asn	Met	Pro	Thr		
195					200					205				210			
TTT	ATT	GGG	ATC	ACG	GAT	TTT	GGA	CAA	AGT	TCG	CTG	AAT	TTC	ACC	ATT	728	
Phe	Ile	Gly	Ile	Thr	Asp	Phe	Gly	Gln	Ser	Ser	Leu	Asn	Phe	Thr	Ile		
				215					220					225			
AGG	GTT	TGG	GCA	AAG	ATT	GAA	GAC	GGA	ATC	TTT	AAT	GTG	CGC	AGC	GAA	776	
Arg	Val	Trp	Ala	Lys	Ile	Glu	Asp	Gly	Ile	Phe	Asn	Val	Arg	Ser	Glu		
			230					235					240				

5

70

75

CTCATAC

311

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

```

Met Val Val Ser Met Asn Cys Ile Gly Ser Lys Tyr Lys Leu Ile Ala
 1             5             10             15
Phe Ile Gln Glu Asn Ile His Ala Val Val Gly Gln Pro Phe Gly Cys
      20             25             30
Asp Phe Leu Arg Ser Val Arg Trp Asp Gly Tyr Arg Gly Val Cys Val
      35             40             45
Lys Trp Ser Leu Gly Ser Thr Leu Lys Asn Ile Phe Ser Leu Asp Ser
      50             55             60
Val Leu Lys Ala Asn Gln Val Ile Pro Lys Asp Ala
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...872
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

```

AAAATTAAGT TGTTTGATCG CTTTAAACG ATTTTAAAA GGAAAAATTT ATG GAT      56
                                     Met Asp
                                     1

GAA ATT AAA ACG CTG TTA GTG GAT TTT TTT CCG CAG GCA AAG CAT TTT      104
Glu Ile Lys Thr Leu Leu Val Asp Phe Phe Pro Gln Ala Lys His Phe
      5             10             15

GGG ATA ATC TTA ATC AAG GCT ATT GTT GTC TTT TGT ATA GGT TTT TAT      152

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

```

Met Ile Val Ser Phe Ile Ala Val Pro Cys Tyr Tyr Val Leu Leu Ala
 1           5           10           15
Met Glu Tyr Gln Ile Ala Tyr Glu His Pro Gly Glu Leu Ile Ser Thr
      20           25           30
Ile Gly Phe Val Ala Leu Ala Val Leu Val Tyr Tyr Leu Trp Gly Lys
      35           40           45
Trp Glu Lys Leu Leu Trp Gly Ala Pro Ser Asn Gln Glu Gln Gln Leu
      50           55           60
Ser Asn Gln Gly Asn Gln Asn Gln
      65           70

```

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...287
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

```

TAGGAAAAAG ACTATCATGC GAGCTATCCA AATTAGATCC GATCAAAAAC TACCCTTTA A      60
                                         Me

TGG TTG TAT CAA TGA ACT GCA TCG GCT CTA AAT ACA AAC TCA TTG CCT      108
t Val Val Ser Met Asn Cys Ile Gly Ser Lys Tyr Lys Leu Ile Ala Ph
1           5           10           15

TTA TTC AAG AAA ATA TCC ATG CGG TTG TGG GGC AAC CTT TTG GGT GTG      156
e Ile Gln Glu Asn Ile His Ala Val Val Gly Gln Pro Phe Gly Cys As
      20           25           30

ATT TTT TGC GAT CTG TTC GCT GGG ACG GGT ATC GTG GGG TGT GCG TAA      204
p Phe Leu Arg Ser Val Arg Trp Asp Gly Tyr Arg Gly Val Cys Val Ly
      35           40           45

AGT GGT CTC TAG GTT CAA CAC TAA AAA ACA TTT TTT CAT TAG ACA GCG      252
s Trp Ser Leu Gly Ser Thr Leu Lys Asn Ile Phe Ser Leu Asp Ser Va
      50           55           60           6

TGT TAA AAG CCA ATC AAG TTA TCC CTA AAG ATG CT TAACATGTTA AAATAAT      304
l Leu Lys Ala Asn Gln Val Ile Pro Lys Asp Ala

```

	180	185	190
Leu Gln Ala Phe Phe Ser Leu Thr Asn Tyr			
195	200		

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 65...280
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

AATTCAAGAA GGCAAAAAAT TATCTTTTTT CCTCGAATCA ATCATTAGGT TATTTTTTTGG	60
TTTT ATG ATA GTT TCT TTT ATT GCC GTT CCA TGC TAC TAT GTT TTA TTG	109
Met Ile Val Ser Phe Ile Ala Val Pro Cys Tyr Tyr Val Leu Leu	
1 5 10 15	
GCG ATG GAA TAC CAA ATA GCC TAT GAA CAC CCA GGA GAA TTA ATA AGC	157
Ala Met Glu Tyr Gln Ile Ala Tyr Glu His Pro Gly Glu Leu Ile Ser	
20 25 30	
ACG ATT GGT TTT GTT GCG TTA GCA GTG CTT GTG TAT TAC TTA TGG GGT	205
Thr Ile Gly Phe Val Ala Leu Ala Val Leu Val Tyr Tyr Leu Trp Gly	
35 40 45	
AAA TGG GAG AAG TTG CTA TGG GGC GCA CCT TCC AAT CAA GAG CAA CAA	253
Lys Trp Glu Lys Leu Leu Trp Gly Ala Pro Ser Asn Gln Glu Gln Gln	
50 55 60	
CTC TCC AAT CAA GGC AAC CAA AAT CAA TGATTGTGAT TGATCGCTAG GTCAATC	307
Leu Ser Asn Gln Gly Asn Gln Asn Gln	
65 70	
TGA	310

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

	140	145	150	
ACC CTT ATG CAG TAT TCG CCC ATT TAC TCC ATA ATC AAA CTT CTT GCT				533
Thr Leu Met Gln Tyr Ser Pro Ile Tyr Ser Ile Ile Lys Leu Leu Ala				
	155	160	165	
CAT TTT AAT ATA GAG ATC ACT TCT AAG ATT ATC ATT TCT CTT GTT TGG				581
His Phe Asn Ile Glu Ile Thr Ser Lys Ile Ile Ile Ser Leu Val Trp				
	170	175	180	
GTG TGT ATA GGG CTG TAT TTT TTG TTA TTG CAA GCG TTT TTT AGT CTT				629
Val Cys Ile Gly Leu Tyr Phe Leu Leu Leu Gln Ala Phe Phe Ser Leu				
	185	190	195	
ACA AAT TAT TAGTTGCAGA AAATTCAAGA AGGCAAAAAA TTATCTTTTT TCCTCGAAT				687
Thr Asn Tyr				
	200			
CAATCATTAG GTTATTTTTT GGTTTTATGA TAG				720

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

Met	Asn	Val	Leu	Ile	Arg	Leu	Cys	Phe	Ile	Phe	Leu	Ile	Gly	Phe	Phe
1				5					10					15	
Gly	Ala	Asn	Lys	Thr	Leu	Asn	Ala	Thr	Ala	Ile	Leu	Ser	Leu	Asp	Phe
			20					25					30		
Gly	Ser	Phe	Ser	Met	Pro	Ile	Thr	Ala	Asn	Phe	Ser	Asp	Gly	Ala	Leu
		35					40					45			
Asn	Val	Phe	Lys	Trp	Phe	Glu	Lys	His	Pro	Ser	Val	Gly	Val	Lys	Val
	50					55				60					
Gly	Arg	Leu	Ala	Asn	Gln	Asp	Asp	Thr	Ile	Phe	Thr	Leu	Val	Phe	Ile
65					70					75				80	
Val	Ile	Val	Val	Ala	Ile	Ile	Ala	Leu	Ile	Ala	Ile	Phe	Ile	Arg	Ser
			85					90					95		
Ile	Leu	Leu	Asn	Thr	Ile	Phe	Val	Gly	Ser	Leu	Ile	Gly	Ser	Leu	Trp
		100						105					110		
Leu	Tyr	Met	Val	Gly	Phe	Tyr	Tyr	Phe	Tyr	Gly	Val	Pro	Phe	Leu	Ser
		115					120					125			
Tyr	Leu	Ser	Gly	Cys	Tyr	Glu	Ser	Phe	Ser	Phe	Ser	Ala	Cys	Tyr	Pro
	130					135					140				
His	Ser	Leu	Gln	Leu	Leu	Pro	Thr	Leu	Met	Gln	Tyr	Ser	Pro	Ile	Tyr
145					150					155					160
Ser	Ile	Ile	Lys	Leu	Leu	Ala	His	Phe	Asn	Ile	Glu	Ile	Thr	Ser	Lys
			165						170					175	
Ile	Ile	Ile	Ser	Leu	Val	Trp	Val	Cys	Ile	Gly	Leu	Tyr	Phe	Leu	Leu

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...638
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

AAGCTTATAA AATCATCAAA AAGAGTGCTG AA ATG AAT GTT TTA ATC AGA TTG	53
Met Asn Val Leu Ile Arg Leu	
1 5	
TGC TTT ATT TTT TTG ATT GGG TTT TTT GGC GCG AAT AAA ACC CTA AAC	101
Cys Phe Ile Phe Leu Ile Gly Phe Phe Gly Ala Asn Lys Thr Leu Asn	
10 15 20	
GCA ACA GCC ATT CTT TCT CTT GAC TTT GGC TCT TTT TCC ATG CCA ATC	149
Ala Thr Ala Ile Leu Ser Leu Asp Phe Gly Ser Phe Ser Met Pro Ile	
25 30 35	
ACT GCC AAT TTC TCA GAT GGT GCG TTA AAT GTA TTC AAA TGG TTT GAA	197
Thr Ala Asn Phe Ser Asp Gly Ala Leu Asn Val Phe Lys Trp Phe Glu	
40 45 50 55	
AAA CAC CCA TCA GTG GGT GTT AAA GTT GGT CGG CTT GCA AAT CAA GAC	245
Lys His Pro Ser Val Gly Val Lys Val Gly Arg Leu Ala Asn Gln Asp	
60 65 70	
GAC ACT ATC TTT ACT CTA GTT TTC ATT GTG ATA GTT GTC GCA ATA ATT	293
Asp Thr Ile Phe Thr Leu Val Phe Ile Val Ile Val Val Ala Ile Ile	
75 80 85	
GCC CTT ATC GCT ATT TTT ATA AGG AGT ATA TTA CTA AAC ACA ATT TTT	341
Ala Leu Ile Ala Ile Phe Ile Arg Ser Ile Leu Leu Asn Thr Ile Phe	
90 95 100	
GTA GGA TCG CTC ATA GGA TCC TTA TGG TTG TAT ATG GTA GGG TTT TAT	389
Val Gly Ser Leu Ile Gly Ser Leu Trp Leu Tyr Met Val Gly Phe Tyr	
105 110 115	
TAT TTT TAT GGT GTT CCC TTT TTG AGT TAT TTG AGC GGT TGT TAT GAA	437
Tyr Phe Tyr Gly Val Pro Phe Leu Ser Tyr Leu Ser Gly Cys Tyr Glu	
120 125 130 135	
TCG TTT TCT TTC TCC GCA TGC TAT CCT CAT AGT TTG CAG CTA CTC CCC	485
Ser Phe Ser Phe Ser Ala Cys Tyr Pro His Ser Leu Gln Leu Leu Pro	

```

Gln Thr Asp Thr Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp Ser Val
 610                      615                      620
Lys Thr Lys Asp Glu Leu Leu Glu Lys Ile Met Asp Ser Leu Lys Asp
625                      630                      635                      640
Phe Lys Gly Ile Asn Phe Ser Phe Thr Gln Pro Ile Glu Met Arg Ile
                      645                      650                      655
Ser Glu Met Leu Thr Gly Val Arg Gly Asp Leu Ala Val Lys Ile Phe
                      660                      665                      670
Gly Asp Gly Ile Ser Glu Leu Asn Glu Leu Ser Phe Gln Ile Ala Gln
                      675                      680                      685
Ala Leu Lys Gly Ile Lys Gly Ser Ser Glu Val Leu Thr Thr Leu Asn
                      690                      695                      700
Glu Gly Val Asn Tyr Leu Tyr Val Thr Pro Asn Lys Glu Ser Met Ala
705                      710                      715                      720
Asp Val Gly Ile Thr Ser Asp Glu Phe Ser Lys Phe Leu Lys Ser Ala
                      725                      730                      735
Leu Glu Gly Leu Val Val Asp Val Ile Pro Thr Gly Ile Ser Arg Thr
                      740                      745                      750
Pro Val Met Ile Arg Gln Glu Ser Asp Phe Ala Ser Ser Ile Thr Lys
                      755                      760                      765
Ile Lys Ser Leu Ala Leu Thr Ser Lys Tyr Gly Val Leu Val Pro Ile
                      770                      775                      780
Thr Ser Ile Ala Lys Ile Glu Glu Val Asp Gly Pro Val Ser Val Val
785                      790                      795                      800
Arg Glu Asn Ser Met Arg Met Ser Val Val Arg Ser Asn Val Val Gly
                      805                      810                      815
Arg Asp Leu Lys Ser Phe Val Glu Glu Ala Lys Lys Val Ile Ala Gln
                      820                      825                      830
Asn Ile Lys Leu Pro Pro Ser Tyr Tyr Ile Thr Tyr Gly Gln Phe
                      835                      840                      845
Glu Asn Gln Gln Arg Ala Asn Lys Arg Leu Ser Thr Val Ile Pro Leu
                      850                      855                      860
Ser Ile Leu Ala Ile Phe Phe Ile Leu Phe Phe Thr Phe Lys Ser Ile
865                      870                      875                      880
Pro Leu Ala Leu Leu Ile Leu Leu Asn Ile Pro Phe Ala Val Thr Gly
                      885                      890                      895
Gly Leu Ile Ala Leu Phe Ala Val Gly Glu Tyr Ile Ser Val Pro Ala
                      900                      905                      910
Ser Val Gly Phe Ile Ala Leu Phe Gly Ile Ala Val Leu Asn Gly Val
                      915                      920                      925
Val Met Ile Gly Tyr Phe Lys Glu Leu Leu Leu Gln Gly Lys Ser Val
                      930                      935                      940
Glu Glu Cys Val Leu Leu Gly Ala Lys Arg Arg Leu Arg Pro Val Leu
945                      950                      955                      960
Met Thr Ala Cys Ile Ala Gly Leu Gly Leu Leu Pro Leu Leu Phe Ser
                      965                      970                      975
His Ser Val Gly Ser Glu Val Gln Lys Pro Leu Ala Ile Val Val Leu
                      980                      985                      990
Gly Gly Leu Val Thr Ser Ser Ala Leu Thr Leu Leu Leu Pro Pro
                      995                      1000                      1005
Met Phe Met Leu Ile Ala Lys Lys Ile Lys Ile Val
1010                      1015                      1020

```

(2) INFORMATION FOR SEQ ID NO:923:

				165					170					175			
Ser	Ile	Gly	Gly	Phe	Ser	Arg	Ala	Phe	Val	Ile	Val	Pro	Asp	Phe	Asn		
			180					185					190				
Asp	Met	Ala	Arg	Leu	Gly	Val	Ser	Ile	Ser	Asp	Leu	Glu	Ser	Ala	Val		
		195					200					205					
Arg	Val	Asn	Leu	Arg	Asn	Ser	Gly	Ala	Gly	Arg	Val	Asp	Arg	Asp	Gly		
	210					215					220						
Glu	Thr	Phe	Leu	Val	Lys	Ile	Gln	Thr	Ala	Ser	Leu	Ser	Leu	Glu	Asp		
225					230					235					240		
Ile	Gly	Lys	Ile	Thr	Val	Ser	Thr	Asn	Leu	Gly	His	Leu	His	Ile	Lys		
			245					250						255			
Asp	Phe	Ala	Lys	Val	Ile	Ser	Gln	Ser	Arg	Thr	Arg	Leu	Gly	Phe	Val		
		260						265					270				
Thr	Lys	Asp	Gly	Val	Gly	Glu	Thr	Thr	Glu	Gly	Leu	Val	Leu	Ser	Leu		
		275					280						285				
Lys	Asp	Ala	Asn	Thr	Lys	Glu	Ile	Ile	Thr	Gln	Val	Tyr	Gln	Lys	Leu		
	290					295					300						
Glu	Glu	Leu	Lys	Pro	Phe	Leu	Pro	Asn	Gly	Val	Ser	Ile	Asn	Val	Phe		
305					310					315					320		
Tyr	Asp	Arg	Ser	Glu	Phe	Thr	Gln	Lys	Ala	Ile	Ala	Thr	Val	Ser	Lys		
			325					330						335			
Thr	Leu	Ile	Glu	Ala	Val	Val	Leu	Ile	Ile	Ile	Thr	Leu	Phe	Leu	Phe		
		340					345						350				
Leu	Gly	Asn	Leu	Arg	Ala	Ser	Val	Ala	Val	Gly	Val	Ile	Leu	Pro	Leu		
	355					360						365					
Ser	Leu	Ser	Val	Ala	Phe	Ile	Phe	Ile	Lys	Phe	Ser	Asp	Leu	Thr	Leu		
	370				375						380						
Asn	Leu	Met	Ser	Leu	Gly	Gly	Leu	Val	Ile	Ala	Ile	Gly	Met	Leu	Ile		
385				390						395				400			
Asp	Ser	Ala	Val	Val	Val	Glu	Asn	Ala	Phe	Glu	Lys	Leu	Ser	Ala			
			405					410						415			
Asn	Thr	Lys	Thr	Lys	Leu	His	Ala	Ile	Tyr	Arg	Ser	Cys	Lys	Glu			
		420					425					430					
Ile	Ala	Val	Ser	Val	Val	Ser	Gly	Val	Val	Ile	Ile	Ile	Val	Phe	Phe		
		435				440						445					
Val	Pro	Ile	Leu	Thr	Leu	Gln	Gly	Leu	Glu	Gly	Lys	Met	Phe	Arg	Pro		
	450				455						460						
Leu	Ala	Gln	Ser	Ile	Val	Tyr	Ala	Leu	Leu	Gly	Thr	Leu	Val	Leu	Ser		
465				470						475				480			
Ile	Thr	Ile	Ile	Pro	Val	Val	Ser	Ser	Leu	Val	Leu	Lys	Ala	Thr	Pro		
			485					490						495			
His	Ser	Glu	Thr	Phe	Leu	Thr	Arg	Phe	Leu	Asn	Arg	Ile	Tyr	Ala	Pro		
		500						505					510				
Leu	Leu	Glu	Phe	Phe	Val	His	Asn	Pro	Lys	Lys	Val	Ile	Leu	Gly	Ala		
	515					520						525					
Phe	Val	Phe	Leu	Ile	Ala	Ser	Leu	Ser	Leu	Phe	Pro	Phe	Val	Gly	Lys		
	530					535					540						
Asn	Phe	Met	Pro	Val	Leu	Asp	Glu	Gly	Asp	Val	Val	Leu	Ser	Val	Glu		
545				550						555				560			
Thr	Thr	Pro	Ser	Ile	Ser	Leu	Asp	Gln	Ser	Arg	Asp	Leu	Met	Leu	Asn		
			565					570						575			
Ile	Glu	Ser	Ala	Ile	Lys	Lys	His	Val	Lys	Glu	Val	Lys	Ser	Ile	Val		
		580						585					590				
Ala	Arg	Thr	Gly	Ser	Asp	Glu	Leu	Gly	Leu	Asp	Leu	Gly	Gly	Leu	Asn		
	595					600						605					

GAA GAA TGC GTT TTA TTG GGC GCT AAA AGG CGT TTG AGA CCG GTT TTA 2940
 Glu Glu Cys Val Leu Leu Gly Ala Lys Arg Arg Leu Arg Pro Val Leu
 945 950 955 960

ATG ACC GCT TGC ATT GCC GGT TTG GGT TTG CTC CCT TTA TTA TTT TCT 2988
 Met Thr Ala Cys Ile Ala Gly Leu Gly Leu Leu Pro Leu Leu Phe Ser
 965 970 975

CAT AGC GTG GGA TCA GAA GTC CAA AAA CCT TTA GCG ATC GTG GTG CTT 3036
 His Ser Val Gly Ser Glu Val Gln Lys Pro Leu Ala Ile Val Val Leu
 980 985 990

GGA GGC TTG GTT ACC TCA AGC GCT CTA ACC TTA CTC CTA CTG CCG CCA 3084
 Gly Gly Leu Val Thr Ser Ser Ala Leu Thr Leu Leu Leu Leu Pro Pro
 995 1000 1005

ATG TTT ATG CTC ATC GCT AAA AAG ATT AAA ATC GTT TGAGTTAAAG GATTTC 3136
 Met Phe Met Leu Ile Ala Lys Lys Ile Lys Ile Val
 1010 1015 1020

ACATGCTCGC TTTAGAAATT TATATTGATA TTTGTTTGAA AGA 3179

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

Met Met Leu Ala Ser Ile Ile Glu Phe Ser Leu Arg Gln Arg Val Ile
 1 5 10 15
 Val Ile Val Gly Ala Ile Leu Ile Leu Phe Phe Gly Thr Tyr Ser Phe
 20 25 30
 Ile Asn Thr Pro Val Asp Ala Phe Pro Asp Ile Ser Pro Thr Gln Val
 35 40 45
 Lys Ile Ile Leu Lys Leu Pro Gly Ser Ser Pro Glu Glu Met Glu Asn
 50 55 60
 Asn Ile Val Arg Pro Leu Glu Leu Glu Leu Leu Gly Leu Lys Gly Gln
 65 70 75 80
 Lys Ser Leu Arg Ser Val Ser Lys Tyr Ser Ile Ser Asp Ile Thr Ile
 85 90 95
 Asp Phe Asp Asp Ser Val Asp Ile Tyr Leu Ala Arg Asn Ile Val Asn
 100 105 110
 Glu Arg Leu Ser Ser Val Met Lys Asp Leu Pro Val Gly Val Glu Gly
 115 120 125
 Gly Met Ala Pro Ile Val Thr Pro Leu Ser Asp Ile Phe Met Phe Thr
 130 135 140
 Ile Asp Gly Asn Ile Thr Glu Ile Glu Lys Arg Gln Leu Leu Asp Phe
 145 150 155 160
 Val Ile Arg Pro Gln Leu Arg Met Ile Ser Gly Val Ala Asp Val Asn

GAT GTG GGG ATC ACT AGC GAT GAA TTT TCC AAG TTT TTA AAA TCC GCT	2268
Asp Val Gly Ile Thr Ser Asp Glu Phe Ser Lys Phe Leu Lys Ser Ala	
725 730 735	
TTA GAG GGC TTG GTT GTA GAT GTG ATC CCT ACA GGG ATT TCA CGC ACG	2316
Leu Glu Gly Leu Val Val Asp Val Ile Pro Thr Gly Ile Ser Arg Thr	
740 745 750	
CCA GTG ATG ATC CGC CAA GAG AGC GAT TTT GCA AGC TCT ATC ACT AAA	2364
Pro Val Met Ile Arg Gln Glu Ser Asp Phe Ala Ser Ser Ile Thr Lys	
755 760 765	
ATC AAA AGT TTA GCC TTG ACT TCA AAA TAT GGC GTT TTA GTG CCT ATC	2412
Ile Lys Ser Leu Ala Leu Thr Ser Lys Tyr Gly Val Leu Val Pro Ile	
770 775 780	
ACT TCT ATC GCC AAA ATT GAA GAA GTG GAT GGC CCT GTT TCT GTT GTG	2460
Thr Ser Ile Ala Lys Ile Glu Glu Val Asp Gly Pro Val Ser Val Val	
785 790 795 800	
CGT GAA AAT TCA ATG CGC ATG AGC GTG GTT CGC AGT AAT GTG GTG GGG	2508
Arg Glu Asn Ser Met Arg Met Ser Val Val Arg Ser Asn Val Val Gly	
805 810 815	
CGC GAT TTG AAA TCT TTT GTA GAA GAG GCT AAA AAA GTG ATC GCT CAA	2556
Arg Asp Leu Lys Ser Phe Val Glu Glu Ala Lys Lys Val Ile Ala Gln	
820 825 830	
AAC ATC AAA CTC CCT CCC AGC TAC TAT ATC ACT TAT GGG GGG CAG TTT	2604
Asn Ile Lys Leu Pro Pro Ser Tyr Tyr Ile Thr Tyr Gly Gly Gln Phe	
835 840 845	
GAA AAC CAG CAA CGG GCC AAT AAA AGG CTC TCC ACC GTT ATC CCT TTA	2652
Glu Asn Gln Gln Arg Ala Asn Lys Arg Leu Ser Thr Val Ile Pro Leu	
850 855 860	
AGC ATC TTA GCG ATT TTT TTC ATT CTT TTT TTC ACT TTT AAA AGC ATT	2700
Ser Ile Leu Ala Ile Phe Phe Ile Leu Phe Phe Thr Phe Lys Ser Ile	
865 870 875 880	
CCT TTA GCC TTG CTC ATT CTT TTG AAT ATC CCT TTT GCG GTT ACC GGA	2748
Pro Leu Ala Leu Leu Ile Leu Leu Asn Ile Pro Phe Ala Val Thr Gly	
885 890 895	
GGC CTT ATT GCG TTG TTT GCG GTC GGG GAG TAT ATT TCA GTG CCA GCG	2796
Gly Leu Ile Ala Leu Phe Ala Val Gly Glu Tyr Ile Ser Val Pro Ala	
900 905 910	
AGC GTG GGC TTT ATC GCT CTT TTT GGG ATT GCG GTT TTA AAT GGC GTG	2844
Ser Val Gly Phe Ile Ala Leu Phe Gly Ile Ala Val Leu Asn Gly Val	
915 920 925	
GTG ATG ATA GGC TAT TTT AAA GAG CTT CTC TTG CAA GGG AAA AGC GTA	2892
Val Met Ile Gly Tyr Phe Lys Glu Leu Leu Leu Gln Gly Lys Ser Val	
930- 935 940	

CAT AGC GAA ACC TTT TTA ACG AGG TTT TTA AAC AGA ATC TAC GCC CCT	1596
His Ser Glu Thr Phe Leu Thr Arg Phe Leu Asn Arg Ile Tyr Ala Pro	
500 505 510	
TTA TTG GAA TTT TTT GTG CAT AAC CCT AAA AAA GTG ATT TTA GGA GCG	1644
Leu Leu Glu Phe Phe Val His Asn Pro Lys Lys Val Ile Leu Gly Ala	
515 520 525	
TTT GTT TTT TTA ATC GCA AGC CTT TCT TTA TTC CCT TTT GTG GGG AAG	1692
Phe Val Phe Leu Ile Ala Ser Leu Ser Leu Phe Pro Phe Val Gly Lys	
530 535 540	
AAT TTC ATG CCC GTT TTA GAT GAG GGC GAT GTG GTT TTG AGC GTG GAA	1740
Asn Phe Met Pro Val Leu Asp Glu Gly Asp Val Val Leu Ser Val Glu	
545 550 555 560	
ACC ACC CCT TCT ATT TCT TTA GAT CAA TCT AGG GAT CTC ATG CTA AAC	1788
Thr Thr Pro Ser Ile Ser Leu Asp Gln Ser Arg Asp Leu Met Leu Asn	
565 570 575	
ATT GAG AGC GCG ATT AAA AAG CAT GTC AAG GAA GTT AAA AGC ATT GTC	1836
Ile Glu Ser Ala Ile Lys Lys His Val Lys Glu Val Lys Ser Ile Val	
580 585 590	
GCG CGC ACA GGG AGC GAT GAA TTG GGG CTG GAT TTA GGA GGT TTG AAT	1884
Ala Arg Thr Gly Ser Asp Glu Leu Gly Leu Asp Leu Gly Gly Leu Asn	
595 600 605	
CAA ACC GAT ACT TTT ATT TCT TTT ATT CCT AAA AAA GAA TGG AGC GTT	1932
Gln Thr Asp Thr Phe Ile Ser Phe Ile Pro Lys Lys Glu Trp Ser Val	
610 615 620	
AAA ACC AAA GAT GAA TTA TTA GAA AAA ATC ATG GAT TCT TTA AAA GAC	1980
Lys Thr Lys Asp Glu Leu Leu Glu Lys Ile Met Asp Ser Leu Lys Asp	
625 630 635 640	
TTT AAG GGG ATT AAC TTT TCT TTC ACC CAA CCC ATT GAA ATG AGA ATT	2028
Phe Lys Gly Ile Asn Phe Ser Phe Thr Gln Pro Ile Glu Met Arg Ile	
645 650 655	
TCT GAA ATG CTG ACA GGG GTT AGG GGG GAT TTA GCG GTT AAG ATT TTT	2076
Ser Glu Met Leu Thr Gly Val Arg Gly Asp Leu Ala Val Lys Ile Phe	
660 665 670	
GGA GAT GGT ATT AGC GAA TTG AAT GAA TTG AGT TTT CAA ATC GCG CAA	2124
Gly Asp Gly Ile Ser Glu Leu Asn Glu Leu Ser Phe Gln Ile Ala Gln	
675 680 685	
GCT CTA AAA GGG ATT AAA GGA TCT AGT GAA GTT TTA ACC ACG CTT AAT	2172
Ala Leu Lys Gly Ile Lys Gly Ser Ser Glu Val Leu Thr Thr Leu Asn	
690 695 700	
GAG GGC GTG AAT TAT TTG TAT GTA ACC CCT AAT AAA GAA TCG ATG GCG	2220
Glu Gly Val Asn Tyr Leu Tyr Val Thr Pro Asn Lys Glu Ser Met Ala	
705 710 715 720	

ACT AAA GAT GGC GTG GGC GAG ACC ACA GAA GGC TTG GTG CTT TCT TTA	924
Thr Lys Asp Gly Val Gly Glu Thr Thr Glu Gly Leu Val Leu Ser Leu	
275 280 285	
AAA GAC GCT AAC ACC AAA GAA ATC ATC ACT CAA GTG TAT CAA AAA CTA	972
Lys Asp Ala Asn Thr Lys Glu Ile Ile Thr Gln Val Tyr Gln Lys Leu	
290 295 300	
GAA GAA TTA AAA CCC TTT TTA CCG AAT GGC GTG TCC ATT AAT GTT TTT	1020
Glu Glu Leu Lys Pro Phe Leu Pro Asn Gly Val Ser Ile Asn Val Phe	
305 310 315 320	
TAT GAT CGC TCA GAA TTT ACG CAA AAA GCC ATT GCC ACC GTT TCT AAA	1068
Tyr Asp Arg Ser Glu Phe Thr Gln Lys Ala Ile Ala Thr Val Ser Lys	
325 330 335	
ACC CTC ATT GAA GCC GTT GTT TTA ATC ATC ATC ACG CTC TTT TTA TTT	1116
Thr Leu Ile Glu Ala Val Val Leu Ile Ile Ile Thr Leu Phe Leu Phe	
340 345 350	
TTA GGG AAT TTG AGG GCG AGC GTG GCT GTG GGG GTG ATT TTA CCT TTA	1164
Leu Gly Asn Leu Arg Ala Ser Val Ala Val Gly Val Ile Leu Pro Leu	
355 360 365	
AGC TTG TCC GTG GCG TTT ATT TTT ATC AAG TTT AGC GAT CTG ACT TTA	1212
Ser Leu Ser Val Ala Phe Ile Phe Ile Lys Phe Ser Asp Leu Thr Leu	
370 375 380	
AAT TTG ATG AGT TTA GGG GGA TTG GTT ATC GCT ATA GGC ATG CTC ATT	1260
Asn Leu Met Ser Leu Gly Gly Leu Val Ile Ala Ile Gly Met Leu Ile	
385 390 395 400	
GAC TCA GCC GTG GTG GTG GTG GAA AAC GCT TTT GAA AAA TTA AGC GCT	1308
Asp Ser Ala Val Val Val Val Glu Asn Ala Phe Glu Lys Leu Ser Ala	
405 410 415	
AAC ACT AAA ACC ACT AAA CTC CAT GCA ATC TAT CGT TCG TGT AAA GAA	1356
Asn Thr Lys Thr Thr Lys Leu His Ala Ile Tyr Arg Ser Cys Lys Glu	
420 425 430	
ATC GCT GTT TCA GTG GTG AGC GGG GTG GTG ATC ATC ATT GTG TTT TTT	1404
Ile Ala Val Ser Val Val Ser Gly Val Val Ile Ile Ile Val Phe Phe	
435 440 445	
GTG CCG ATT TTA ACC TTA CAG GGG TTA GAG GGT AAG ATG TTT AGG CCT	1452
Val Pro Ile Leu Thr Leu Gln Gly Leu Glu Gly Lys Met Phe Arg Pro	
450 455 460	
TTA GCG CAA AGC ATT GTG TAT GCG CTT TTA GGC ACT TTA GTT CTA TCT	1500
Leu Ala Gln Ser Ile Val Tyr Ala Leu Leu Gly Thr Leu Val Leu Ser	
465 470 475 480	
ATT ACA ATC ATT CCT GTA GTC AGC TCT CTT GTC TTA AAA GCC ACG CCC	1548
Ile Thr Ile Ile Pro Val Val Ser Ser Leu Val Leu Lys Ala Thr Pro	
485 490 495	

Lys	Ile	Ile	Leu	Lys	Leu	Pro	Gly	Ser	Ser	Pro	Glu	Glu	Met	Glu	Asn	
50						55					60					
AAC	ATC	GTG	CGC	CCT	TTA	GAA	TTG	GAG	CTT	TTA	GGC	TTG	AAA	GGG	CAA	300
Asn	Ile	Val	Arg	Pro	Leu	Glu	Leu	Glu	Leu	Leu	Gly	Leu	Lys	Gly	Gln	
65					70					75					80	
AAA	TCT	TTA	AGG	AGT	GTT	TCA	AAA	TAT	TCT	ATT	TCA	GAT	ATT	ACG	ATA	348
Lys	Ser	Leu	Arg	Ser	Val	Ser	Lys	Tyr	Ser	Ile	Ser	Asp	Ile	Thr	Ile	
				85					90					95		
GAT	TTT	GAT	GAC	AGC	GTG	GAT	ATT	TAT	TTA	GCG	AGG	AAT	ATT	GTC	AAT	396
Asp	Phe	Asp	Asp	Ser	Val	Asp	Ile	Tyr	Leu	Ala	Arg	Asn	Ile	Val	Asn	
				100				105						110		
GAG	CGC	TTG	AGC	AGC	GTG	ATG	AAA	GAT	TTA	CCC	GTG	GGG	GTT	GAG	GGG	444
Glu	Arg	Leu	Ser	Ser	Val	Met	Lys	Asp	Leu	Pro	Val	Gly	Val	Glu	Gly	
		115					120					125				
GGC	ATG	GCG	CCC	ATT	GTT	ACG	CCG	CTA	TCA	GAT	ATC	TTT	ATG	TTC	ACT	492
Gly	Met	Ala	Pro	Ile	Val	Thr	Pro	Leu	Ser	Asp	Ile	Phe	Met	Phe	Thr	
	130					135					140					
ATT	GAT	GGC	AAT	ATC	ACT	GAG	ATA	GAA	AAA	CGA	CAG	CTT	TTA	GAT	TTT	540
Ile	Asp	Gly	Asn	Ile	Thr	Glu	Ile	Glu	Lys	Arg	Gln	Leu	Leu	Asp	Phe	
145					150					155					160	
GTG	ATC	CGC	CCA	CAA	TTA	AGA	ATG	ATT	AGC	GGC	GTA	GCA	GAT	GTC	AAT	588
Val	Ile	Arg	Pro	Gln	Leu	Arg	Met	Ile	Ser	Gly	Val	Ala	Asp	Val	Asn	
				165					170					175		
TCC	ATT	GGA	GGC	TTT	AGC	AGA	GCG	TTT	GTG	ATC	GTG	CCG	GAT	TTT	AAT	636
Ser	Ile	Gly	Gly	Phe	Ser	Arg	Ala	Phe	Val	Ile	Val	Pro	Asp	Phe	Asn	
			180					185					190			
GAC	ATG	GCA	AGG	CTT	GGG	GTG	AGT	ATT	TCT	GAT	TTA	GAA	TCG	GCT	GTG	684
Asp	Met	Ala	Arg	Leu	Gly	Val	Ser	Ile	Ser	Asp	Leu	Glu	Ser	Ala	Val	
		195					200					205				
AGA	GTG	AAT	TTA	AGA	AAC	AGC	GGA	GCG	GGG	CGC	GTG	GAT	AGA	GAT	GGC	732
Arg	Val	Asn	Leu	Arg	Asn	Ser	Gly	Ala	Gly	Arg	Val	Asp	Arg	Asp	Gly	
	210					215					220					
GAA	ACC	TTT	TTA	GTC	AAA	ATC	CAA	ACC	GCT	TCT	TTG	AGT	TTA	GAA	GAC	780
Glu	Thr	Phe	Leu	Val	Lys	Ile	Gln	Thr	Ala	Ser	Leu	Ser	Leu	Glu	Asp	
225					230					235					240	
ATT	GGC	AAA	ATC	ACC	GTT	TCC	ACT	AAT	TTA	GGG	CAT	TTG	CAC	ATT	AAG	828
Ile	Gly	Lys	Ile	Thr	Val	Ser	Thr	Asn	Leu	Gly	His	Leu	His	Ile	Lys	
				245					250					255		
GAT	TTT	GCG	AAA	GTC	ATC	AGC	CAG	TCT	CGC	ACC	CGT	TTG	GGG	TTT	GTT	876
Asp	Phe	Ala	Lys	Val	Ile	Ser	Gln	Ser	Arg	Thr	Arg	Leu	Gly	Phe	Val	
			260					265					270			

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

```

Met Ile Leu Gly Asn Asn Val Ser Lys Ser Phe Lys Arg Asp Phe Asn
 1             5             10             15
Pro Cys Lys Ile Ser Ala Asn Gly Leu Val Thr Gly Phe Leu Glu Lys
      20             25             30
Ile Thr Leu Lys Ala Leu Ile Pro Asn Ser Ile Pro Cys Ser Lys Phe
      35             40             45
Thr Asp Arg Ser Leu Glu Ser Leu Phe Arg Leu Ser Asn Ser Ala Trp
      50             55             60
Lys Ser Phe Glu Lys Glu Arg Leu Ile Phe Ser Ile Ser Asn Leu Ala
65             70             75             80
Phe Leu Ile Lys Leu Cys Cys Met Met Leu Ser Ile Ser Leu Leu Asn
      85             90             95
Ser Leu Gly Leu Leu Ile Lys Glu Ala Lys
      100             105

```

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 61...3120
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

```

CAGCGTGGCA GTGGGGTCAT TGATAGGGTT AAAAGGCATG ATCAACAATT TAGGGGAGGA      60
ATG ATG CTC GCT TCC ATT ATT GAA TTT TCC TTA CGC CAA AGA GTG ATC      108
Met Met Leu Ala Ser Ile Ile Glu Phe Ser Leu Arg Gln Arg Val Ile
 1             5             10             15

GTG ATT GTT GGT GCG ATT CTT ATT TTA TTT TTT GGG ACT TAT AGT TTT      156
Val Ile Val Gly Ala Ile Leu Ile Leu Phe Phe Gly Thr Tyr Ser Phe
      20             25             30

ATC AAC ACT CCA GTG GAC GCT TTC CCG GAT ATT TCG CCC ACT CAA GTT      204
Ile Asn Thr Pro Val Asp Ala Phe Pro Asp Ile Ser Pro Thr Gln Val
      35             40             45

AAA ATC ATT TTA AAA CTC CCC GGC TCT AGC CCT GAA GAA ATG GAA AAC      252

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...348
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

```

TCTTTTCTT CATTCCTAAA GAATGAAGCG  ATG ATA TTA GGC AAC AAT GTC AGT      54
                               Met Ile Leu Gly Asn Asn Val Ser
                               1                               5

AAA TCT TTT AAA AGA GAT TTT AAC CCT TGC AAA ATC AGC GCG AAT GGC      102
Lys Ser Phe Lys Arg Asp Phe Asn Pro Cys Lys Ile Ser Ala Asn Gly
  10                               15                               20

CTT GTA ACC GGA TTC TTG GAA AAA ATC ACG CTT AAA GCG TTG ATC CCT      150
Leu Val Thr Gly Phe Leu Glu Lys Ile Thr Leu Lys Ala Leu Ile Pro
  25                               30                               35                               40

AAT TCA ATC CCA TGC TCT AAA TTC ACA GAC AGA TCG CTA GAA AGC TTG      198
Asn Ser Ile Pro Cys Ser Lys Phe Thr Asp Arg Ser Leu Glu Ser Leu
                45                               50                               55

TTC AGG CTT TCA AAT TCC GCA TGG AAA TCT TTT GAA AAA GAA AGG TTG      246
Phe Arg Leu Ser Asn Ser Ala Trp Lys Ser Phe Glu Lys Glu Arg Leu
                60                               65                               70

ATC TTT TCA ATC TCT AAT TTA GCG TTT TTG ATC AAG CTT TGT TGC ATG      294
Ile Phe Ser Ile Ser Asn Leu Ala Phe Leu Ile Lys Leu Cys Cys Met
                75                               80                               85

ATG CTT TCT ATT TCG CTA TTG AAC TCG TTA GGC TTG TTG ATT AAA GAG      342
Met Leu Ser Ile Ser Leu Leu Asn Ser Leu Gly Leu Leu Ile Lys Glu
                90                               95                               100

GCT AAA TAGGATTTTT GA                                             360
Ala Lys
105

```

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid

130						135					140				
Gly	Phe	Asp	Ser	Pro	Ile	Ser	Ser	His	Thr	His	Ala	Ile	Leu	Glu	Tyr
145					150					155					160
Leu	Glu	Arg	Gly	Val	His	Phe	Val	Ile	Leu	Thr	Ser	Val	Glu	Glu	Gly
				165					170						175
Asn	Leu	Thr	Lys	Arg	Met	Val	Arg	Glu	Leu	Lys	Asn	Leu	Leu	Glu	Phe
			180					185					190		
Asp	Lys	Gly	Leu	Ser	Phe	Ile	Leu	Ser	Lys	Thr	Asn	Leu	Arg	Thr	Pro
	195						200					205			
Ser	Gln	Val	Gly	Glu	Ile	Ser	His	Tyr	Ile	Gln	Asp	Gln	Ile	Gln	Asp
210					215					220					
His	Leu	Asp	Leu	Thr	Thr	His	Leu	Ile	His	Ser	Asn	Lys	Asp	Asn	Asn
225					230					235					240
Ala	Leu	Leu	Glu	Val	Ala	Asp	Lys	Ile	Asp	Ala	Glu	Lys	Leu	Phe	Ser
				245					250						255
Ala	Leu	Tyr	Leu	Lys	Arg	Leu	Lys	Phe	Leu	Asn	Ser	Lys	Leu	Gln	Asn
			260					265					270		
Ser	Leu	Lys	Ser	Val	Met	Glu	Ser	Phe	Asp	Tyr	Ser	Lys	Glu	Lys	Ala
	275						280					285			
Leu	Glu	Glu	Ile	Gln	Ala	Leu	Asp	Leu	Gly	Val	Lys	Asp	Ile	Glu	Lys
290					295					300					
Thr	Tyr	Glu	Lys	Leu	Arg	Ala	Asn	Leu	Glu	Glu	Glu	Tyr	Ser	Ser	Val
305					310					315					320
Ala	Val	Gly	Ser	Val	Val	Lys	Lys	Val	Val	Glu	Glu	Val	Arg	Asp	Gln
			325					330						335	
Lys	Ser	Tyr	Leu	Ala	Ser	Leu	Ile	Asn	Lys	Pro	Asn	Glu	Phe	Asn	Ser
		340						345				350			
Glu	Ile	Glu	Ser	Ile	Met	Gln	Gln	Ser	Leu	Ile	Lys	Asn	Ala	Lys	Leu
	355						360					365			
Glu	Ile	Glu	Lys	Ile	Asn	Leu	Ser	Phe	Ser	Lys	Asp	Phe	His	Ala	Glu
370					375					380					
Phe	Glu	Ser	Leu	Asn	Lys	Leu	Ser	Ser	Asp	Leu	Ser	Val	Asn	Leu	Glu
385					390					395					400
His	Gly	Ile	Glu	Leu	Gly	Ile	Asn	Ala	Leu	Ser	Val	Ile	Phe	Ser	Lys
			405					410						415	
Asn	Pro	Val	Thr	Arg	Pro	Phe	Ala	Leu	Ile	Leu	Gln	Gly	Leu	Lys	Ser
			420					425					430		
Leu	Leu	Lys	Asp	Leu	Leu	Thr	Leu	Leu	Pro	Asn	Ile	Ile	Ala	Ser	Phe
	435						440					445			
Phe	Arg	Asn	Glu	Glu	Lys	Glu	Arg	Ala	Lys	Leu	Glu	Asn	Leu	Ile	Glu
450					455					460					
Val	Arg	Val	Ile	Pro	Glu	Ile	Gln	Tyr	Lys	Leu	Lys	Lys	Val	Leu	Pro
465					470					475					480
Gly	Leu	Phe	Asn	Glu	Ala	Leu	Gln	Asn	Ser	Leu	Lys	Ser	Leu	Lys	Asp
			485					490						495	
Arg	Cys	Glu	Leu	Glu	Ile	Thr	His	Lys	Lys	Gln	Glu	Ile	Ala	Leu	Ala
			500					505					510		
Gln	Lys	Glu	Lys	Glu	Lys	His	Leu	Asn	Asp	Leu	Glu	Asp	Gln	Lys	Gln
	515						520					525			
Ile	Leu	Glu	Asn	Lys	Ile	Asn	Ala	Leu	Ser	Asp	Leu	Glu	Gln	Gln	Tyr
530					535					540					
Leu	Lys	Asp	Gln	Gln											
545															

(2) INFORMATION FOR SEQ ID NO:919:

AAA TTA GAA AAT CTG ATT GAA GTC AGA GTG ATT CCA GAA ATC CAA TAC	1446
Lys Leu Glu Asn Leu Ile Glu Val Arg Val Ile Pro Glu Ile Gln Tyr	
460 465 470	
AAG CTT AAA AAA GTT TTA CCG GGA TTG TTT AAT GAA GCT TTG CAA AAT	1494
Lys Leu Lys Lys Val Leu Pro Gly Leu Phe Asn Glu Ala Leu Gln Asn	
475 480 485	
TCC CTA AAA TCT CTA AAA GAT CGG TGC GAG CTA GAA ATC ACG CAT AAA	1542
Ser Leu Lys Ser Leu Lys Asp Arg Cys Glu Glu Ile Thr His Lys	
490 495 500 505	
AAA CAA GAA ATC GCG CTC GCT CAA AAG GAA AAA GAA AAA CAC CTA AAC	1590
Lys Gln Glu Ile Ala Leu Ala Gln Lys Glu Lys Glu Lys His Leu Asn	
510 515 520	
GAT TTA GAA GAT CAA AAA CAA ATC TTA GAA AAT AAG ATC AAC GCT TTA	1638
Asp Leu Glu Asp Gln Lys Gln Ile Leu Glu Asn Lys Ile Asn Ala Leu	
525 530 535	
AGC GAT TTA GAA CAA CAA TAT TTA AAG GAT CAA CAA TGAACGAGCA AGAACT	1690
Ser Asp Leu Glu Gln Gln Tyr Leu Lys Asp Gln Gln	
540 545	
CATTCAAAAA AGCGCTTTAA TTGAAAAA	1718

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

Met Met Val Leu Arg Thr Gln Thr Asn Phe Val Glu Phe Leu Glu Gln	
1 5 10 15	
Val Leu Glu Val Leu Lys Glu Val Glu Ile Asp Lys Thr Glu Cys Ser	
20 25 30	
Thr Leu Leu Ala Ser Val Gln Lys Gln Gln Leu Val Ile Pro Val Val	
35 40 45	
Gly Asn Phe Ser Ala Gly Lys Ser Thr Leu Leu Asn Arg Phe Leu Gly	
50 55 60	
Ser Ser Val Leu Pro Thr Gly Ile Thr Pro Glu Thr Ser Leu Ala Thr	
65 70 75 80	
Glu Leu His Tyr Ser Ala Lys Glu Arg Ile Glu Ala Phe Ser Asn Asn	
85 90 95	
Asp Glu Lys Thr Glu Ser Phe Glu Leu Asn Glu Gln Ser Phe Glu Ala	
100 105 110	
Ile Lys Glu Asn Ala Thr Lys Tyr Ser Tyr Leu Lys Val Tyr Leu Asn	
115 120 125	
Asn Glu Ala Leu Lys Asn Ser Ala Pro Leu Val Phe Val Asp Met Pro	

CAT TCC AAT AAA GAC AAT AAC GCC CTT TTA GAG GTA GCG GAT AAA ATA	774
His Ser Asn Lys Asp Asn Asn Ala Leu Leu Glu Val Ala Asp Lys Ile	
235 240 245	
GAC GCT GAA AAG CTT TTT AGC GCT TTG TAT TTG AAA CGA TTG AAG TTT	822
Asp Ala Glu Lys Leu Phe Ser Ala Leu Tyr Leu Lys Arg Leu Lys Phe	
250 255 260 265	
TTA AAT TCT AAG TTA CAA AAT AGC CTA AAA AGC GTG ATG GAA AGC TTT	870
Leu Asn Ser Lys Leu Gln Asn Ser Leu Lys Ser Val Met Glu Ser Phe	
270 275 280	
GAT TAT TCT AAA GAA AAG GCT TTA GAA GAA ATA CAA GCT TTG GAT TTG	918
Asp Tyr Ser Lys Glu Lys Ala Leu Glu Glu Ile Gln Ala Leu Asp Leu	
285 290 295	
GGC GTT AAA GAC ATT GAA AAA ACC TAT GAA AAA TTA AGG GCT AAT TTA	966
Gly Val Lys Asp Ile Glu Lys Thr Tyr Glu Lys Leu Arg Ala Asn Leu	
300 305 310	
GAA GAA GAA TAT TCT AGC GTG GCT GTG GGA TCG GTG GTT AAA AAA GTA	1014
Glu Glu Glu Tyr Ser Ser Val Ala Val Gly Ser Val Val Lys Lys Val	
315 320 325	
GTA GAA GAG GTT AGG GAT CAA AAA TCC TAT TTA GCC TCT TTA ATC AAC	1062
Val Glu Glu Val Arg Asp Gln Lys Ser Tyr Leu Ala Ser Leu Ile Asn	
330 335 340 345	
AAG CCT AAC GAG TTC AAT AGC GAA ATA GAA AGC ATC ATG CAA CAA AGC	1110
Lys Pro Asn Glu Phe Asn Ser Glu Ile Glu Ser Ile Met Gln Gln Ser	
350 355 360	
TTG ATC AAA AAC GCT AAA TTA GAG ATT GAA AAG ATC AAC CTT TCT TTT	1158
Leu Ile Lys Asn Ala Lys Leu Glu Ile Glu Lys Ile Asn Leu Ser Phe	
365 370 375	
TCA AAA GAT TTC CAT GCG GAA TTT GAA AGC CTG AAC AAG CTT TCT AGC	1206
Ser Lys Asp Phe His Ala Glu Phe Glu Ser Leu Asn Lys Leu Ser Ser	
380 385 390	
GAT CTG TCT GTG AAT TTA GAG CAT GGG ATT GAA TTA GGG ATC AAC GCT	1254
Asp Leu Ser Val Asn Leu Glu His Gly Ile Glu Leu Gly Ile Asn Ala	
395 400 405	
TTA AGC GTG ATT TTT TCC AAG AAT CCG GTT ACA AGG CCA TTC GCG CTG	1302
Leu Ser Val Ile Phe Ser Lys Asn Pro Val Thr Arg Pro Phe Ala Leu	
410 415 420 425	
ATT TTG CAA GGG TTA AAA TCT CTT TTA AAA GAT TTA CTG ACA TTG TTG	1350
Ile Leu Gln Gly Leu Lys Ser Leu Leu Lys Asp Leu Leu Thr Leu Leu	
430 435 440	
CCT AAT ATC ATC GCT TCA TTC TTT AGG AAT GAA GAA AAA GAG CGG GCG	1398
Pro Asn Ile Ile Ala Ser Phe Phe Arg Asn Glu Glu Lys Glu Arg Ala	
445 450 455	

Phe	Val	Glu	Phe	Leu	Glu	Gln	Val	Leu	Glu	Val	Leu	Lys	Glu	Val	Glu		
10					15				20					25			
ATC	GAT	AAA	ACA	GAA	TGC	TCC	ACG	CTT	TTA	GCA	AGC	GTT	CAA	AAA	CAA	150	
Ile	Asp	Lys	Thr	Glu	Cys	Ser	Thr	Leu	Leu	Ala	Ser	Val	Gln	Lys	Gln		
				30				35					40				
CAG	CTA	GTG	ATA	CCC	GTT	GTG	GGG	AAT	TTT	AGC	GCA	GGG	AAA	AGC	ACG	198	
Gln	Leu	Val	Ile	Pro	Val	Val	Gly	Asn	Phe	Ser	Ala	Gly	Lys	Ser	Thr		
			45				50					55					
CTA	TTA	AAC	CGC	TTT	TTA	GGC	AGC	AGC	GTT	TTG	CCT	ACC	GGT	ATC	ACG	246	
Leu	Leu	Asn	Arg	Phe	Leu	Gly	Ser	Ser	Val	Leu	Pro	Thr	Gly	Ile	Thr		
		60				65					70						
CCA	GAG	ACT	TCT	TTA	GCC	ACT	GAG	TTG	CAC	TAT	AGC	GCT	AAG	GAA	CGC	294	
Pro	Glu	Thr	Ser	Leu	Ala	Thr	Glu	Leu	His	Tyr	Ser	Ala	Lys	Glu	Arg		
	75					80				85							
ATA	GAG	GCT	TTT	TCA	AAC	AAT	GAT	GAA	AAA	ACA	GAG	AGT	TTT	GAA	CTG	342	
Ile	Glu	Ala	Phe	Ser	Asn	Asn	Asp	Glu	Lys	Thr	Glu	Ser	Phe	Glu	Leu		
90					95					100				105			
AAT	GAG	CAA	AGT	TTT	GAA	GCG	ATT	AAA	GAG	AAT	GCC	ACG	AAG	TAT	TCC	390	
Asn	Glu	Gln	Ser	Phe	Glu	Ala	Ile	Lys	Glu	Asn	Ala	Thr	Lys	Tyr	Ser		
				110				115				120					
TAC	CTT	AAG	GTT	TAT	TTG	AAT	AAT	GAA	GCT	TTG	AAA	AAC	AGC	GCT	CCT	438	
Tyr	Leu	Lys	Val	Tyr	Leu	Asn	Asn	Glu	Ala	Leu	Lys	Asn	Ser	Ala	Pro		
			125					130				135					
TTA	GTG	TTT	GTG	GAT	ATG	CCA	GGC	TTT	GAT	AGC	CCC	ATT	TCA	AGC	CAC	486	
Leu	Val	Phe	Val	Asp	Met	Pro	Gly	Phe	Asp	Ser	Pro	Ile	Ser	Ser	His		
		140					145					150					
ACC	CAT	GCC	ATT	TTG	GAA	TAT	TTA	GAA	AGG	GGC	GTG	CAT	TTT	GTC	ATT	534	
Thr	His	Ala	Ile	Leu	Glu	Tyr	Leu	Glu	Arg	Gly	Val	His	Phe	Val	Ile		
	155					160				165							
CTC	ACA	AGC	GTA	GAA	GAG	GGC	AAT	CTC	ACT	AAA	CGC	ATG	GTT	AGG	GAG	582	
Leu	Thr	Ser	Val	Glu	Glu	Gly	Asn	Leu	Thr	Lys	Arg	Met	Val	Arg	Glu		
170					175					180				185			
TTA	AAA	AAC	CTT	TTA	GAG	TTT	GAC	AAA	GGC	CTT	AGC	TTT	ATT	TTG	AGT	630	
Leu	Lys	Asn	Leu	Leu	Glu	Phe	Asp	Lys	Gly	Leu	Ser	Phe	Ile	Leu	Ser		
			190					195				200					
AAA	ACG	AAT	TTA	AGA	ACG	CCT	TCG	CAA	GTG	GGA	GAA	ATC	TCT	CAC	TAC	678	
Lys	Thr	Asn	Leu	Arg	Thr	Pro	Ser	Gln	Val	Gly	Glu	Ile	Ser	His	Tyr		
			205					210				215					
ATT	CAA	GAT	CAA	ATC	CAG	GAT	CAC	CTT	GAT	TTG	ACA	ACG	CAC	CTC	ATC	726	
Ile	Gln	Asp	Gln	Ile	Gln	Asp	His	Leu	Asp	Leu	Thr	Thr	His	Leu	Ile		
		220				225						230					

```

Ala Lys Gln Gly Tyr Thr Gly Gly Asp Lys Glu Ala Ser Lys Glu Ser
 210                215                220
Leu Lys His Ala Lys His Ile Leu Trp Leu Ile Ser Cys Glu Ser Gly
225                230                235                240
Glu Ile His Glu Asp Asp Leu Glu Tyr Leu Gln Glu Leu Tyr Glu Glu
                245                250                255
Gly Lys Gln Val Phe Ile Val Leu Ser Arg Ala Asp Arg Arg Thr Lys
 260                265                270
Arg Gln Leu Glu Glu Val Val Ile Lys Ile Lys Glu Thr Leu Lys Asp
 275                280                285
Asn Gly Ile Glu Phe Leu Gly Ile Gly Ala Tyr Ser Ser Thr Arg Tyr
 290                295                300
Gln Glu Tyr Lys Glu Phe Ser Glu Lys Ser Lys Val Phe Asn Ser Leu
305                310                315                320
Glu Glu Phe Leu Met Lys Leu Asn Gln Arg Ser Glu Lys Gln Asn Glu
                325                330                335
Ile Leu Gly Tyr Leu Tyr Glu Val His Ser Met Tyr Glu Lys Ala Ile
 340                345                350
Glu Gln Asp Ala Asn Gln Phe Lys Arg Tyr Gln Ser Glu Leu His Ser
 355                360                365
Val Arg Leu Asp Leu Met Gln Lys Gly Phe Asp Asp Phe Ser Asp Lys
 370                375                380
Ile Phe Arg Arg Ile Glu Asn Leu Glu Lys Glu Phe Ser Glu Gln Glu
385                390                395                400
Arg Ser Lys Arg Glu Ser Leu Ala Arg Leu Asn Glu Val Ile Asp Leu
 405                410                415
Phe Lys Glu Gly Ile Asp Lys Val Phe Asp Arg Val Ser Ala Phe Thr
 420                425                430
Trp Glu Lys Tyr Lys Glu Gln Asn Asp Asp Glu Glu Asp Asp Asp
 435                440                445

```

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1674
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

```

ATTTTAGTTT TTAATTTTAA AGGATTG ATG ATG GTT TTA CGC ACA CAG ACA AAT      54
          Met Met Val Leu Arg Thr Gln Thr Asn
              1                      5

TTT GTG GAG TTT TTA GAA CAG GTT TTA GAA GTT TTA AAA GAA GTG GAG      102

```

```

Asn Leu Glu Lys Glu Phe Ser Glu Gln Glu Arg Ser Lys Arg Glu Ser
      395                                400                        405

TTA GCG CGA TTG AAT GAA GTG ATT GAC TTG TTT AAA GAA GGT ATT GAT      1364
Leu Ala Arg Leu Asn Glu Val Ile Asp Leu Phe Lys Glu Gly Ile Asp
      410                                415                        420

AAG GTT TTT GAT CGC GTG AGC GCT TTC ACT TGG GAA AAA TAC AAA GAA      1412
Lys Val Phe Asp Arg Val Ser Ala Phe Thr Trp Glu Lys Tyr Lys Glu
      425                                430                        435

CAA AAT GAC GAT GAA GAG GAC GAT GAT TGAAGAAAAC TACAAAGAAG AGCGTTA  1466
Gln Asn Asp Asp Glu Glu Asp Asp Asp
      440                                445

CACCGAAAGG GTGAATCAAG GCGG                                          1490

```

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

```

Met Ser Val Asn Phe Phe Lys Gly Ile Phe Asn Asp Asn Ser Arg Ala
  1              5              10              15
Glu Asn His Gln Asp Asn His Gln Asn Asn His Gln Val Gly Leu Lys
      20              25              30
Glu Arg Tyr Asp Leu Ile Ala Arg Ile Leu Asn Ala Arg Ile Glu Asn
      35              40              45
Glu Gly Leu Glu Glu Tyr Gln Ser Val Leu Asp Asn Glu Phe Leu Glu
      50              55              60
Phe Ala Ser Gly Val Asp Ser Leu Lys Glu Lys Glu Ile Ala Leu Leu
      65              70              75              80
Thr Leu Gln Glu Ile Gln Lys Glu Leu Gln Leu Val Ala Ser Tyr Pro
      85              90              95
Ser Leu Phe Gln Lys Thr Ile Val Ala Val Gly Gly Gly Phe Ser Ala
      100             105             110
Gly Lys Ser Thr Phe Leu Asn Asn Leu Leu Gly Leu Lys Leu Lys Leu
      115             120             125
Pro Glu Asp Met Asn Pro Thr Thr Ala Ile Pro Thr Tyr Cys Leu Lys
      130             135             140
Gly Lys Arg Glu Val Leu Met Gly Phe Ser Gln Asn Gly Gly Met Val
      145             150             155             160
Glu Leu Pro His Leu Ala Phe Asp His Gln Phe Leu Asn Ser Leu Gly
      165             170             175
Phe Asn Leu Lys Glu Ile Met Pro Phe Met Leu Leu Ser Ala Pro Ser
      180             185             190
Val Pro Phe Glu Phe Leu Cys Phe Ile Asp Thr Pro Gly Phe Asn Ser
      195             200             205

```

170						175						180						
ATG	CCT	TTC	ATG	CTT	TTA	AGC	GCT	CCT	AGC	GTG	CCT	TTT	GAA	TTT	TTA	692		
Met	Pro	Phe	Met	Leu	Leu	Ser	Ala	Pro	Ser	Val	Pro	Phe	Glu	Phe	Leu			
185						190						195						
TGC	TTC	ATA	GAC	ACG	CCT	GGT	TTT	AAC	TCC	GCC	AAG	CAA	GGC	TAT	ACG	740		
Cys	Phe	Ile	Asp	Thr	Pro	Gly	Phe	Asn	Ser	Ala	Lys	Gln	Gly	Tyr	Thr			
200						205						210						
GGT	GGG	GAT	AAA	GAA	GCC	TCT	AAA	GAA	TCC	CTA	AAA	CAC	GCC	AAA	CAC	788		
Gly	Gly	Asp	Lys	Glu	Ala	Ser	Lys	Glu	Ser	Leu	Lys	His	Ala	Lys	His			
215						220						225						
ATT	CTG	TGG	CTC	ATT	AGT	TGC	GAG	AGT	GGG	GAG	ATT	CAC	GAA	GAT	GAT	836		
Ile	Leu	Trp	Leu	Ile	Ser	Cys	Glu	Ser	Gly	Glu	Ile	His	Glu	Asp	Asp			
235						240						245						
TTA	GAA	TAT	TTG	CAA	GAA	TTA	TAC	GAA	GAA	GGC	AAG	CAG	GTT	TTT	ATC	884		
Leu	Glu	Tyr	Leu	Gln	Glu	Leu	Tyr	Glu	Glu	Gly	Lys	Gln	Val	Phe	Ile			
250						255						260						
GTA	TTG	AGT	AGG	GCT	GAT	AGG	CGC	ACA	AAA	AGG	CAA	TTA	GAA	GAA	GTC	932		
Val	Leu	Ser	Arg	Ala	Asp	Arg	Arg	Thr	Lys	Arg	Gln	Leu	Glu	Glu	Val			
265						270						275						
GTT	ATT	AAA	ATT	AAA	GAG	ACT	TTA	AAA	GAT	AAT	GGC	ATT	GAA	TTT	TTA	980		
Val	Ile	Lys	Ile	Lys	Glu	Thr	Leu	Lys	Asp	Asn	Gly	Ile	Glu	Phe	Leu			
280						285						290						
GGG	ATT	GGT	GCT	TAT	AGT	TCT	ACA	AGG	TAT	CAA	GAA	TAT	AAA	GAA	TTC	1028		
Gly	Ile	Gly	Ala	Tyr	Ser	Ser	Thr	Arg	Tyr	Gln	Glu	Tyr	Lys	Glu	Phe			
295						300						305						
AGC	GAA	AAA	AGC	AAA	GTT	TTT	AAC	TCG	CTT	GAG	GAA	TTT	CTA	ATG	AAG	1076		
Ser	Glu	Lys	Ser	Lys	Val	Phe	Asn	Ser	Leu	Glu	Glu	Phe	Leu	Met	Lys			
315						320						325						
TTA	AAT	CAA	AGG	AGC	GAG	AAA	CAA	AAC	GAA	ATT	TTA	GGA	TAT	TTA	TAC	1124		
Leu	Asn	Gln	Arg	Ser	Glu	Lys	Gln	Asn	Glu	Ile	Leu	Gly	Tyr	Leu	Tyr			
330						335						340						
GAG	GTG	CAT	TCC	ATG	TAT	GAA	AAG	GCT	ATT	GAG	CAA	GAC	GCT	AAC	CAA	1172		
Glu	Val	His	Ser	Met	Tyr	Glu	Lys	Ala	Ile	Glu	Gln	Asp	Ala	Asn	Gln			
345						350						355						
TTC	AAA	CGC	TAC	CAA	AGC	GAA	TTG	CAT	TCT	GTT	AGA	TTG	GAT	TTG	ATG	1220		
Phe	Lys	Arg	Tyr	Gln	Ser	Glu	Leu	His	Ser	Val	Arg	Leu	Asp	Leu	Met			
360						365						370						
CAA	AAA	GGC	TTT	GAT	GAT	TTT	AGC	GAT	AAA	ATT	TTT	AGA	AGA	ATT	GAG	1268		
Gln	Lys	Gly	Phe	Asp	Asp	Phe	Ser	Asp	Lys	Ile	Phe	Arg	Arg	Ile	Glu			
375						380						385						
AAT	TTA	GAA	AAA	GAA	TTT	TCC	GAG	CAA	GAG	CGA	TCC	AAA	AGA	GAG	AGT	1316		

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 99...1439
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

CTTAAAGAAA ACATGCAAAA TTTGCAAAAT CAAGTTCAAA ACAAAGAGCA ATCCATCGCT	60
CAATTAGATG CACAAATCCA AGCTTTAAAG GGGATTCA ATG AGC GTT AAT TTT TTT	116
Met Ser Val Asn Phe Phe	
1 5	
AAG GGC ATT TTT AAT GAC AAT AGC AGG GCT GAA AAC CAC CAA GAC AAC	164
Lys Gly Ile Phe Asn Asp Asn Ser Arg Ala Glu Asn His Gln Asp Asn	
10 15 20	
CAC CAA AAC AAC CAT CAA GTG GGC TTA AAA GAG CGT TAC GAT TTG ATC	212
His Gln Asn Asn His Gln Val Gly Leu Lys Glu Arg Tyr Asp Leu Ile	
25 30 35	
GCT CGT ATT TTA AAC GCC AGA ATT GAA AAT GAA GGG CTA GAA GAA TAT	260
Ala Arg Ile Leu Asn Ala Arg Ile Glu Asn Glu Gly Leu Glu Glu Tyr	
40 45 50	
CAG AGC GTC TTG GAT AAC GAG TTT TTA GAG TTC GCT AGC GGC GTG GAT	308
Gln Ser Val Leu Asp Asn Glu Phe Leu Glu Phe Ala Ser Gly Val Asp	
55 60 65 70	
TCG CTC AAA GAA AAG GAA ATA GCG TTA CTG ACG CTC CAA GAA ATC CAA	356
Ser Leu Lys Glu Lys Glu Ile Ala Leu Leu Thr Leu Gln Glu Ile Gln	
75 80 85	
AAA GAA TTG CAA TTG GTA GCG AGC TAC CCT AGT TTG TTC CAA AAA ACC	404
Lys Glu Leu Gln Leu Val Ala Ser Tyr Pro Ser Leu Phe Gln Lys Thr	
90 95 100	
ATC GTT GCG GTG GGG GGA GGG TTT AGC GCG GGC AAA TCC ACT TTT TTA	452
Ile Val Ala Val Gly Gly Gly Phe Ser Ala Gly Lys Ser Thr Phe Leu	
105 110 115	
AAC AAC TTG TTG GGC TTG AAA TTA AAA CTC CCT GAA GAC ATG AAT CCC	500
Asn Asn Leu Leu Gly Leu Lys Leu Lys Leu Pro Glu Asp Met Asn Pro	
120 125 130	
ACC ACA GCT ATC CCC ACT TAT TGC TTA AAG GGT AAA AGA GAA GTT TTA	548
Thr Thr Ala Ile Pro Thr Tyr Cys Leu Lys Gly Lys Arg Glu Val Leu	
135 140 145 150	
ATG GGG TTT TCT CAA AAT GGG GGC ATG GTG GAA TTG CCA CAT CTC GCT	596
Met Gly Phe Ser Gln Asn Gly Gly Met Val Glu Leu Pro His Leu Ala	
155 160 165	
TTT GAC CAT CAG TTT TTA AAC TCC CTT GGC TTT AAT TTG AAA GAG ATC	644
Phe Asp His Gln Phe Leu Asn Ser Leu Gly Phe Asn Leu Lys Glu Ile	

Ser Lys Val Asp Ala Ile Thr Trp Leu
 205 210

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met	Lys	Phe	Leu	Asp	Gln	Glu	Lys	Arg	Arg	Gln	Leu	Leu	Asn	Glu	Arg	1	5	10	15
His	Ser	Cys	Lys	Met	Phe	Asp	Ser	His	Tyr	Glu	Phe	Ser	Ser	Thr	Glu	20	25	30	
Leu	Glu	Glu	Ile	Ala	Glu	Ile	Ala	Arg	Leu	Ser	Pro	Ser	Ser	Tyr	Asn	35	40	45	
Thr	Gln	Pro	Trp	His	Phe	Val	Met	Val	Thr	Asp	Lys	Asp	Leu	Lys	Lys	50	55	60	
Gln	Ile	Ala	Ala	His	Ser	Tyr	Phe	Asn	Glu	Glu	Met	Ile	Lys	Ser	Ala	65	70	75	80
Ser	Ala	Leu	Met	Val	Val	Cys	Ser	Leu	Arg	Pro	Ser	Glu	Leu	Leu	Pro	85	90	95	
His	Gly	His	Tyr	Met	Gln	Asn	Leu	Tyr	Pro	Glu	Ser	Tyr	Lys	Val	Arg	100	105	110	
Val	Ile	Pro	Ser	Phe	Ala	Gln	Met	Leu	Gly	Val	Arg	Phe	Asn	His	Ser	115	120	125	
Met	Gln	Arg	Leu	Glu	Ser	Tyr	Ile	Leu	Glu	Gln	Cys	Tyr	Ile	Ala	Val	130	135	140	
Gly	Gln	Ile	Cys	Met	Gly	Val	Ser	Leu	Met	Gly	Leu	Asp	Ser	Cys	Ile	145	150	155	160
Ile	Gly	Gly	Phe	Asp	Pro	Leu	Lys	Val	Gly	Glu	Val	Leu	Glu	Glu	Arg	165	170	175	
Ile	Asn	Lys	Pro	Lys	Ile	Ala	Cys	Leu	Ile	Ala	Leu	Gly	Lys	Arg	Val	180	185	190	
Ala	Glu	Ala	Ser	Gln	Lys	Ser	Arg	Lys	Ser	Lys	Val	Asp	Ala	Ile	Thr	195	200	205	
Trp	Leu															210			

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

AAATTCTAAA AAAATAAAGG AAAATCA ATG AAA TTT TTG GAT CAA GAA AAA AGA	54
Met Lys Phe Leu Asp Gln Glu Lys Arg	
1 5	
AGA CAA TTA TTA AAC GAG CGC CAT TCT TGC AAG ATG TTT GAT AGC CAT	102
Arg Gln Leu Leu Asn Glu Arg His Ser Cys Lys Met Phe Asp Ser His	
10 15 20 25	
TAT GAG TTT TCT AGC ACA GAA TTA GAA GAA ATC GCT GAA ATC GCC AGG	150
Tyr Glu Phe Ser Ser Thr Glu Leu Glu Glu Ile Ala Glu Ile Ala Arg	
30 35 40	
CTA TCG CCA AGC TCT TAC AAC ACG CAG CCA TGG CAT TTT GTG ATG GTT	198
Leu Ser Pro Ser Ser Tyr Asn Thr Gln Pro Trp His Phe Val Met Val	
45 50 55	
ACT GAT AAG GAT TTA AAA AAA CAA ATT GCA GCG CAC AGC TAT TTC AAT	246
Thr Asp Lys Asp Leu Lys Lys Gln Ile Ala Ala His Ser Tyr Phe Asn	
60 65 70	
GAA GAG ATG ATT AAA AGC GCT TCA GCG TTA ATG GTG GTA TGC TCT TTA	294
Glu Glu Met Ile Lys Ser Ala Ser Ala Leu Met Val Val Cys Ser Leu	
75 80 85	
AGA CCC AGC GAG TTG TTA CCA CAC GGC CAC TAC ATG CAA AAT CTC TAT	342
Arg Pro Ser Glu Leu Leu Pro His Gly His Tyr Met Gln Asn Leu Tyr	
90 95 100 105	
CCG GAG TCT TAT AAA GTT AGA GTG ATC CCC TCT TTT GCT CAA ATG CTT	390
Pro Glu Ser Tyr Lys Val Arg Val Ile Pro Ser Phe Ala Gln Met Leu	
110 115 120	
GGC GTG AGA TTC AAC CAC AGC ATG CAA AGA TTA GAA AGC TAT ATT TTA	438
Gly Val Arg Phe Asn His Ser Met Gln Arg Leu Glu Ser Tyr Ile Leu	
125 130 135	
GAG CAA TGC TAT ATC GCT GTG GGG CAA ATT TGC ATG GGC GTG AGC TTA	486
Glu Gln Cys Tyr Ile Ala Val Gly Gln Ile Cys Met Gly Val Ser Leu	
140 145 150	
ATG GGA TTG GAT AGT TGC ATT ATT GGA GGC TTT GAT CCT TTA AAG GTG	534
Met Gly Leu Asp Ser Cys Ile Ile Gly Gly Phe Asp Pro Leu Lys Val	
155 160 165	
GGC GAA GTT TTA GAA GAG CGT ATC AAT AAG CCT AAA ATC GCA TGC TTG	582
Gly Glu Val Leu Glu Arg Ile Asn Lys Pro Lys Ile Ala Cys Leu	
170 175 180 185	
ATC GCT TTG GGC AAG AGG GTG GCA GAA GCG AGT CAA AAA TCA AGA AAA	630
Ile Ala Leu Gly Lys Arg Val Ala Glu Ala Ser Gln Lys Ser Arg Lys	
190 195 200	
TCA AAA GTT GAT GCG ATT ACT TGG TTG TGATTAAACA AAATCAAAAA CTTT	681

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

```

Met Lys Phe Lys Phe Leu Asn Met Asp Asn Glu Ser Gly Phe Ile Leu
 1             5             10             15
Ile Glu Lys Glu Leu Lys Arg Leu Asn Ile Leu Ala Gln Val Lys Glu
      20             25             30
Asp Cys Ile Glu Leu Lys Gly Glu Asn Thr Glu Gln Ala Arg Ile Tyr
      35             40             45
Leu Lys Thr Leu Phe Asn Ser Asn Ile Val Glu Leu Asp Asp His Gln
      50             55             60
Lys Ser Ala Asn Ala Leu Ile Glu Arg Leu Lys Ser Leu Asp Leu Lys
      65             70             75             80
Ile Ala Val Ala Glu Ser Cys Ser Gly Gly Leu Leu Ser His Ala Phe
      85             90             95
Thr Ser Ile Ser Gly Ala Ser Ala Val Phe Met Gly Gly Ile Val Cys
      100            105            110
Tyr Asn Glu Glu Val Lys Arg Glu Leu Leu Lys Val Asn Ala Thr Thr
      115            120            125
Leu Lys Val Phe Gly Val Tyr Ser Glu Glu Cys Val Lys Glu Met Leu
      130            135            140
Leu Gly Val Phe Leu Asn Phe Lys Val Asp Leu Ala Leu Ala Met Ser
      145            150            155            160
Gly Val Ala Gly Pro Asn Gly Gly Asn Lys Ala Asn Pro Val Gly Thr
      165            170            175
Ile Tyr Ile Gly Ala Gln Lys Leu Gly Ser Gln Ala Leu Ile Asp Arg
      180            185            190
Cys Phe Phe Glu Gly Asn Arg Glu Ser Ile Gln Asn Lys Ser Val Glu
      195            200            205
His Ala Leu Asn Met Leu Ala Arg Met Leu
      210            215

```

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...657
- (D) OTHER INFORMATION:

CGA TTA AAC ATT CTC GCT CAA GTC AAA GAA GAT TGC ATT GAA TTA AAA	149
Arg Leu Asn Ile Leu Ala Gln Val Lys Glu Asp Cys Ile Glu Leu Lys	
25 30 35	
GGC GAA AAC ACA GAA CAA GCG AGA ATT TAT CTT AAA ACG CTT TTT AAC	197
Gly Glu Asn Thr Glu Gln Ala Arg Ile Tyr Leu Lys Thr Leu Phe Asn	
40 45 50	
TCC AAT ATT GTA GAA TTA GAC GAT CAT CAA AAA AGT GCA AAC GCT TTA	245
Ser Asn Ile Val Glu Leu Asp Asp His Gln Lys Ser Ala Asn Ala Leu	
55 60 65 70	
ATA GAG CGC TTG AAA TCT TTA GAT TTA AAA ATT GCG GTG GCT GAA AGC	293
Ile Glu Arg Leu Lys Ser Leu Asp Leu Lys Ile Ala Val Ala Glu Ser	
75 80 85	
TGC TCT GGG GGG CTA TTA TCG CAT GCA TTC ACT TCC ATT AGC GGG GCT	341
Cys Ser Gly Gly Leu Leu Ser His Ala Phe Thr Ser Ile Ser Gly Ala	
90 95 100	
TCA GCG GTT TTT ATG GGG GGT ATT GTG TGC TAC AAT GAA GAG GTT AAG	389
Ser Ala Val Phe Met Gly Gly Ile Val Cys Tyr Asn Glu Glu Val Lys	
105 110 115	
CGC GAA TTA TTG AAG GTC AAT GCC ACG ACT TTA AAA GTC TTT GGG GTT	437
Arg Glu Leu Leu Lys Val Asn Ala Thr Thr Leu Lys Val Phe Gly Val	
120 125 130	
TAT AGC GAA GAA TGC GTG AAA GAA ATG CTA CTA GGC GTG TTT TTG AAT	485
Tyr Ser Glu Glu Cys Val Lys Glu Met Leu Leu Gly Val Phe Leu Asn	
135 140 145 150	
TTT AAA GTG GAT TTA GCG CTT GCG ATG AGT GGG GTG GCT GGC CCT AAT	533
Phe Lys Val Asp Leu Ala Leu Ala Met Ser Gly Val Ala Gly Pro Asn	
155 160 165	
GGG GGG AAC AAG GCT AAT CCT GTA GGC ACG ATT TAC ATT GGC GCG CAA	581
Gly Gly Asn Lys Ala Asn Pro Val Gly Thr Ile Tyr Ile Gly Ala Gln	
170 175 180	
AAG TTA GGA TCT CAA GCT TTA ATC GAT CGC TGT TTT TTT GAA GGG AAC	629
Lys Leu Gly Ser Gln Ala Leu Ile Asp Arg Cys Phe Phe Glu Gly Asn	
185 190 195	
AGA GAA AGC ATT CAA AAT AAA AGC GTA GAG CAT GCC TTA AAC ATG CTC	677
Arg Glu Ser Ile Gln Asn Lys Ser Val Glu His Ala Leu Asn Met Leu	
200 205 210	
GCT AGA ATG CTA TAAACTACC TTAACGCACA AACGCTACCA AATTCTTTTT GAGCG	734
Ala Arg Met Leu	
215	
ACCTTAGCGA TGTAAGCGAT TT	756

(2) INFORMATION FOR SEQ ID NO:912:

85

90

95

CCGGATAAGG CTCTGTAA

367

(2) INFORMATION FOR SEO ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

Met	Ser	Phe	Arg	Val	Ser	Asn	Thr	Thr	Pro	Gly	His	Glu	Ser	Gly	Ala
1				5					10					15	
Phe	Leu	Asn	Ala	Glu	Ile	Ser	Pro	Ala	Phe	Pro	Lys	Glu	Val	Pro	Phe
			20					25					30		
Ala	Pro	Ser	Phe	Phe	Ser	Ile	Thr	Gln	Thr	Leu	Cys	Pro	Asn	Leu	Cys
		35					40					45			
Ile	Glu	Tyr	Ala	Gln	Glu	Ser	Pro	Thr	Ile	Pro	Pro	Pro	Met	Thr	Thr
	50					55					60				
Thr	Ser	Phe	Phe	Met	Leu	Ile	Val	Pro	Leu	Ile	Asn	Tyr	Leu	Met	Ala
65					70					75					80
Ile	Ala	Ser	Ile	Ser	Thr	Lys	Ala	Ser	Leu	Gly	Ser	Leu	Ala	Thr	
				85					90					95	

(2) INFORMATION FOR SEO ID NO:911:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 36...689
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

GCGCACGCTG AATTTAGGGT TTTGAAAGGT TAAAA ATG AAA TTT AAA TTT TTG 53
Met Lys Phe Lys Phe Leu
1 5

AAT ATG GAT AAT GAA AGC GGT TTT ATT TTG ATT GAA AAA GAA TTG AAA 101
Asn Met Asp Asn Glu Ser Gly Phe Ile Leu Ile Glu Lys Glu Leu Lys
10 15 20

```

385          390          395          400
Val Gly Ala Met Ala Lys Ile Asp Phe Val Trp Asn Leu Ala Asp Leu
          405          410          415
Ser Asn Gly Leu Met Ala Ile Pro Asn Leu Ile Ala Leu Ile Leu Leu
          420          425          430
His Lys Val Val Tyr Ser Glu Thr Arg Trp Tyr Phe Ser Lys His Ser
          435          440          445
Asn Lys
          450

```

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...333
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

```

TTTAAATTAA GCCCGAAATG GAATTTTAAA GGGGCTTGGT TTTTGAGC ATG AGC TTC      57
                                     Met Ser Phe
                                     1

AGG GTG TCT AAC ACC ACA CCA GGG CAT GAG AGT GGG GCT TTT TTA AAC      105
Arg Val Ser Asn Thr Thr Pro Gly His Glu Ser Gly Ala Phe Leu Asn
   5              10              15

GCA GAA ATA AGC CCA GCA TTC CCA AAA GAA GTG CCG TTT GCG CCA TCG      153
Ala Glu Ile Ser Pro Ala Phe Pro Lys Glu Val Pro Phe Ala Pro Ser
  20              25              30              35

TTT TTT TCT ATC ACG CAG ACC TTA TGC CCT AAC TTG TGC ATA GAA TAC      201
Phe Phe Ser Ile Thr Gln Thr Leu Cys Pro Asn Leu Cys Ile Glu Tyr
          40              45              50

GCA CAA GAA AGC CCT ACA ATC CCA CCG CCT ATG ACC ACG ACC TCT TTT      249
Ala Gln Glu Ser Pro Thr Ile Pro Pro Pro Met Thr Thr Ser Phe
          55              60              65

TTC ATG CTG ATA GTC CCT TTA ATA AAT TAC TTA ATG GCT ATC GCT TCA      297
Phe Met Leu Ile Val Pro Leu Ile Asn Tyr Leu Met Ala Ile Ala Ser
          70              75              80

ATT TCT ACT AAA GCG TCT TTA GGC AGT TTA GCC ACT TGAAAGGTCG CTCTGG      349
Ile Ser Thr Lys Ala Ser Leu Gly Ser Leu Ala Thr

```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

```

Met Glu Thr Ile Asp Ser Val Val Arg Leu Leu Ser Asn Leu Val Trp
 1           5           10           15
Gly Ile Pro Met Gln Ile Leu Leu Val Gly Thr Gly Leu Phe Leu Thr
          20           25           30
Phe Tyr Leu Arg Gly Leu Gln Phe Ser Lys Ile Phe Tyr Ala Ile Lys
          35           40           45
Ile Leu Phe Asp Lys Glu Ser Gln Ser Lys Gly Asp Ile Ser Gln Phe
          50           55           60
Ser Ala Leu Met Leu Ser Leu Gly Ala Thr Val Gly Ile Gly Ser Ile
65           70           75           80
Val Gly Val Ala Thr Ala Ile Ser Ile Ala Gly Pro Gly Ala Val Phe
          85           90           95
Trp Met Trp Val Thr Gly Leu Val Gly Met Ala Thr Lys Tyr Ser Glu
          100          105          110
Gly Ile Leu Ala Val Lys Tyr Arg Glu Lys Gly Ala Phe Gly Tyr Asn
          115          120          125
Gly Gly Pro Met Tyr Tyr Ile Lys Asn Gly Leu Asn Met Pro Lys Leu
          130          135          140
Ala Met Ala Phe Ala Ile Phe Thr Ile Ile Ala Ser Ile Gly Thr Gly
145          150          155          160
Asn Met Thr Gln Ser Asn Ala Val Ser Ser Ile Leu Ser Glu Gln Ala
          165          170          175
Asn Leu Pro Asn Trp Val Ser Gly Leu Leu Thr Leu Leu Thr Ala
          180          185          190
Phe Ile Val Ile Gly Gly Ile Lys Ser Ile Gly Lys Phe Thr Ser Tyr
          195          200          205
Leu Ala Pro Val Met Val Leu Leu Tyr Leu Ile Ala Ile Ile Tyr Ile
          210          215          220
Ile Val Ser His Phe Asp Leu Ala Leu Gln Ala Ile Lys Leu Ile Phe
225          230          235          240
Glu Glu Ala Phe Asn Pro Lys Pro Val Val Gly Gly Ala Ser Gly Ala
          245          250          255
Leu Ile Ala Thr Met Ile Lys Thr Gly Val Ala Arg Gly Leu Tyr Ser
          260          265          270
Asn Glu Ala Gly Leu Gly Ser Ser Ala Ile Ile Ala Ala Ser Ala Gln
          275          280          285
Thr Arg His Pro Val Arg Gln Ala Leu Val Ser Met Leu Gln Thr Phe
          290          295          300
Ile Val Thr Leu Ile Val Cys Ser Ala Thr Ala Ser Val Ile Leu Met
305          310          315          320
Ala Pro Glu Tyr Asn Thr Leu Leu Pro Asn Gly Glu Lys Leu Ser Ala
          325          330          335
Asn Leu Leu Thr Leu Lys Ser Thr Glu Tyr Phe Leu Gly Ser Leu Gly
          340          345          350
Thr Val Val Ile Phe Thr Thr Met Ile Phe Phe Ala Tyr Ser Thr Ile
          355          360          365
Ile Gly Trp Ala Tyr Tyr Gly Glu Lys Cys Thr Glu Tyr Ala Phe Gly
          370          375          380
Glu Lys Lys Val Lys Tyr Tyr Arg Leu Ile Phe Leu Ala Ser Val Met

```

Ala Arg Gly Leu Tyr Ser Asn Glu Ala Gly Leu Gly Ser Ser Ala Ile	
270 275 280	
ATT GCC GCG AGC GCT CAA ACA CGC CAC CCG GTG CGC CAA GCC TTA GTG	916
Ile Ala Ala Ser Ala Gln Thr Arg His Pro Val Arg Gln Ala Leu Val	
285 290 295	
TCC ATG CTC CAA ACT TTT ATT GTA ACC TTA ATA GTG TGT TCG GCA ACA	964
Ser Met Leu Gln Thr Phe Ile Val Thr Leu Ile Val Cys Ser Ala Thr	
300 305 310	
GCG AGC GTG ATT TTA ATG GCT CCA GAA TAC AAC ACC TTG CTC CCT AAT	1012
Ala Ser Val Ile Leu Met Ala Pro Glu Tyr Asn Thr Leu Leu Pro Asn	
315 320 325 330	
GGG GAA AAA TTA AGC GCT AAT TTG CTC ACT CTA AAA AGC ACG GAG TAT	1060
Gly Glu Lys Leu Ser Ala Asn Leu Leu Thr Leu Lys Ser Thr Glu Tyr	
335 340 345	
TTT CTA GGC TCA TTA GGG ACG GTG GTG ATT TTT ACA ACC ATG ATC TTT	1108
Phe Leu Gly Ser Leu Gly Thr Val Val Ile Phe Thr Thr Met Ile Phe	
350 355 360	
TTT GCC TAC TCT ACG ATC ATT GGT TGG GCT TAT TAT GGG GAA AAA TGC	1156
Phe Ala Tyr Ser Thr Ile Ile Gly Trp Ala Tyr Tyr Gly Glu Lys Cys	
365 370 375	
ACT GAA TAC GCC TTT GGT GAA AAA AAA GTG AAA TAT TAC CGC TTG ATC	1204
Thr Glu Tyr Ala Phe Gly Glu Lys Lys Val Lys Tyr Tyr Arg Leu Ile	
380 385 390	
TTT TTA GCG AGT GTG ATG GTG GGG GCT ATG GCC AAA ATT GAT TTT GTG	1252
Phe Leu Ala Ser Val Met Val Gly Ala Met Ala Lys Ile Asp Phe Val	
395 400 405 410	
TGG AAT TTA GCG GAT CTT TCT AAC GGG CTT ATG GCT ATC CCT AAT TTA	1300
Trp Asn Leu Ala Asp Leu Ser Asn Gly Leu Met Ala Ile Pro Asn Leu	
415 420 425	
ATC GCT TTG ATT TTA TTG CAT AAA GTG GTT TAT TCT GAA ACT CGT TGG	1348
Ile Ala Leu Ile Leu Leu His Lys Val Val Tyr Ser Glu Thr Arg Trp	
430 435 440	
TAT TTT AGC AAG CAT TCT AAC AAG TAAATGGCA TGTTAAAAAG GGCGAGTTTT	1402
Tyr Phe Ser Lys His Ser Asn Lys	
445 450	
GTAGAAGTGG ATACCGCTTC T	1423

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

45	50	55	
GGC GAC ATT TCA CAA TTT TCC GCT CTC ATG CTC TCT TTG GGG GCG ACT			244
Gly Asp Ile Ser Gln Phe Ser Ala Leu Met Leu Ser Leu Gly Ala Thr			
60	65	70	
GTA GGC ATT GGG AGT ATC GTA GGC GTA GCG ACC GCT ATT AGC ATC GCA			292
Val Gly Ile Gly Ser Ile Val Gly Val Ala Thr Ala Ile Ser Ile Ala			
75	80	85	90
GGG CCA GGA GCG GTG TTT TGG ATG TGG GTT ACT GGG CTT GTT GGC ATG			340
Gly Pro Gly Ala Val Phe Trp Met Trp Val Thr Gly Leu Val Gly Met			
	95	100	105
GCG ACT AAG TAT TCT GAG GGG ATT TTA GCG GTG AAA TAC CGG GAA AAA			388
Ala Thr Lys Tyr Ser Glu Gly Ile Leu Ala Val Lys Tyr Arg Glu Lys			
	110	115	120
GGG GCG TTT GGA TAC AAC GGA GGG CCC ATG TAT TAC ATC AAA AAC GGT			436
Gly Ala Phe Gly Tyr Asn Gly Gly Pro Met Tyr Tyr Ile Lys Asn Gly			
	125	130	135
CTT AAC ATG CCC AAA CTC GCC ATG GCG TTT GCG ATT TTT ACG ATT ATT			484
Leu Asn Met Pro Lys Leu Ala Met Ala Phe Ala Ile Phe Thr Ile Ile			
	140	145	150
GCA AGC ATT GGC ACC GGT AAC ATG ACG CAA TCT AAT GCG GTT TCT TCC			532
Ala Ser Ile Gly Thr Gly Asn Met Thr Gln Ser Asn Ala Val Ser Ser			
155	160	165	170
ATT TTA AGC GAA CAA GCG AAC CTG CCT AAT TGG GTT TCA GGT TTA TTG			580
Ile Leu Ser Glu Gln Ala Asn Leu Pro Asn Trp Val Ser Gly Leu Leu			
	175	180	185
CTC ACT CTT TTA ACC GCT TTC ATT GTC ATA GGG GGG ATC AAA TCC ATT			628
Leu Thr Leu Leu Thr Ala Phe Ile Val Ile Gly Gly Ile Lys Ser Ile			
	190	195	200
GGT AAA TTC ACT TCT TAC TTA GCT CCT GTT ATG GTG CTT TTA TAT TTG			676
Gly Lys Phe Thr Ser Tyr Leu Ala Pro Val Met Val Leu Leu Tyr Leu			
	205	210	215
ATC GCT ATT ATT TAT ATT ATT GTT AGC CAT TTT GAT TTA GCC CTT CAA			724
Ile Ala Ile Ile Tyr Ile Ile Val Ser His Phe Asp Leu Ala Leu Gln			
	220	225	230
GCG ATC AAA CTC ATT TTT GAA GAA GCC TTT AAC CCT AAA CCC GTT GTG			772
Ala Ile Lys Leu Ile Phe Glu Glu Ala Phe Asn Pro Lys Pro Val Val			
235	240	245	250
GGC GGA GCG AGC GGC GCG TTG ATA GCG ACG ATG ATA AAA ACG GGC GTG			820
Gly Gly Ala Ser Gly Ala Leu Ile Ala Thr Met Ile Lys Thr Gly Val			
	255	260	265
GCT AGG GGG TTG TAT TCT AAT GAA GCG GGG TTA GGG AGC TCA GCC ATT			868

(2) INFORMATION FOR SEO ID NO:907:

(A) LENGTH: 1423 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 23...1372
(D) OTHER INFORMATION:

CCTAGT	TTTAT	TAAGGAG	TTT	TT	ATG	GAA	ACG	ATT	GAT	TCG	GTG	GTG	CGT	TTG		52
					Met	Glu	Thr	Ile	Asp	Ser	Val	Val	Arg	Leu		
					1				5					10		
TTA	TCT	AAT	TTG	GTG	TGG	GGG	ATT	CCC	ATG	CAA	ATT	TTA	TTA	GTA	GGC	100
Leu	Ser	Asn	Leu	Val	Trp	Gly	Ile	Pro	Met	Gln	Ile	Leu	Leu	Val	Gly	
				15				20						25		
ACC	GGC	TTG	TTT	TTA	ACC	TTT	TAT	CTT	AGG	GGT	TTG	CAA	TTC	AGT	AAG	148
Thr	Gly	Leu	Phe	Leu	Thr	Phe	Tyr	Leu	Arg	Gly	Leu	Gln	Phe	Ser	Lys	
			30					35					40			
ATT	TTT	TAT	GCG	ATC	AAA	ATC	CTT	TTT	GAC	AAA	GAG	TCC	CAA	TCT	AAG	196
Ile	Phe	Tyr	Ala	Ile	Lys	Ile	Leu	Phe	Asp	Lys	Glu	Ser	Gln	Ser	Lys	

140	145	150	
TTT AAA TAC GAC GCT CAA ATC GTT TCG GTG GAT TCT ATG GCG CAA GCT			532
Phe Lys Tyr Asp Ala Gln Ile Val Ser Val Asp Ser Met Ala Gln Ala			
155	160	165	
TTG TTG CTG GTG GCG CAA AAA CGA GCC GAT TTG ACC TTA AAT AGT TCT			580
Leu Leu Leu Val Ala Gln Lys Arg Ala Asp Leu Thr Leu Asn Ser Ser			
170	175	180	185
TTA GCG ATC TTA AAC TAC CTT AAC ACC CAC AAA GAT AAC CCC TTT AAA			628
Leu Ala Ile Leu Asn Tyr Leu Asn Thr His Lys Asp Asn Pro Phe Lys			
	190	195	200
ATC GCA TGG GAG TCC AAA GAA AAA GAT GGG GGC GCT TCC TTT GTT ATT			676
Ile Ala Trp Glu Ser Lys Glu Lys Asp Gly Gly Ala Ser Phe Val Ile			
	205	210	215
AAC AAG CAC CAA GAA AAA GCC TTA GAG CTT ATC AAC CAA GCG ATG CAA			724
Asn Lys His Gln Glu Lys Ala Leu Glu Leu Ile Asn Gln Ala Met Gln			
	220	225	230
AGA TTG ATC AAC AAA GGG GTT TTA AAA CGC TTA GGC GAA CAA TTT TTT			772
Arg Leu Ile Asn Lys Gly Val Leu Lys Arg Leu Gly Glu Gln Phe Phe			
	235	240	245
GGA AAA GAT GTC AGC CAG CCC TAATCTGTCT TTGTTTTTTG AATCTTTAGA TTTG			827
Gly Lys Asp Val Ser Gln Pro			
250	255		
AGCAAGGAGC GTTTGAAT			846

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

Met	Lys	Lys	Val	Leu	Phe	Leu	Xaa	Val	Ile	Ser	Phe	Phe	Gly	Gly	Phe
1				5				10					15		
Leu	Asn	Ala	Ser	Ser	Leu	Tyr	Glu	Lys	Leu	Ile	Asn	Lys	Glu	Thr	Ile
		20					25					30			
Ser	Val	Gly	Thr	Glu	Gly	Ile	Tyr	Pro	Pro	Phe	Thr	Tyr	His	Asn	Lys
		35				40					45				
Glu	Gly	Lys	Leu	Thr	Gly	Tyr	Asp	Val	Glu	Val	Ala	Arg	Glu	Leu	Ala
	50				55				60						
Lys	Glu	Leu	Gly	Val	Lys	Ile	Lys	Phe	His	Glu	Thr	Ser	Trp	Asp	Ile
65				70			75							80	
Met	Leu	Thr	Gly	Leu	Lys	Ser	Gly	Arg	Phe	Asp	Met	Val	Ala	Asn	Gln

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...793
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

AAAAAATTCA GGATTAAAT ATAAA ATG AAA AAA GTT TTA TTT TTG TNG GTA	52
Met Lys Lys Val Leu Phe Leu Xaa Val	
1 5	
ATA AGC TTT TTT GGG GGT TTT TTG AAC GCT TCT AGC TTG TAT GAA AAA	100
Ile Ser Phe Phe Gly Gly Phe Leu Asn Ala Ser Ser Leu Tyr Glu Lys	
10 15 20 25	
CTG ATT AAT AAA GAA ACG ATC AGC GTT GGC ACA GAA GGC ATT TAC CCC	148
Leu Ile Asn Lys Glu Thr Ile Ser Val Gly Thr Glu Gly Ile Tyr Pro	
30 35 40	
CCT TTC ACT TAC CAC AAT AAA GAA GGC AAG CTC ACC GGC TAT GAT GTG	196
Pro Phe Thr Tyr His Asn Lys Glu Gly Lys Leu Thr Gly Tyr Asp Val	
45 50 55	
GAA GTG GCT AGG GAG TTG GCC AAA GAG CTT GGC GTG AAG ATC AAA TTC	244
Glu Val Ala Arg Glu Leu Ala Lys Glu Leu Gly Val Lys Ile Lys Phe	
60 65 70	
CAC GAA ACT TCA TGG GAT ATC ATG CTG ACA GGT TTG AAA TCG GGG CGT	292
His Glu Thr Ser Trp Asp Ile Met Leu Thr Gly Leu Lys Ser Gly Arg	
75 80 85	
TTT GAT ATG GTC GCT AAC CAA GTG AGT TTG GCG ACT AAA AAA CGC CAA	340
Phe Asp Met Val Ala Asn Gln Val Ser Leu Ala Thr Lys Lys Arg Gln	
90 95 100 105	
GCG GCT TTT GAT AAA AGC TTG CCT TAT AGC TAT TCA GGC ACG ATC ATG	388
Ala Ala Phe Asp Lys Ser Leu Pro Tyr Ser Tyr Ser Gly Thr Ile Met	
110 115 120	
CTG GTC AGG AAA GAT GAA AAC CGC ATT AAA GAT ATT AAA GAC ATC AAG	436
Leu Val Arg Lys Asp Glu Asn Arg Ile Lys Asp Ile Lys Asp Ile Lys	
125 130 135	
GGT TTG AGA GCG GCT AAC ACT TTA AGC TCC ACT TAT GGG GAA ATC GCT	484
Gly Leu Arg Ala Ala Asn Thr Leu Ser Ser Thr Tyr Gly Glu Ile Ala	

```

TTA CAG CAT TTC CAC CTC ACT TTC ACT AAA ATC GCT CAA GGC GTG CCT      530
Leu Gln His Phe His Leu Thr Phe Thr Lys Ile Ala Gln Gly Val Pro
155                      160                      165                      170

ACT GGA GTG AAT TTT GAA AAC ATT GAC TCA GTT TCG CTC TCA AGG GCG      578
Thr Gly Val Asn Phe Glu Asn Ile Asp Ser Val Ser Leu Ser Arg Ala
                      175                      180                      185

TTT AAT TCA AGG ATC AAA GCA TGAATTTAAA TTTTATGCCC CTATTGCATG CTTA    633
Phe Asn Ser Arg Ile Lys Ala
                      190

TAACCATGCG AGCATTGATT TTCATTTCAA TTCTAGTG                                671

```

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

```

Met Asn Thr Tyr Lys Asn Ser Leu Asn His Phe Leu Asn Leu Val Asp
 1           5           10           15
Cys Leu Glu Lys Ile Pro Asn Val Gly Lys Lys Ser Ala Phe Lys Met
          20           25           30
Ala Tyr His Leu Gly Leu Glu Asn Pro Tyr Leu Ala Leu Lys Ile Thr
          35           40           45
His Ala Leu Glu Asn Ala Leu Glu Asn Leu Lys Thr Cys Ser Ser Cys
          50           55           60
Asn Ala Leu Ser Glu Ser Glu Val Cys Glu Ile Cys Ser Asp Glu Ser
65           70           75           80
Arg Gln Asn Ser Gln Leu Cys Met Val Leu His Pro Arg Asp Val Phe
          85           90           95
Ile Leu Glu Asp Leu Lys Asp Phe Leu Gly Arg Tyr Tyr Val Leu Asn
          100          105          110
Ser Ile Glu Glu Val Asp Phe Asn Ala Leu Glu Lys Arg Leu Ile Glu
          115          120          125
Glu Asn Ile Lys Glu Ile Ile Phe Ala Phe Pro Pro Thr Leu Ala Asn
          130          135          140
Asp Ser Leu Met Leu Tyr Ile Glu Asp Lys Leu Gln His Phe His Leu
145          150          155          160
Thr Phe Thr Lys Ile Ala Gln Gly Val Pro Thr Gly Val Asn Phe Glu
          165          170          175
Asn Ile Asp Ser Val Ser Leu Ser Arg Ala Phe Asn Ser Arg Ile Lys
          180          185          190
Ala

```

(2) INFORMATION FOR SEQ ID NO:905:

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 21...599
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

AAGTTTGATA TACTAACAGA	ATG AAT ACT TAT AAA AAC AGC TTG AAT CAC	50
	Met Asn Thr Tyr Lys Asn Ser Leu Asn His	
	1 5 10	
TTT TTA AAT TTA GTG GAT TGT TTA GAA AAA ATC CCC AAT GTG GGT AAA	98	
Phe Leu Asn Leu Val Asp Cys Leu Glu Lys Ile Pro Asn Val Gly Lys		
	15 20 25	
AAG TCC GCC TTT AAA ATG GCG TAT CAT TTG GGT TTA GAA AAC CCC TAT	146	
Lys Ser Ala Phe Lys Met Ala Tyr His Leu Gly Leu Glu Asn Pro Tyr		
	30 35 40	
CTG GCG CTA AAA ATC ACG CAC GCT TTA GAG AAC GCC CTA GAA AAC CTT	194	
Leu Ala Leu Lys Ile Thr His Ala Leu Glu Asn Ala Leu Glu Asn Leu		
	45 50 55	
AAA ACA TGT TCA TCT TGT AAC GCG CTC AGC GAG AGT GAG GTT TGT GAG	242	
Lys Thr Cys Ser Ser Cys Asn Ala Leu Ser Glu Ser Glu Val Cys Glu		
	60 65 70	
ATT TGC TCT GAT GAA AGC CGA CAA AAT TCT CAG CTT TGC ATG GTT TTA	290	
Ile Cys Ser Asp Glu Ser Arg Gln Asn Ser Gln Leu Cys Met Val Leu		
	75 80 85 90	
CAC CCA AGA GAT GTG TTT ATT TTA GAA GAT TTA AAG GAT TTT TTA GGG	338	
His Pro Arg Asp Val Phe Ile Leu Glu Asp Leu Lys Asp Phe Leu Gly		
	95 100 105	
CGC TAT TAT GTG TTA AAC TCC ATA GAA GAA GTG GAT TTT AAC GCC CTA	386	
Arg Tyr Tyr Val Leu Asn Ser Ile Glu Glu Val Asp Phe Asn Ala Leu		
	110 115 120	
GAA AAA CGC CTG ATT GAA GAA AAC ATT AAA GAA ATC ATT TTT GCT TTC	434	
Glu Lys Arg Leu Ile Glu Glu Asn Ile Lys Glu Ile Ile Phe Ala Phe		
	125 130 135	
CCT CCC ACT TTA GCT AAT GAT TCT CTA ATG CTT TAT ATT GAA GAC AAA	482	
Pro Pro Thr Leu Ala Asn Asp Ser Leu Met Leu Tyr Ile Glu Asp Lys		
	140 145 150	

GCA TAC ACG CTC ATC AAA CCA AAG ACA ATA GTT GTC ATG CCC AAA GCC	198
Ala Tyr Thr Leu Ile Lys Pro Lys Thr Ile Val Val Met Pro Lys Ala	
45 50 55	
TGC CAA ATC GCT CCT AAA CCA GCT TTT GCA ATC ACC ATA CCC AAC AAA	246
Cys Gln Ile Ala Pro Lys Pro Ala Phe Ala Ile Thr Ile Pro Asn Lys	
60 65 70	
GGC ACT AGC GTA ACC CCT GAT AAT GAA GTG AAA GCA AAC AGC ATG AAC	294
Gly Thr Ser Val Thr Pro Asp Asn Glu Val Lys Ala Asn Ser Met Asn	
75 80 85	
AGA TTC AAT CCG GGT TTA GAT TTA GAA AAC ATC AAA CCA AAA AAC GCC	342
Arg Phe Asn Pro Gly Leu Asp Leu Glu Asn Ile Lys Pro Lys Asn Ala	
90 95 100	
GCA ATT TCA GCG ATA AAA AAC ACC CAT TTA TAC TGC ACT ACG GCT TGAAA	392
Ala Ile Ser Ala Ile Lys Asn Thr His Leu Tyr Cys Thr Thr Ala	
105 110 115	
ATTCATTAAA CCTAGTAACG CCCCAATAGT CGCTAATAA	431

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

Met Thr Thr Trp Asn Met Gly Leu Pro Lys Asn Lys Leu Met Ser Glu	
1 5 10 15	
His Thr Thr Thr Thr Ile Lys Ala Met Lys Ser Ile Leu Pro Ile Phe	
20 25 30	
Ala Arg Ser Phe Leu Val Leu Arg Ala Tyr Thr Leu Ile Lys Pro Lys	
35 40 45	
Thr Ile Val Val Met Pro Lys Ala Cys Gln Ile Ala Pro Lys Pro Ala	
50 55 60	
Phe Ala Ile Thr Ile Pro Asn Lys Gly Thr Ser Val Thr Pro Asp Asn	
65 70 75 80	
Glu Val Lys Ala Asn Ser Met Asn Arg Phe Asn Pro Gly Leu Asp Leu	
85 90 95	
Glu Asn Ile Lys Pro Lys Asn Ala Ala Ile Ser Ala Ile Lys Asn Thr	
100 105 110	
His Leu Tyr Cys Thr Thr Ala	
115	

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs

```

Val Ile His Thr Ile Asp His Lys Asn Asp Asn Leu Leu Glu Tyr Gly
      180                      185                      190
Leu Asn Tyr Gln Asn Leu Thr Thr Phe Asp Lys Ala Ile Pro Asn Ser
      195                      200                      205
Glu Leu Val Lys Pro Gly Asp Ala Pro Asp Ala Cys Leu Arg Val Thr
      210                      215                      220
Ser Pro Asn Asp Pro Asn Met Asn Gly Arg Cys Gln Arg Asn Gly Ala
      225                      230                      235                      240
Thr Ala Asn Val Ile Gly Val Tyr Ala Gln Ala Asn Tyr Thr Leu His
      245                      250                      255
Pro Met Val Thr Leu Gly Ala Gly Thr Arg Tyr Asp Val Tyr Thr Leu
      260                      265                      270
Val Asp Lys Asp Trp Gln Leu His Ile Thr Gln Gly Phe Ser Pro Ser
      275                      280                      285
Ala Ala Leu Asn Val Ser Pro Leu Glu Asn Leu Asn Phe Arg Leu Ser
      290                      295                      300
Tyr Ala Tyr Val Thr Arg Gly Pro Met Pro Gly Gly Leu Val Trp Met
      305                      310                      315                      320
Arg Gln Asp Asn Leu Xaa Leu Gln Pro Gln Phe Lys Ala Arg Asn Trp
      325                      330                      335
Ala Lys Cys Gly Ile Leu Thr Pro Asn Thr Ala Val Ser Ile Leu Ile
      340                      345                      350
Leu Glu Pro Pro Val Leu Ser Asn
      355                      360

```

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...387
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

```

AGACTGAATA AAATCGCACT CGCTCCCGCA  ATG ACA ACC TGG AAC ATG GGG CTG      54
                               Met Thr Thr Trp Asn Met Gly Leu
                               1                      5

CCC AAA AAC AAG TTA ATG AGC GAA CAC ACC ACC ACC ACA ATC AAA GCG      102
Pro Lys Asn Lys Leu Met Ser Glu His Thr Thr Thr Thr Ile Lys Ala
      10                      15                      20

ATG AAG AGC ATT TTA CCC ATA TTC GCT AGA TCG TTT TTA GTC TTA AGG      150
Met Lys Ser Ile Leu Pro Ile Phe Ala Arg Ser Phe Leu Val Leu Arg
      25                      30                      35                      40

```

```

Leu Asn Val Ser Pro Leu Glu Asn Leu Asn Phe Arg Leu Ser Tyr Ala
      295                      300                      305

TAT GTA ACC AGA GGC CCT ATG CCT GGA GGT TTG GTG TGG ATG CGT CAA      1016
Tyr Val Thr Arg Gly Pro Met Pro Gly Gly Leu Val Trp Met Arg Gln
      310                      315                      320

GAT AAT TTG CGN CTA CAA CCG CAA TTT AAA GCC AGA AAT TGG GCA AAA      1064
Asp Asn Leu Xaa Leu Gln Pro Gln Phe Lys Ala Arg Asn Trp Ala Lys
      325                      330                      335

TGT GGA ATT TTA ACA CCG AAT ACA GCA GTC AGT ATT TTG ATT TTA GAG      1112
Cys Gly Ile Leu Thr Pro Asn Thr Ala Val Ser Ile Leu Ile Leu Glu
      340                      345                      350

CCG CCG GTT TTG TCC AAT TGATTTCTAA TTACATCAAT CAATTTTCTT CAACGCTT      1168
Pro Pro Val Leu Ser Asn
355                      360

TTTGTAACCA ACTTG                                                    1183

```

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

```

Met Ala Lys Ile Asn Gly Tyr Leu Ser Glu Arg Asp Ile Leu Thr Leu
  1           5           10           15
Ser Tyr Asn Met Thr Arg Asp Asn Ala Asn Arg Pro Leu Arg Ala Asn
      20           25           30
Phe Thr Gly Thr Phe Leu Pro Tyr Ser Cys Gly Asp Phe Asn Ala Phe
      35           40           45
Pro Asn Glu Lys Asn Pro Ser Asp Cys Leu Phe Glu Asn Asp Ala Ser
      50           55           60
Leu Phe Lys Thr Tyr Ser Val Asn Leu Val His Asn Val Ser Leu Asn
      65           70           75           80
Tyr Glu Arg Glu Gly Gly Ser Arg Phe Gly Asp Pro Lys Leu Lys Ile
      85           90           95
Asn Gly Tyr Thr Ser Ile Arg Asn Val Gln Ile Asp Pro Leu Phe Lys
      100          105          110
Pro Asn Asp Ile Ala Ala Ser Ile Pro Phe Thr Pro Asn Pro Lys Leu
      115          120          125
Gly Glu Glu Asn Glu Cys Val Ala Gln Gly Gly Ile Tyr Asp Ala Leu
      130          135          140
Lys Gln Thr Cys Ser Ile Thr Phe Lys Ser Leu Gly Gly Gly Ser Val
      145          150          155          160
Val Ala Asn Lys Asn Leu Phe Ile Ile Asn Ser Gly Phe Asn Ala Asn
      165          170          175

```

70						75						80						
AGA Arg	GAA Glu	GGG Gly	GGG Gly	AGC Ser	CGT Arg	TTT Phe	GGT Gly	GAT Asp	CCT Pro	AAA Lys	TTA Leu	AAA Lys	ATC Ile	AAT Asn	GGC Gly	344		
		85					90					95						
TAT Tyr	ACA Thr	AGC Ser	ATT Ile	AGG Arg	AAT Asn	GTC Val	CAA Gln	ATT Ile	GAT Asp	CCG Pro	CTT Leu	TTT Phe	AAG Lys	CCT Pro	AAC Asn	392		
		100					105					110						
GAC Asp	ATA Ile	GCG Ala	GCT Ala	AGT Ser	ATT Ile	CCT Pro	TTC Phe	ACC Thr	CCA Pro	AAC Asn	CCA Pro	AAA Lys	CTT Leu	GGC Gly	GAA Glu	440		
		115					120					125			130			
GAG Glu	AAT Asn	GAA Glu	TGC Cys	GTG Val	GCG Ala	CAA Gln	GGG Gly	GGC Gly	ATT Ile	TAT Tyr	GAC Asp	GCT Ala	CTT Leu	AAA Lys	CAA Gln	488		
				135					140					145				
ACT Thr	TGC Cys	TCC Ser	ATC Ile	ACT Thr	TTT Phe	AAA Lys	AGC Ser	CTT Leu	GGA Gly	GGG Gly	GGT Gly	TCT Ser	GTG Val	GTG Val	GCT Ala	536		
				150					155					160				
AAT Asn	AAA Lys	AAT Asn	TTA Leu	TTC Phe	ATC Ile	ATC Ile	AAT Asn	TCT Ser	GGG Gly	TTT Phe	AAT Asn	GCG Ala	AAC Asn	GTG Val	ATC Ile	584		
				165					170					175				
CAC His	ACC Thr	ATA Ile	GAC Asp	CAT His	AAG Lys	AAT Asn	GAC Asp	AAC Asn	CTT Leu	TTG Leu	GAA Glu	TAC Tyr	GGG Gly	TTG Leu	AAT Asn	632		
				180					185					190				
TAC Tyr	CAA Gln	AAC Asn	TTA Leu	ACC Thr	ACT Thr	TTT Phe	GAT Asp	AAA Lys	GCG Ala	ATC Ile	CCT Pro	AAT Asn	AGC Ser	GAA Glu	TTA Leu	680		
						200					205							
GTC Val	AAA Lys	CCC Pro	GGC Gly	GAT Asp	GCC Ala	CCT Pro	GAC Asp	GCA Ala	TGC Cys	TTA Leu	AGG Arg	GTT Val	ACA Thr	AGC Ser	CCC Pro	728		
				215					220					225				
AAT Asn	GAT Asp	CCC Pro	AAC Asn	ATG Met	AAC Asn	GGG Gly	CGT Arg	TGC Cys	CAA Gln	CGA Arg	AAT Asn	GGC Gly	GCT Ala	ACG Thr	GCG Ala	776		
				230					235					240				
AAT Asn	GTG Val	ATT Ile	GGG Gly	GTG Val	TAT Tyr	GCG Ala	CAA Gln	GCG Ala	AAT Asn	TAC Tyr	ACC Thr	TTG Leu	CAT His	CCT Pro	ATG Met	824		
				245					250					255				
GTA Val	ACT Thr	TTA Leu	GGG Gly	GCA Ala	GGG Gly	ACT Thr	CGT Arg	TAT Tyr	GAT Asp	GTC Val	TAT Tyr	ACT Thr	TTA Leu	GTG Val	GAT Asp	872		
				260					265					270				
AAA Lys	GAC Asp	TGG Trp	CAA Gln	TTG Leu	CAC His	ATA Ile	ACC Thr	CAA Gln	GGG Gly	TTT Phe	AGC Ser	CCT Pro	AGC Ser	GCG Ala	GCT Ala	920		
						280					285							
TTA Asn	AAT Lys	GTC Glu	TCG Cys	CCT Pro	TTA Asn	GAA Glu	AAT Lys	TTG Gln	AAT Lys	TTC Phe	AGG Ser	CTT Pro	TCT Ser	TAT Ala	GCG Gly	968		


```

                260                265                270
Ile Ser Pro Lys Lys Arg Ile Tyr Val Asn Ala Lys Thr His Gln Lys
                275                280                285
Asn Pro Phe Phe Ile His Gln Cys Pro Asn Tyr Asp Gly Ser Ile Leu
                290                295                300
Ala Leu Phe Pro Tyr Asn Gln Asn Leu Asp Leu Gln Asn Leu Cys Asp
305                310                315                320
Lys Leu Asn Ala Ile Asn Trp Gln Glu Leu Gly Phe Val Cys Gly Gly
                325                330                335
Arg Phe Leu Phe Ser Gln Arg Ser Leu Glu Asn Ala Leu Leu Pro Lys
                340                345                350
Asp Phe Leu Asn Leu Gly
                355

```

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1130
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

```

CCTAAAGCGG AGAATAAAGT TACAGAAAGTC CTAGCGAGCA AAACAATGTG  ATG GCT      56
                                     Met Ala
                                     1

AAG ATC AAT GGT TAT TTG AGC GAA AGG GAT ATT TTA ACG CTC AGT TAT      104
Lys Ile Asn Gly Tyr Leu Ser Glu Arg Asp Ile Leu Thr Leu Ser Tyr
      5                10                15

AAC ATG ACC AGA GAC AAC GCT AAC CGC CCT TTA AGA GCG AAT TTT ACA      152
Asn Met Thr Arg Asp Asn Ala Asn Arg Pro Leu Arg Ala Asn Phe Thr
      20                25                30

GGC ACT TTT TTA CCC TAT TCT TGC GGT GAT TTT AAC GCT TTC CCT AAC      200
Gly Thr Phe Leu Pro Tyr Ser Cys Gly Asp Phe Asn Ala Phe Pro Asn
      35                40                45                50

GAG AAA AAC CCT AGC GAT TGT TTG TTT GAA AAC GAC GCT AGT TTG TTT      248
Glu Lys Asn Pro Ser Asp Cys Leu Phe Glu Asn Asp Ala Ser Leu Phe
                55                60                65

AAA ACT TAT AGC GTC AAT TTA GTG CAT AAT GTG AGT TTG AAT TAT GAA      296
Lys Thr Tyr Ser Val Asn Leu Val His Asn Val Ser Leu Asn Tyr Glu

```

TGG CAA GAA TTA GGC TTT GTG TGC GGC GGG CGT TTT TTG TTT TCG CAG 1063
 Trp Gln Glu Leu Gly Phe Val Cys Gly Gly Arg Phe Leu Phe Ser Gln
 330 335 340

CGC TCT TTA GAA AAC GCG CTT TTG CCT AAA GAC TTT TTA AAT CTA GGA T 1112
 Arg Ser Leu Glu Asn Ala Leu Leu Pro Lys Asp Phe Leu Asn Leu Gly
 345 350 355

AAAACCTTGTT AGAAACTTTG CAATTAAACC CTGAGCAGC 1151

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

Met	Leu	Thr	Leu	Lys	His	Asn	His	Gly	Ser	Val	Leu	Glu	Pro	Ser	Ala
1				5				10					15		
Gly	Asp	Gly	Ser	Phe	Leu	Lys	Arg	Leu	Lys	Lys	Ala	Val	Arg	Ile	Glu
	20							25					30		
Ile	Asp	Pro	Lys	Ile	Cys	Pro	Lys	Asn	Ala	Leu	Cys	Met	Asp	Phe	Phe
	35						40					45			
Asp	Tyr	Pro	Leu	Glu	Asn	Gln	Phe	Asp	Thr	Ile	Ile	Gly	Asn	Pro	Pro
	50					55					60				
Tyr	Val	Lys	His	Lys	Asp	Ile	Ala	Pro	Ser	Thr	Lys	Glu	Lys	Leu	His
	65				70					75					80
Tyr	Ser	Leu	Phe	Asp	Glu	Arg	Ser	Asn	Leu	Tyr	Leu	Phe	Phe	Ile	Glu
			85					90						95	
Lys	Ala	Ile	Lys	His	Leu	Lys	Pro	Lys	Gly	Glu	Leu	Ile	Phe	Ile	Thr
		100						105					110		
Pro	Arg	Asp	Phe	Leu	Lys	Ser	Thr	Ser	Ser	Val	Lys	Leu	Asn	Glu	Trp
		115					120					125			
Ile	Tyr	Lys	Glu	Gly	Thr	Ile	Thr	His	Phe	Phe	Glu	Leu	Gly	Asp	Gln
	130					135					140				
Lys	Val	Phe	Pro	Asn	Ala	Met	Pro	Asn	Cys	Val	Ile	Phe	Arg	Phe	Cys
	145				150				155						160
Lys	Gly	Asn	Phe	Ser	Arg	Ile	Thr	Asn	Asp	Gly	Leu	Gln	Phe	Leu	Cys
			165					170						175	
Lys	Lys	Gly	Ile	Leu	Tyr	Phe	Leu	Asn	Gln	Ser	Tyr	Thr	Gln	Lys	Leu
		180						185					190		
Ser	Glu	Val	Phe	Lys	Val	Lys	Val	Gly	Ala	Val	Ser	Gly	Cys	Asp	Lys
		195					200					205			
Ile	Phe	Lys	Asn	Glu	Lys	Tyr	Gly	Asn	Leu	Glu	Phe	Val	Thr	Ser	Ile
	210					215					220				
Thr	Lys	Arg	Thr	Asn	Ala	Leu	Glu	Lys	Met	Val	Phe	Val	Asn	Glu	Pro
	225				230				235						240
Asn	Asp	Tyr	Leu	Leu	Gln	His	Lys	Asp	Ser	Leu	Met	Gln	Arg	Lys	Ile
			245					250						255	
Lys	Lys	Phe	Asn	Glu	Asn	Asn	Trp	Phe	Glu	Trp	Gly	Arg	Met	His	His

AAA CCT AAA GGC GAA TTG ATT TTC ATC ACC CCA AGG GAT TTT TTA AAA	391
Lys Pro Lys Gly Glu Leu Ile Phe Ile Thr Pro Arg Asp Phe Leu Lys	
105 110 115	
TCC ACT TCT AGC GTG AAA TTA AAC GAA TGG ATT TAT AAA GAA GGC ACG	439
Ser Thr Ser Ser Val Lys Leu Asn Glu Trp Ile Tyr Lys Glu Gly Thr	
120 125 130	
ATA ACG CAT TTT TTT GAA CTG GGC GAT CAA AAG GTT TTC CCA AAC GCC	487
Ile Thr His Phe Phe Glu Leu Gly Asp Gln Lys Val Phe Pro Asn Ala	
135 140 145 150	
ATG CCT AAT TGC GTG ATT TTT CGT TTT TGT AAG GGT AAT TTC AGT AGA	535
Met Pro Asn Cys Val Ile Phe Arg Phe Cys Lys Gly Asn Phe Ser Arg	
155 160 165	
ATC ACC AAC GAT GGT TTG CAA TTT TTG TGC AAA AAA GGC ATT TTG TAT	583
Ile Thr Asn Asp Gly Leu Gln Phe Leu Cys Lys Lys Gly Ile Leu Tyr	
170 175 180	
TTC CTC AAC CAA TCT TAC ACG CAA AAA TTA AGC GAG GTT TTT AAG GTT	631
Phe Leu Asn Gln Ser Tyr Thr Gln Lys Leu Ser Glu Val Phe Lys Val	
185 190 195	
AAA GTG GGG GCA GTG AGC GGG TGC GAT AAG ATT TTT AAA AAT GAA AAA	679
Lys Val Gly Ala Val Ser Gly Cys Asp Lys Ile Phe Lys Asn Glu Lys	
200 205 210	
TAC GGG AAT TTA GAA TTT GTC ACC TCA ATC ACG AAA AGA ACC AAT GCT	727
Tyr Gly Asn Leu Glu Phe Val Thr Ser Ile Thr Lys Arg Thr Asn Ala	
215 220 225 230	
TTA GAA AAA ATG GTT TTT GTC AAT GAG CCT AAT GAT TAT TTA CTC CAG	775
Leu Glu Lys Met Val Phe Val Asn Glu Pro Asn Asp Tyr Leu Leu Gln	
235 240 245	
CAT AAA GAC AGC TTA ATG CAA AGA AAG ATT AAA AAA TTC AAT GAA AAT	823
His Lys Asp Ser Leu Met Gln Arg Lys Ile Lys Lys Phe Asn Glu Asn	
250 255 260	
AAC TGG TTT GAG TGG GGG AGA ATG CAT CAC ATA TCC CCT AAA AAA CGC	871
Asn Trp Phe Glu Trp Gly Arg Met His His Ile Ser Pro Lys Lys Arg	
265 270 275	
ATT TAT GTC AAC GCC AAA ACG CAC CAA AAA AAC CCC TTT TTT ATC CAC	919
Ile Tyr Val Asn Ala Lys Thr His Gln Lys Asn Pro Phe Phe Ile His	
280 285 290	
CAA TGC CCT AAT TAT GAC GGC TCT ATT TTA GCG CTA TTC CCT TAT AAC	967
Gln Cys Pro Asn Tyr Asp Gly Ser Ile Leu Ala Leu Phe Pro Tyr Asn	
295 300 305 310	
CAA AAC CTG GAC TTA CAA AAT CTC TGC GAC AAA CTC AAC GCT ATC AAC	1015
Gln Asn Leu Asp Leu Gln Asn Leu Cys Asp Lys Leu Asn Ala Ile Asn	
315 320 325	

Glu Ala Leu Thr Ile Ala Gln Lys Leu Asp Pro Gln Leu Glu Ile Asp
 65 70 75 80
 Gly Pro Leu Gln Phe Asp Ala Ser Ile Asp Lys Ser Val Ala Lys Lys
 85 90 95
 Lys Cys Leu Thr Ala Lys Trp Leu Gly Lys Leu Ala Phe Leu Phe Ser
 100 105 110
 Arg Ile

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 38...1111
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

AGGGCAGGTT TTCACCCCTA AAAAGATAGT GGATTTTC ATG CTC ACT CTC AAA CAC 55
 Met Leu Thr Leu Lys His
 1 5

AAT CAT GGG AGT GTT TTA GAA CCG AGT GCT GGC GAT GGG AGT TTT TTA 103
 Asn His Gly Ser Val Leu Glu Pro Ser Ala Gly Asp Gly Ser Phe Leu
 10 15 20

AAG CGC TTA AAA AAG GCC GTA AGG ATT GAA ATC GAT CCT AAA ATC TGC 151
 Lys Arg Leu Lys Lys Ala Val Arg Ile Glu Ile Asp Pro Lys Ile Cys
 25 30 35

CCT AAA AAT GCC CTT TGC ATG GAC TTT TTT GAC TAC CCT TTA GAA AAT 199
 Pro Lys Asn Ala Leu Cys Met Asp Phe Phe Asp Tyr Pro Leu Glu Asn
 40 45 50

CAA TTT GAC ACC ATT ATT GGT AAC CCG CCC TAT GTC AAG CAC AAG GAT 247
 Gln Phe Asp Thr Ile Ile Gly Asn Pro Pro Tyr Val Lys His Lys Asp
 55 60 65 70

ATT GCG CCA AGC ACC AAA GAA AAA CTC CAT TAC AGC CTT TTT GAT GAA 295
 Ile Ala Pro Ser Thr Lys Glu Lys Leu His Tyr Ser Leu Phe Asp Glu
 75 80 85

AGG AGT AAT CTC TAC TTG TTT TTC ATA GAA AAA GCG ATC AAG CAT TTA 343
 Arg Ser Asn Leu Tyr Leu Phe Phe Ile Glu Lys Ala Ile Lys His Leu
 90 95 100

```

TGAATCACAG CTGAGACCAT TAGACCCGCT TTACAAATCA TCAAACTAA ACCCGGCGTG      60
AGCCTGGTTT CAAGCGTGTT TTTA ATG TGT TTA GAC ACT CAA GTG CTA GTC      111
          Met Cys Leu Asp Thr Gln Val Leu Val
                1                5

TTT GGG GAT TGC GCG ATT ATC CCT AAC CCT AGC CCT AAA GAA TTA GCC      159
Phe Gly Asp Cys Ala Ile Ile Pro Asn Pro Ser Pro Lys Glu Leu Ala
10                15                20                25

GAG ATC GCT ACC ACT TCC GCA CAA ACC GCC AAG CAA TTC AAT ATT GCG      207
Glu Ile Ala Thr Thr Ser Ala Gln Thr Ala Lys Gln Phe Asn Ile Ala
                30                35                40

CCT AAA GTG GCC TTG CTT TCT TAT GCG ACA GGC GAT TCC GCT CAA GGC      255
Pro Lys Val Ala Leu Leu Ser Tyr Ala Thr Gly Asp Ser Ala Gln Gly
                45                50                55

GAA ATG ATA GAC AAA ATC AAC GAA GCT TTA ACA ATC GCT CAA AAG TTG      303
Glu Met Ile Asp Lys Ile Asn Glu Ala Leu Thr Ile Ala Gln Lys Leu
                60                65                70

GAT CCC CAA TTA GAA ATT GAT GGC CCC TTA CAA TTT GAC GCT TCC ATT      351
Asp Pro Gln Leu Glu Ile Asp Gly Pro Leu Gln Phe Asp Ala Ser Ile
                75                80                85

GAT AAA AGC GTA GCC AAG AAA AAA TGC CTA ACA GCC AAG TGG CTG GGC      399
Asp Lys Ser Val Ala Lys Lys Lys Cys Leu Thr Ala Lys Trp Leu Gly
90                95                100                105

AAG CTA GCG TTT TTA TTT TCC CGG ATT TAAACGCTGG GAACATCGCT TATAAAG      453
Lys Leu Ala Phe Leu Phe Ser Arg Ile
                110

CGGTGCAACG GAGCGCTAAA GCCGTGGCGA TAG      486

```

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

```

Met Cys Leu Asp Thr Gln Val Leu Val Phe Gly Asp Cys Ala Ile Ile
1                5                10                15
Pro Asn Pro Ser Pro Lys Glu Leu Ala Glu Ile Ala Thr Thr Ser Ala
                20                25                30
Gln Thr Ala Lys Gln Phe Asn Ile Ala Pro Lys Val Ala Leu Leu Ser
                35                40                45
Tyr Ala Thr Gly Asp Ser Ala Gln Gly Glu Met Ile Asp Lys Ile Asn
50                55                60

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

```

Met Pro Gly Pro Lys Pro Gly Ala Leu Pro Leu Gly Asp Thr Pro Lys
 1           5           10           15
Thr Lys Glu Ser Ile Ile Gln Lys Leu Phe Lys Lys Val Lys Leu Lys
      20           25           30
Arg Tyr Asn Phe Ile Met Glu Asn Gly Phe Asp Pro Ile Ile Tyr Lys
      35           40           45
Arg Tyr Leu Lys Lys Lys Glu Thr Phe Leu Leu Phe Lys Lys Ile Ala
      50           55           60
Gln Ala Ser Ala Phe Lys Asn Leu Lys Leu Gln Leu Lys Arg Arg Glu
65           70           75           80
Ile Ile Asn Arg Tyr Val Ser Gln Ala Leu Gly Asp Leu Lys Lys Gly
      85           90           95
Phe Arg Tyr Ala Lys Val Glu His Gln Ile Leu Lys Ile Tyr Phe Thr
      100          105          110
His Pro Ser Tyr Leu Lys Ala Phe Lys Ile Glu Glu Ala Tyr Tyr Thr
      115          120          125
Asn His Leu Lys Ala His Leu Lys Glu Thr Gln Lys Thr Leu Lys Ala
      130          135          140
Leu Asp Tyr Pro Phe Asp Phe Lys Thr Ile Gln Ala Ser Val Lys Lys
145          150          155          160
Arg Ala Tyr Gln Lys Pro Val Val Lys Lys Glu Lys Pro Pro Lys Ser
      165          170          175
Val Asn Val Asn Cys Glu Gly Leu Ser Asp Phe Thr Lys Lys Gln Phe
      180          185          190
Leu Lys Leu Lys Arg Ala Cys Asn Asp Asn Thr Leu Arg Thr Pro Pro
      195          200          205

```

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 85...426
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GGT GCC TTA CCG CTT GGC GAC ACC CCA AAA ACT AAA GAA AGC ATT ATA	104
Gly Ala Leu Pro Leu Gly Asp Thr Pro Lys Thr Lys Glu Ser Ile Ile	
10 15 20	
CAA AAG CTT TTT AAA AAA GTC AAG CTA AAA CGC TAT AAT TTT ATC ATG	152
Gln Lys Leu Phe Lys Lys Val Lys Leu Lys Arg Tyr Asn Phe Ile Met	
25 30 35	
GAA AAT GGA TTT GAC CCC ATC ATT TAT AAA CGC TAT TTG AAA AAG AAA	200
Glu Asn Gly Phe Asp Pro Ile Ile Tyr Lys Arg Tyr Leu Lys Lys Lys	
40 45 50	
GAA ACC TTT TTG CTG TTT AAA AAA ATC GCT CAA GCG TCT GCG TTT AAA	248
Glu Thr Phe Leu Leu Phe Lys Lys Ile Ala Gln Ala Ser Ala Phe Lys	
55 60 65 70	
AAT TTA AAA CTC CAA CTC AAA CGA AGA GAA ATA ATC AAC CGC TAT GTT	296
Asn Leu Lys Leu Gln Leu Lys Arg Arg Glu Ile Ile Asn Arg Tyr Val	
75 80 85	
TCT CAA GCT TTG GGG GAT TTA AAA AAA GGG TTT AGA TAC GCT AAA GTA	344
Ser Gln Ala Leu Gly Asp Leu Lys Lys Gly Phe Arg Tyr Ala Lys Val	
90 95 100	
GAA CAC CAA ATC CTA AAA ATC TAT TTC ACG CAC CCT AGC TAT TTG AAA	392
Glu His Gln Ile Leu Lys Ile Tyr Phe Thr His Pro Ser Tyr Leu Lys	
105 110 115	
GCC TTT AAA ATA GAA GAA GCC TAT TAC ACC AAC CAC CTG AAA GCC CAT	440
Ala Phe Lys Ile Glu Glu Ala Tyr Tyr Thr Asn His Leu Lys Ala His	
120 125 130	
TTA AAA GAA ACG CAA AAA ACC CTA AAA GCC CTA GAT TAC CCC TTT GAT	488
Leu Lys Glu Thr Gln Lys Thr Leu Lys Ala Leu Asp Tyr Pro Phe Asp	
135 140 145 150	
TTT AAG ACT ATC CAA GCG AGC GTG AAA AAA AGG GCT TAT CAA AAA CCA	536
Phe Lys Thr Ile Gln Ala Ser Val Lys Lys Arg Ala Tyr Gln Lys Pro	
155 160 165	
GTT GTT AAA AAA GAA AAA CCC CCT AAA AGC GTG AAT GTC AAT TGC GAA	584
Val Val Lys Lys Glu Lys Pro Pro Lys Ser Val Asn Val Asn Cys Glu	
170 175 180	
GGT TTG AGC GAT TTC ACT AAA AAG CAA TTT TTA AAG CTC AAA CGC GCT	632
Gly Leu Ser Asp Phe Thr Lys Lys Gln Phe Leu Lys Leu Lys Arg Ala	
185 190 195	
TGT AAC GAT AAT ACG CTG CGC ACG CCC CCT TGAGAGCTGA CCATGCAACT GCC	685
Cys Asn Asp Asn Thr Leu Arg Thr Pro Pro	
200 205	
GATCGGGTTT TCGGGGTGC AAGTTT	711

(2) INFORMATION FOR SEQ ID NO:894:

Ile Thr Gln Ala Lys Ala Ile
105

ACGATTAATC TGA

410

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

Met	Leu	Asp	Ser	Thr	Thr	Ala	Ile	Ala	Ile	Ala	Thr	Pro	Ser	Ile	Ala
1				5				10						15	
Pro	Leu	Glu	Ile	Pro	Ser	Lys	Lys	Gly	Ser	Thr	Lys	Gly	Phe	Leu	Lys
			20					25					30		
Ile	Val	Cys	Ile	Thr	Thr	Pro	Leu	Pro	Asp	Lys	Leu	Ala	Pro	Thr	Arg
		35				40						45			
Ser	Ala	Lys	Ile	Thr	Arg	Gly	Ser	Arg	Ile	Ser	Lys	Ile	Ile	Ile	Leu
	50					55					60				
Lys	Glu	Leu	Ser	Ser	Ser	Leu	Cys	Lys	Lys	Trp	Phe	Phe	Thr	Leu	Arg
65					70					75				80	
His	Thr	Ser	Cys	His	Ser	Ser	Lys	Leu	Lys	Asp	Ser	Pro	Pro	Asn	Asn
			85					90						95	
Ser	Thr	Thr	Thr	Ala	Lys	Ile	Thr	Gln	Ala	Lys	Ala	Ile			
			100					105							

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...662
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

AGGAAAAATG	GCTGGGGTGC	AAGGATTCGA	ACCTCGGA	ATG	CCA	GGA	CCA	AAA	CCT	56
				Met	Pro	Gly	Pro	Lys	Pro	
				1				5		


```

Leu Ala Asp Val Val Ala Lys Thr Ile Thr Pro Tyr Asp Leu Pro Val
  290                      295                      300
Gly Ile Ala Thr Ser Val Leu Gly Ala Pro Phe Phe Leu Trp Leu Leu
305                      310                      315                      320
Phe Arg Thr Arg Gly Val
                      325

```

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...363
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

```

CTAGCTAAAA TCGCCCCAAA AAACGCCAAA ATCGCA ATG TTA GAC TCC ACT ACC      54
                      Met Leu Asp Ser Thr Thr
                      1                      5

GCT ATC GCC ATC GCC ACG CCT AGC ATC GCC CCG CTA GAA ATC CCT AGT      102
Ala Ile Ala Ile Ala Thr Pro Ser Ile Ala Pro Leu Glu Ile Pro Ser
                      10                      15                      20

AAA AAG GGA TCC ACT AAG GGG TTT CTA AAA ATC GTT TGC ATC ACC ACC      150
Lys Lys Gly Ser Thr Lys Gly Phe Leu Lys Ile Val Cys Ile Thr Thr
                      25                      30                      35

CCA CTC CCA GAC AAA CTC GCT CCC ACC AGG AGC GCT AAA ATC ACT CGT      198
Pro Leu Pro Asp Lys Leu Ala Pro Thr Arg Ser Ala Lys Ile Thr Arg
                      40                      45                      50

GGT AGT CGT ATT TCT AAA ATA ATA ATA CTT AAA GAG CTC AGT TCT TCA      246
Gly Ser Arg Ile Ser Lys Ile Ile Ile Leu Lys Glu Leu Ser Ser Ser
55                      60                      65                      70

TTG TGC AAA AAG TGG TTT TTC ACA TTA AGG CAC ACT TCT TGC CAT TCT      294
Leu Cys Lys Lys Trp Phe Phe Thr Leu Arg His Thr Ser Cys His Ser
                      75                      80                      85

TCC AAG CTC AAG GAC TCC CCT CCA AAC AAC AGC ACC ACC ACC GCT AAA      342
Ser Lys Leu Lys Asp Ser Pro Pro Asn Asn Ser Thr Thr Thr Ala Lys
                      90                      95                      100

ATC ACG CAA GCT AAG GCG ATA TGATAGGTTT TAAGCATCAC GCTTCCTTTT AAGA      397

```

GATGGTTTTA GAAGTTAAAA ACCTGTCCTT TAAATATTCT CAAAAACTCA TTTTGGATAA	1077
ATT	1080

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEO ID NO:890:

-1321-

CCC TTA GTG GAT CCC TTT TTA CTA GGG ATT TCT AGC GGG GCG ATG CTA	344
Pro Leu Val Asp Pro Phe Leu Leu Gly Ile Ser Ser Gly Ala Met Leu	
90 95 100	
GGC GTG GCG ATG GCG ATA GCG GTA GTG GAG TCT AAC ATT GCG ATT TTG	392
Gly Val Ala Met Ala Ile Ala Val Val Glu Ser Asn Ile Ala Ile Leu	
105 110 115	
GCG TTT TTT GGG GCG ATT TTA GCT AGC CTT GCT GTT TTG GCG ATG AAT	440
Ala Phe Phe Gly Ala Ile Leu Ala Ser Leu Ala Val Leu Ala Met Asn	
120 125 130	
AGG GTT TTG GGT AAT TCC GTC CTT TCG TTG GTG CTT TCA GGG GTG GTG	488
Arg Val Leu Gly Asn Ser Val Leu Ser Leu Val Leu Ser Gly Val Val	
135 140 145 150	
TTG AGC GCG TTT TTA AGC GCC TTA GCC GGA GCG ATA AAA TTC TTT GTG	536
Leu Ser Ala Phe Leu Ser Ala Leu Ala Gly Ala Ile Lys Phe Phe Val	
155 160 165	
ATC CCC CAA AAA GCG CAA GCG ATT GTC GTG TGG CTT TTA GGG AGC TTG	584
Ile Pro Gln Lys Ala Gln Ala Ile Val Val Trp Leu Leu Gly Ser Leu	
170 175 180	
TCG TTG AGC AGT TAT AAG GAT TGC TTG ATC GCT TTC ATA GGG CTA TCT	632
Ser Leu Ser Ser Tyr Lys Asp Cys Leu Ile Ala Phe Ile Gly Leu Ser	
185 190 195	
TTA GGC TTT ATC CCG CTT TTT TTG TTA AGG TGG CGC ATC AAT TTA TTG	680
Leu Gly Phe Ile Pro Leu Phe Leu Leu Arg Trp Arg Ile Asn Leu Leu	
200 205 210	
AGC TTG AGC GAT GCG CAA AGT TTG AGC TTG GGG ATT AAC CCG GTG CTG	728
Ser Leu Ser Asp Ala Gln Ser Leu Ser Leu Gly Ile Asn Pro Val Leu	
215 220 225 230	
TTG CGA TCG CTT TGT TTG GTG TGC GTG AGC GTT GCG AGC GCT TTA GCG	776
Leu Arg Ser Leu Cys Leu Val Cys Val Ser Val Ala Ser Ala Leu Ala	
235 240 245	
GTG AGC GTG TCC GGC ACG ATT GGC TGG ATT GGG TTA GTC ATT CCG CAT	824
Val Ser Val Ser Gly Thr Ile Gly Trp Ile Gly Leu Val Ile Pro His	
250 255 260	
GTG GCT AGG TTG TTT TTT GGG GCG AAT TTG CAA AAA CTG CTT TTA AGT	872
Val Ala Arg Leu Phe Phe Gly Ala Asn Leu Gln Lys Leu Leu Leu Ser	
265 270 275	
TCT TTG TTA ATG GGA GCG TTT TTC TTG CTT CTA GCG GAT GTG GTG GCT	920
Ser Leu Leu Met Gly Ala Phe Phe Leu Leu Leu Ala Asp Val Val Ala	
280 285 290	
AAA ACC ATT ACC CCC TAT GAT TTA CCG GTA GGC ATT GCG ACA AGC GTT	968
Lys Thr Ile Thr Pro Tyr Asp Leu Pro Val Gly Ile Ala Thr Ser Val	
295 300 305 310	

```

65          70          75          80
Gly Leu Ile Phe Cys Ile Val Leu Phe Met Trp Cys Leu Leu Val Ala
          85          90          95
Leu Asn Pro Leu Trp Leu Ala Lys Leu Leu Ala Tyr Gly Phe Asp Glu
          100          105          110
Glu Thr Leu Lys Leu Cys Ala Pro Ile Val Ala Ile Asn Phe Trp Xaa
          115          120          125
Leu Leu Leu Val Phe Ile Thr Thr Phe Leu Gly Ala Leu Leu Gln Xaa
          130          135          140
Gln Thr Gln Leu Phe Cys Gln Arg Leu
145          150

```

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...1016
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

```

TTCTTTGTTC AGATTAATCG TTCTTAAAAG GAAGCGTG ATG CTT AAA ACC TAT CAT      56
                               Met Leu Lys Thr Tyr His
                               1           5

ATC GCC TTA GCT TGC GTG ATT TTA GCG GTG GTG GTG CTG TTG TTT GGA      104
Ile Ala Leu Ala Cys Val Ile Leu Ala Val Val Val Leu Leu Phe Gly
          10           15           20

GGG GAG TCC TTG AGC TTG GAA GAA TGG CAA GAA GTG TGC CTT AAT GTG      152
Gly Glu Ser Leu Ser Leu Glu Glu Trp Gln Glu Val Cys Leu Asn Val
          25           30           35

AAA AAC CAC TTT TTG CAC AAT GAA GAA CTG AGC TCT TTA AGT ATT ATT      200
Lys Asn His Phe Leu His Asn Glu Glu Leu Ser Ser Leu Ser Ile Ile
          40           45           50

ATT TTA GAA ATA CGA CTA CCA CGA GTG ATT TTA GCG CTC CTG GTG GGA      248
Ile Leu Glu Ile Arg Leu Pro Arg Val Ile Leu Ala Leu Leu Val Gly
55           60           65           70

GCG AGT TTG TCT GGG AGT GGG GTG GTG ATG CAA ACG ATT TTT AGA AAC      296
Ala Ser Leu Ser Gly Ser Gly Val Val Met Gln Thr Ile Phe Arg Asn
          75           80           85

```

ATG ATG GCT AAT ATT CTA GGG GCT GGG GTG TAT AGC GAT ATT TTC TTT	150
Met Met Ala Asn Ile Leu Gly Ala Gly Val Tyr Ser Asp Ile Phe Phe	
30 35 40	
GTG GCT TTC AAA TTG CCT AAT TTA TTC AGG CGT ATT TTT GCG GAG GGC	198
Val Ala Phe Lys Leu Pro Asn Leu Phe Arg Arg Ile Phe Ala Glu Gly	
45 50 55	
TCT TTT TCA CAA AGC TTT TTA CCG AGC TTC ATA CGA AGT TCT ATT AAA	246
Ser Phe Ser Gln Ser Phe Leu Pro Ser Phe Ile Arg Ser Ser Ile Lys	
60 65 70	
GGG AGC TTT GCG AGT TTG GTA GGG CTT ATT TTT TGT ATC GTT TTA TTC	294
Gly Ser Phe Ala Ser Leu Val Gly Leu Ile Phe Cys Ile Val Leu Phe	
75 80 85	
ATG TGG TGC TTA TTG GTG GCG TTA AAT CCC TTA TGG CTA GCT AAA CTC	342
Met Trp Cys Leu Leu Val Ala Leu Asn Pro Leu Trp Leu Ala Lys Leu	
90 95 100 105	
CTA GCT TAC GGC TTT GAT GAA GAA ACG CTC AAA TTA TGC GCC CCT ATT	390
Leu Ala Tyr Gly Phe Asp Glu Glu Thr Leu Lys Leu Cys Ala Pro Ile	
110 115 120	
GTA GCG ATC AAT TTT TGG NAT CTT TTA TTG GTG TTT ATC ACC ACC TTT	438
Val Ala Ile Asn Phe Trp Xaa Leu Leu Leu Val Phe Ile Thr Thr Phe	
125 130 135	
TTA GGC GCG CTT TTA CAA NTA CAA ACA CAG CTT TTT TGC CAG CGC TTA T	487
Leu Gly Ala Leu Leu Gln Xaa Gln Thr Gln Leu Phe Cys Gln Arg Leu	
140 145 150	
AGCGCAAGCT TACTCAATGT ATGCATGATT TTAGCCCTTT TGATTTCTAA AGA	540

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

Met Leu Lys Lys Ile Phe Leu Thr Asn Ser Leu Gly Ile Leu Cys Ser	
1 5 10 15	
Arg Ile Phe Gly Phe Leu Arg Asp Leu Met Met Ala Asn Ile Leu Gly	
20 25 30	
Ala Gly Val Tyr Ser Asp Ile Phe Phe Val Ala Phe Lys Leu Pro Asn	
35 40 45	
Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser Phe Ser Gln Ser Phe Leu	
50 55 60	
Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly Ser Phe Ala Ser Leu Val	

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

```

Met Lys Thr Ser Ala Lys Val Leu Leu Thr Leu Leu Ile Val Ile Ser
 1             5             10             15
Leu Gly Lys Gly Leu Asn Ser Leu Ile Ser Ala Trp Arg Gly Lys Asp
          20             25             30
Asp Ala Ile Pro Ile Glu Thr Arg Leu His Lys Asn Lys Leu Thr Ile
          35             40             45
Ile Ser Lys Thr Asp Ser Ile Glu Ile Gln Asp Ile Gln Phe Asn Arg
          50             55             60
Glu Asn Cys Ser His Thr Tyr Thr Ser Lys Asp Leu Glu Lys Ile Gln
          65             70             75             80
Lys Asp Leu Glu Glu Leu Glu Glu Gly Val Pro Glu Leu Phe Glu Glu
          85             90             95
Leu Glu Arg Asp Glu Glu Ser Ile Ala Lys Asn Lys Lys Thr Ile Gln
          100            105            110
Glu Tyr Gln Asn Lys Ile Ala Asn Phe Gln Lys Tyr Tyr Lys Asp Ile
          115            120            125
Lys Asp Ile Asp Asp Tyr Ser Ala Leu Met Ala Gln
          130            135            140

```

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...486
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

```

GAAAATTAGG TAATAAATAC AACCAGT ATG CTA AAA AAA ATA TTT TTA ACC AAC      54
                Met Leu Lys Lys Ile Phe Leu Thr Asn
                  1             5

AGC TTA GGG ATT TTA TGC TCT AGG ATT TTT GGC TTT TTA CGG GAT TTG      102
Ser Leu Gly Ile Leu Cys Ser Arg Ile Phe Gly Phe Leu Arg Asp Leu
10             15             20             25

```

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 22...441
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

ATATTGAAAG ATAATCAAAA A ATG AAG ACA AGC GCT AAA GTA TTA TTG ACT	51
Met Lys Thr Ser Ala Lys Val Leu Leu Thr	
1 5 10	
TTA TTG ATT GTA ATA TCA TTA GGT AAG GGA TTA AAT AGT CTC ATA TCA	99
Leu Leu Ile Val Ile Ser Leu Gly Lys Gly Leu Asn Ser Leu Ile Ser	
15 20 25	
GCT TGG CGT GGC AAA GAT GAT GCG ATC CCC ATT GAA ACA AGA CTC CAT	147
Ala Trp Arg Gly Lys Asp Asp Ala Ile Pro Ile Glu Thr Arg Leu His	
30 35 40	
AAA AAC AAA CTG ACA ATC ATT TCT AAA ACA GAC AGC ATA GAA ATC CAA	195
Lys Asn Lys Leu Thr Ile Ile Ser Lys Thr Asp Ser Ile Glu Ile Gln	
45 50 55	
GAC ATT CAG TTT AAT AGA GAG AAT TGT TCT CAC ACT TAT ACT AGT AAG	243
Asp Ile Gln Phe Asn Arg Glu Asn Cys Ser His Thr Tyr Thr Ser Lys	
60 65 70	
GAT TTG GAA AAA ATT CAA AAA GAT TTA GAA GAG CTT GAA GAA GGA GTG	291
Asp Leu Glu Lys Ile Gln Lys Asp Leu Glu Glu Leu Glu Glu Gly Val	
75 80 85 90	
CCT GAA TTG TTC GAG GAG CTT GAG CGT GAT GAA GAG TCC ATC GCT AAA	339
Pro Glu Leu Phe Glu Glu Leu Glu Arg Asp Glu Glu Ser Ile Ala Lys	
95 100 105	
AAT AAA AAA ACG ATC CAA GAG TAT CAA AAT AAA ATT GCT AAT TTT CAA	387
Asn Lys Lys Thr Ile Gln Glu Tyr Gln Asn Lys Ile Ala Asn Phe Gln	
110 115 120	
AAA TAC TAT AAA GAT ATA AAA GAT ATT GAC GAT TAT TCG GCG TTA ATG	435
Lys Tyr Tyr Lys Asp Ile Lys Asp Ile Asp Asp Tyr Ser Ala Leu Met	
125 130 135	
GCT CAA TGAACATAAA GATTCTTATA CTTGGGATAA TGATCTTGAT	481
Ala Gln	
140	

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

TTAGATTCTT AAGCTTGAGC GATAACCTTT AAAAAGCGTT ATGGGGTGGT GTTGCAAAAC 838
CC 840

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

```

Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile Val Val
 1           5           10           15
Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile Val Phe
          20           25           30
Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys
          35           40           45
Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile Asn
          50           55           60
Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly Ile
65           70           75           80
Glu Ser Pro Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu
          85           90           95
Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile
          100          105          110
Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser
          115          120          125
Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu Ala Arg
          130          135          140
Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro
145          150          155          160
Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val Thr
          165          170          175
Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn Lys Glu
          180          185          190
Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala Val Val
          195          200          205
Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn Pro
          210          215          220
Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys
225          230          235          240
Ala Ile Leu His

```

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Asp	Pro	Asn	Val	Leu	Arg	Lys	Ile	Val	Phe	Glu	Lys	Cys	Leu	Pro	Asn		
		25					30					35					
TAT	GAG	AAA	AAT	CAG	AAT	CCT	TCG	CCA	TGC	ATA	GAA	GTC	AAA	CCC	GAT	199	
Tyr	Glu	Lys	Asn	Gln	Asn	Pro	Ser	Pro	Cys	Ile	Glu	Val	Lys	Pro	Asp		
	40					45					50						
GCC	GGC	TAT	GTG	GTT	TTA	AAA	GAT	ATT	AAC	GGC	CCG	TTG	CAA	TAT	TTG	247	
Ala	Gly	Tyr	Val	Val	Leu	Lys	Asp	Ile	Asn	Gly	Pro	Leu	Gln	Tyr	Leu		
	55				60					65					70		
TTG	ATG	CCA	ACA	ACT	CAC	ATT	AGC	GGT	ATT	GAA	AGC	CCT	TTG	TTA	CTT	295	
Leu	Met	Pro	Thr	Thr	His	Ile	Ser	Gly	Ile	Glu	Ser	Pro	Leu	Leu	Leu		
				75					80					85			
GAT	CCT	TCT	ACG	CCT	AAC	TTT	TTT	TAT	TTA	TCC	TGG	CAA	GCG	CGT	GAT	343	
Asp	Pro	Ser	Thr	Pro	Asn	Phe	Phe	Tyr	Leu	Ser	Trp	Gln	Ala	Arg	Asp		
			90					95					100				
TTT	ATG	AGT	AAA	AAA	TAC	GGC	CAA	CCC	ATT	CCT	GAT	TAT	GCG	ATT	TCT	391	
Phe	Met	Ser	Lys	Lys	Tyr	Gly	Gln	Pro	Ile	Pro	Asp	Tyr	Ala	Ile	Ser		
		105					110					115					
TTG	ACG	ATT	AAC	TCT	AGC	AAA	GGG	CGA	TCG	CAA	AAC	CAT	TTT	CAT	ATC	439	
Leu	Thr	Ile	Asn	Ser	Ser	Lys	Gly	Arg	Ser	Gln	Asn	His	Phe	His	Ile		
	120					125					130						
CAT	ATC	TCT	TGC	ATT	AGT	CTT	GAA	GCA	CGC	AAA	CAG	CTG	GAT	AAT	AAC	487	
His	Ile	Ser	Cys	Ile	Ser	Leu	Glu	Ala	Arg	Lys	Gln	Leu	Asp	Asn	Asn		
	135				140					145					150		
CTA	AAA	AAA	ATC	AAC	AGC	CGT	TGG	TCG	CCA	TTA	CCG	GGC	GGT	TTG	AAT	535	
Leu	Lys	Lys	Ile	Asn	Ser	Arg	Trp	Ser	Pro	Leu	Pro	Gly	Gly	Leu	Asn		
				155					160					165			
GGG	CAT	AAA	TAC	TTG	GCG	CGT	CGG	GTA	ACA	GAG	AGC	GAG	TTA	GTG	CAA	583	
Gly	His	Lys	Tyr	Leu	Ala	Arg	Arg	Val	Thr	Glu	Ser	Glu	Leu	Val	Gln		
			170					175					180				
AAA	AGC	CCG	TTT	GTC	ATG	CTT	AAT	AAA	GAA	GTG	CCT	AAT	GCG	TAC	AAA	631	
Lys	Ser	Pro	Phe	Val	Met	Leu	Asn	Lys	Glu	Val	Pro	Asn	Ala	Tyr	Lys		
		185					190					195					
CGC	ATG	GGG	GAC	TAT	GGC	TTA	GCG	GTG	GTG	CAA	CAA	AGC	GAT	AAC	TCC	679	
Arg	Met	Gly	Asp	Tyr	Gly	Leu	Ala	Val	Val	Gln	Gln	Ser	Asp	Asn	Ser		
	200					205						210					
TTT	GTC	TTA	TTA	GCG	ACA	CAA	TTT	AAC	CCA	TTG	ACT	TTA	AAT	CGC	GCT	727	
Phe	Val	Leu	Leu	Ala	Thr	Gln	Phe	Asn	Pro	Leu	Thr	Leu	Asn	Arg	Ala		
	215				220					225				230			
TCA	GCC	GAA	GAG	ATT	CAA	GAT	CAT	GAA	TGC	GCG	ATT	TTG	CAC	TAAAGCGAG	778		
Ser	Ala	Glu	Glu	Ile	Gln	Asp	His	Glu	Cys	Ala	Ile	Leu	His				
				235					240								

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

```

Met His Glu Tyr Ser Val Val Ser Ser Leu Ile Ala Leu Cys Glu Glu
 1             5             10             15
His Ala Lys Lys Asn Gln Ala His Lys Ile Glu Arg Val Val Val Gly
      20             25             30
Ile Gly Glu Arg Ser Ala Met Asp Lys Ser Leu Phe Val Ser Ala Phe
      35             40             45
Glu Thr Phe Arg Glu Glu Ser Leu Val Cys Lys Asp Ala Ile Leu Asp
      50             55             60
Ile Val Asp Glu Lys Val Glu Leu Glu Cys Lys Asp Cys Ser His Val
      65             70             75             80
Phe Lys Pro Asn Ala Leu Asp Tyr Gly Val Cys Glu Lys Cys His Ser
      85             90             95
Lys Asn Val Ile Ile Thr Gln Gly Asn Glu Met Arg Leu Leu Ser Leu
      100             105             110
Glu Met Leu Ala Glu
      115

```

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 38...769
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

```

TTGCAAAAAC TCTCATTA AAACAAGGAGC AAAAAAG ATG AAA AAG GCG GGC TTT      55
                                     Met Lys Lys Ala Gly Phe
                                     1             5

CTT TTT TTA GCG GTA ATG GCT ATC GTT GTT ATG AGT TTA AAC GCT AAA      103
Leu Phe Leu Ala Val Met Ala Ile Val Val Met Ser Leu Asn Ala Lys
      10             15             20

GAT CCG AAT GTG TTG CGT AAG ATT GTT TTT GAG AAA TGT CTG CCT AAT      151

```

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...366
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

```

AGATTAAGGT TTAGT ATG CAT GAA TAC TCG GTC GTT TCT TCT TTA ATC GCT      51
      Met His Glu Tyr Ser Val Val Ser Ser Leu Ile Ala
           1                      5                      10

CTT TGC GAA GAG CAT GCG AAG AAA AAT CAA GCC CAT AAG ATT GAA AGA      99
Leu Cys Glu Glu His Ala Lys Lys Asn Gln Ala His Lys Ile Glu Arg
           15                      20                      25

GTC GTG GTC GGT ATT GGT GAA AGA AGT GCT ATG GAT AAG AGC TTG TTT      147
Val Val Val Gly Ile Gly Glu Arg Ser Ala Met Asp Lys Ser Leu Phe
           30                      35                      40

GTG AGT GCG TTT GAG ACT TTT AGA GAA GAA TCT TTG GTG TGT AAA GAC      195
Val Ser Ala Phe Glu Thr Phe Arg Glu Glu Ser Leu Val Cys Lys Asp
           45                      50                      55                      60

GCT ATT TTA GAC ATT GTA GAT GAA AAG GTT GAA TTA GAA TGC AAG GAT      243
Ala Ile Leu Asp Ile Val Asp Glu Lys Val Glu Leu Glu Cys Lys Asp
           65                      70                      75

TGT TCG CAT GTT TTT AAG CCT AAC GCG CTA GAT TAT GGG GTG TGT GAG      291
Cys Ser His Val Phe Lys Pro Asn Ala Leu Asp Tyr Gly Val Cys Glu
           80                      85                      90

AAA TGC CAC AGC AAG AAT GTT ATT ATC ACT CAA GGC AAT GAA ATG CGT      339
Lys Cys His Ser Lys Asn Val Ile Ile Thr Gln Gly Asn Glu Met Arg
           95                      100                      105

TTG TTG TCT TTA GAA ATG TTA GCG GAA TAACCGATGC AAGAAGAATT GAACGCT      393
Leu Leu Ser Leu Glu Met Leu Ala Glu
           110                      115

TACCAGCAAG AAATTGA      410

```

(2) INFORMATION FOR SEQ ID NO:882:

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

```

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Val Phe Ser
 1             5             10             15
Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
             20             25             30
Gly Glu Ala Tyr Phe Pro Asn His Leu Gln Glu Ser Ile Val Ser Ser
             35             40             45
Asn Arg Tyr Gly Ala Ile Leu Lys Asn Gly Ala Val Ile Gly Asp Lys
             50             55             60
Gly Leu Thr Gln Leu Arg Ile Gly Lys Asn Phe Asn Tyr Glu Ser Ser
             65             70             75             80
Phe Leu Asn Glu Ser Gln Gly Phe Phe Ile Leu Ala Gln Asp Cys Leu
             85             90             95
Asn Lys Ile Asp Lys Lys Thr Asn Lys Ser Lys Val Ala Lys Thr Glu
             100            105            110
Glu Thr Glu Leu Lys Leu Lys Gly Val Glu Ala Glu Val Gln Asp Lys
             115            120            125
Val Cys His Gln Val Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln
             130            135            140
Gln Ser Ile Val Ile Pro Leu Glu Thr Phe Ala Leu Ser Ala Ser Val
             145            150            155            160
Lys Gly Asn Leu Leu Ala Val Val Leu Ala Asp Asn Ser Ala Asn Leu
             165            170            175
Tyr Asp Ile Thr Ser Gln Lys Leu Leu Phe Ser Glu Lys Gly Ser Pro
             180            185            190
Ser Thr Thr Ile Asn Ser Leu Met Ala Met Pro Ile Phe Met Asp Thr
             195            200            205
Val Val Val Phe Pro Met Leu Asp Gly Arg Leu Leu Val Val Asp Tyr
             210            215            220
Val His Gly Asn Pro Thr Pro Ile Arg Asn Ile Val Ile Ser Ser Asp
             225            230            235            240
Lys Phe Phe Asn Asn Ile Thr Tyr Leu Ile Val Asp Gly Asn Asn Met
             245            250            255
Ile Ala Ser Thr Gly Lys Arg Ile Leu Ser Val Val Ser Gly Gln Glu
             260            265            270
Phe Asn Tyr Asp Gly Asp Ile Val Asp Leu Leu Tyr Asp Lys Gly Thr
             275            280            285
Leu Tyr Val Leu Thr Leu Asp Gly Gln Ile Leu Gln Met Asp Lys Ser
             290            295            300
Leu Arg Glu Leu Asn Ser Val Lys Leu Pro Xaa Xaa Ala Gln His Asp
             305            310            315            320
Cys Ile Lys Pro

```

105	110	115	
GGC GTT GAA GCG GAA GTC CAA GAT AAA GTC TGT CAT CAA GTG GAA TTG			438
Gly Val Glu Ala Glu Val Gln Asp Lys Val Cys His Gln Val Glu Leu			
120	125	130	135
ATT AGC AAT AAC CCT AAC GCC AGC CAA CAA TCT ATC GTT ATT CCT TTG			486
Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val Ile Pro Leu			
	140	145	150
GAG ACT TTT GCC TTG AGC GCA AGC GTT AAA GGG AAT CTT TTA GCG GTG			534
Glu Thr Phe Ala Leu Ser Ala Ser Val Lys Gly Asn Leu Leu Ala Val			
	155	160	165
GTG TTA GCG GAC AAT TCA GCG AAC TTA TAC GAC ATC ACT TCT CAA AAA			582
Val Leu Ala Asp Asn Ser Ala Asn Leu Tyr Asp Ile Thr Ser Gln Lys			
	170	175	180
TTG CTT TTT AGT GAG AAA GGT TCC CCA AGC ACC ACG ATC AAT TCT TTA			630
Leu Leu Phe Ser Glu Lys Gly Ser Pro Ser Thr Thr Ile Asn Ser Leu			
	185	190	195
ATG GCG ATG CCT ATT TTT ATG GAT ACG GTC GTG GTG TTC CCC ATG CTA			678
Met Ala Met Pro Ile Phe Met Asp Thr Val Val Val Phe Pro Met Leu			
	200	205	210
GAT GGG CGC TTG TTG GTC GTG GAT TAT GTG CAC GGA AAC CCT ACG CCT			726
Asp Gly Arg Leu Leu Val Val Asp Tyr Val His Gly Asn Pro Thr Pro			
	220	225	230
ATT AGA AAC ATT GTT ATC AGC AGC GAT AAG TTT TTT AAC AAT ATC ACC			774
Ile Arg Asn Ile Val Ile Ser Ser Asp Lys Phe Phe Asn Asn Ile Thr			
	235	240	245
TAC CTT ATC GTA GAT GGC AAT AAC ATG ATC GCT TCT ACA GGG AAA AGG			822
Tyr Leu Ile Val Asp Gly Asn Asn Met Ile Ala Ser Thr Gly Lys Arg			
	250	255	260
ATA CTC TCA GTA GTG AGC GGT CAA GAG TTC AAC TAT GAT GGG GAT ATT			870
Ile Leu Ser Val Val Ser Gly Gln Glu Phe Asn Tyr Asp Gly Asp Ile			
	265	270	275
GTG GAT TTG CTT TAT GAT AAG GGG ACT TTA TAT GTG CTC ACG CTA GAC			918
Val Asp Leu Leu Tyr Asp Lys Gly Thr Leu Tyr Val Leu Thr Leu Asp			
	280	285	290
GGG CAG ATT TTG CAA ATG GAT AAG AGT TTG AGG GAA TTA AAC AGC GTG			966
Gly Gln Ile Leu Gln Met Asp Lys Ser Leu Arg Glu Leu Asn Ser Val			
	300	305	310
AAA CTG CCT NTC NTC GCT CAA CAC GAT TGT ATT AAA CCA TAATAAATTG TA			1017
Lys Leu Pro Xaa Xaa Ala Gln His Asp Cys Ile Lys Pro			
	315	320	
TTCTTTAGAA AAACGAGGGT ATGTGATAGA			1047

```

          195                200                205
Arg Glu His Gln Glu Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys
          210                215                220
Ala Leu Glu Met Asn Lys Lys
          225                230

```

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1005
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

```

AGAAAGAAAC CATTCAAGGA ACGCATTGAT TTG ATG AAT AAA CCA TTT TTA ATC      54
                               Met Asn Lys Pro Phe Leu Ile
                               1               5

TTA CTC ATA GCC CTA ATT GTC TTT AGC GGC TGT AAC ATG AGA AAA TAT      102
Leu Leu Ile Ala Leu Ile Val Phe Ser Gly Cys Asn Met Arg Lys Tyr
          10                15                20

TTC AAA CCC GCT AAA CAC CAA ATT AAA GGC GAA GCG TAT TTC CCT AAC      150
Phe Lys Pro Ala Lys His Gln Ile Lys Gly Glu Ala Tyr Phe Pro Asn
          25                30                35

CAT TTG CAA GAA AGT ATC GTT TCG TCT AAT CGT TAT GGA GCC ATT TTG      198
His Leu Gln Glu Ser Ile Val Ser Ser Asn Arg Tyr Gly Ala Ile Leu
          40                45                50                55

AAA AAT GGA GCG GTT ATA GGC GAT AAA GGT TTA ACG CAG CTA AGA ATC      246
Lys Asn Gly Ala Val Ile Gly Asp Lys Gly Leu Thr Gln Leu Arg Ile
                60                65                70

GGT AAG AAC TTC AAT TAC GAA AGC AGT TTT TTA AAT GAG AGT CAA GGG      294
Gly Lys Asn Phe Asn Tyr Glu Ser Ser Phe Leu Asn Glu Ser Gln Gly
                75                80                85

TTT TTT ATT CTT GCG CAA GAT TGT TTG AAC AAG ATT GAT AAA AAA ACA      342
Phe Phe Ile Leu Ala Gln Asp Cys Leu Asn Lys Ile Asp Lys Lys Thr
          90                95                100

AAC AAA AGC AAG GTG GCT AAG ACT GAA GAA ACG GAA TTG AAA TTA AAG      390
Asn Lys Ser Lys Val Ala Lys Thr Glu Glu Thr Glu Leu Lys Leu Lys

```

```

CCA AAA CCA AAT TCT AAA GAA GAA AAA CGC CGC TTG AAA GAA GAA AAG      576
Pro Lys Pro Asn Ser Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys
      180                      185                      190

AAA AAA GCC AAA GCC GAA CAA AGA GCG AGA GAA TTT GAA CAA AGA GCG      624
Lys Lys Ala Lys Ala Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala
      195                      200                      205

AGA GAG CAT CAA GAA AGA GAT GAA AAA GAG CTT GAA GAA AGA AGA AAA      672
Arg Glu His Gln Glu Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys
      210                      215                      220

GCT TTA GAA ATG AAT AAG AAG TAGGCCTATG CCAGCTAGGC AATCTTTTAC AGAT      727
Ala Leu Glu Met Asn Lys Lys
      225                      230

TTGAAAAA      735

```

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

```

Asn Cys Xaa Xaa Ser Leu Asn Thr Ile Val Leu Asn His Asn Lys Leu
 1           5           10           15
Tyr Ser Leu Glu Lys Arg Gly Tyr Val Ile Glu Val Asp Leu Asn Asp
      20           25           30
Phe Asp Ser Tyr Asn Val Tyr Lys Thr Pro Thr Ile Gly Ser Phe Lys
      35           40           45
Phe Phe Ser Ser Asn Arg Leu Asp Lys Gly Val Phe Tyr Asp Lys Asn
      50           55           60
Arg Val Tyr Tyr Asp Arg Tyr Tyr Leu Asp Tyr Asn Asp Phe Lys Pro
      65           70           75           80
Lys Leu Tyr Pro Val Val Glu Lys Ser Ala Ser Lys Lys Ser Gln Lys
      85           90           95
Gly Glu Lys Gly Asn Ala Pro Ile Tyr Leu Gln Glu Arg His Lys Ala
      100          105          110
Lys Glu Asn Lys Gln Pro Leu Glu Asn Lys Val Lys Pro Arg Asn
      115          120          125
Ser Gly Phe Glu Glu Glu Glu Val Lys Thr Arg Arg Pro Glu Pro Ile
      130          135          140
Arg Asp Gln Asn Asn Ala Thr Gln Gln Gly Glu Thr Lys Asn Asn Glu
      145          150          155          160
Ser Lys Asn Ala Pro Val Leu Lys Glu Asn Ala Ala Lys Lys Glu Val
      165          170          175
Pro Lys Pro Asn Ser Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys
      180          185          190
Lys Lys Ala Lys Ala Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala

```

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...693
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

AAC TGC CTN TCN TCG CTC AAC ACG ATT GTA TTA AAC CAT AAT AAA TTG	48
Asn Cys Xaa Xaa Ser Leu Asn Thr Ile Val Leu Asn His Asn Lys Leu	
1 5 10 15	
TAT TCT TTA GAA AAA CGA GGG TAT GTG ATA GAG GTG GAT TTA AAT GAT	96
Tyr Ser Leu Glu Lys Arg Gly Tyr Val Ile Glu Val Asp Leu Asn Asp	
20 25 30	
TTT GAT TCG TAT AAT GTC TAT AAA ACG CCA ACT ATA GGC AGT TTT AAG	144
Phe Asp Ser Tyr Asn Val Tyr Lys Thr Pro Thr Ile Gly Ser Phe Lys	
35 40 45	
TTT TTT TCA TCT AAT CGT TTG GAT AAA GGG GTG TTT TAT GAT AAA AAT	192
Phe Phe Ser Ser Asn Arg Leu Asp Lys Gly Val Phe Tyr Asp Lys Asn	
50 55 60	
CGG GTG TAT TAC GAT CGC TAC TAT TTA GAT TAT AAC GAT TTT AAA CCA	240
Arg Val Tyr Tyr Asp Arg Tyr Tyr Leu Asp Tyr Asn Asp Phe Lys Pro	
65 70 75 80	
AAA CTT TAT CCC GTT GTG GAA AAA TCG GCA TCT AAA AAA TCT CAA AAA	288
Lys Leu Tyr Pro Val Val Glu Lys Ser Ala Ser Lys Lys Ser Gln Lys	
85 90 95	
GGC GAA AAA GGG AAC GCT CCT ATT TAT TTG CAA GAA AGG CAT AAA GCT	336
Gly Glu Lys Gly Asn Ala Pro Ile Tyr Leu Gln Glu Arg His Lys Ala	
100 105 110	
AAA GAA AAT AAA CAG CCT TTA GAA GAA AAC AAA GTT AAA CCA AGA AAT	384
Lys Glu Asn Lys Gln Pro Leu Glu Glu Asn Lys Val Lys Pro Arg Asn	
115 120 125	
AGC GGG TTT GAA GAA GAA GAG GTT AAA ACC AGA AGG CCT GAG CCT ATT	432
Ser Gly Phe Glu Glu Glu Glu Val Lys Thr Arg Arg Pro Glu Pro Ile	
130 135 140	
AGG GAT CAA AAT AAC GCC ACC CAA CAA GGC GAA ACA AAA AAC AAT GAA	480
Arg Asp Gln Asn Asn Ala Thr Gln Gln Gly Glu Thr Lys Asn Asn Glu	
145 150 155 160	
AGT AAA AAC GCT CCT GTC TTA AAA GAA AAC GCC GCT AAA AAA GAA GTG	528
Ser Lys Asn Ala Pro Val Leu Lys Glu Asn Ala Ala Lys Lys Glu Val	
165 170 175	

ACAGAGACGG CATTATCAAT ATTGA

801

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

```

Met Gln Met Met His Asn Leu Ser Phe Leu Gly Met Phe Leu Ala Ala
 1           5           10           15
Leu Ser Met Ser Leu Gly His Cys Val Gly Met Cys Gly Gly Ile Val
          20           25           30
Ser Ala Phe Ser Gln Ile Arg Phe Ser Lys Val Thr Ser Phe Ser Tyr
          35           40           45
Gln Leu Thr Cys His Ala Leu Tyr Asn Val Gly Arg Ile Ser Thr Tyr
          50           55           60
Met Leu Leu Gly Ala Ile Ala Ala Ser Leu Gly His Ser Leu Ser Val
65           70           75           80
Ser Met Gly Phe Arg Gly Val Leu Phe Ile Ser Met Gly Ile Ile Leu
          85           90           95
Ile Cys Leu Ala Leu Leu Gly Ala Arg Met Glu Lys Leu Ser Phe Gln
          100          105          110
Ile Pro Phe Ile Ser Phe Leu Met Lys Lys Thr Leu Gln Ser Gln Asn
          115          120          125
Ile Leu Gly Leu Tyr Phe Leu Gly Val Leu Asn Gly Phe Leu Pro Cys
          130          135          140
Met Met Val Tyr Ser Phe Leu Ala Ser Val Ile Leu Ser His Ser Ala
145          150          155          160
Phe Met Gly Ala Met Leu Gly Leu Ser Phe Gly Leu Gly Thr Ser Met
          165          170          175
Pro Leu Phe Leu Met Gly Ile Phe Leu Ser Lys Ile Ser Val Ser Tyr
          180          185          190
Arg Lys Phe Phe Asn Leu Leu Ser Lys Ile Leu Met Gly Val Phe Gly
          195          200          205
Leu Tyr Ile Leu Tyr Met Gly Ile Met Leu Ile Asn His Lys Met Pro
          210          215          220
His Ala Met His His Gln Asn Asn Thr Thr Gln His Asp His Lys Gly
225          230          235          240
Val His Ser His Glu His
          245

```

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Cys Gly Gly Ile Val Ser Ala Phe Ser Gln Ile Arg Phe Ser Lys Val	
30 35 40	
ACA AGC TTT TCT TAC CAG CTC ACT TGC CAT GCC CTT TAT AAT GTA GGG	195
Thr Ser Phe Ser Tyr Gln Leu Thr Cys His Ala Leu Tyr Asn Val Gly	
45 50 55	
AGG ATC AGC ACT TAC ATG CTT TTA GGG GCT ATA GCG GCA AGT TTG GGG	243
Arg Ile Ser Thr Tyr Met Leu Leu Gly Ala Ile Ala Ala Ser Leu Gly	
60 65 70 75	
CAT AGT CTT AGC GTG AGC ATG GGT TTT AGG GGT GTT TTA TTC ATT AGC	291
His Ser Leu Ser Val Ser Met Gly Phe Arg Gly Val Leu Phe Ile Ser	
80 85 90	
ATG GGG ATT ATT TTG ATC TGT TTA GCG TTG CTA GGG GCA AGA ATG GAA	339
Met Gly Ile Ile Leu Ile Cys Leu Ala Leu Leu Gly Ala Arg Met Glu	
95 100 105	
AAA TTA AGC TTT CAA ATC CCT TTT ATT TCT TTT TTG ATG AAA AAA ACC	387
Lys Leu Ser Phe Gln Ile Pro Phe Ile Ser Phe Leu Met Lys Lys Thr	
110 115 120	
TTG CAA TCT CAA AAC ATT CTA GGG CTG TAT TTC TTA GGC GTG TTG AAC	435
Leu Gln Ser Gln Asn Ile Leu Gly Leu Tyr Phe Leu Gly Val Leu Asn	
125 130 135	
GGG TTT TTA CCT TGC ATG ATG GTG TAT TCG TTT TTA GCG AGC GTG ATT	483
Gly Phe Leu Pro Cys Met Met Val Tyr Ser Phe Leu Ala Ser Val Ile	
140 145 150 155	
CTC AGT CAT AGC GCG TTT ATG GGA GCG ATG CTA GGC CTT TCT TTT GGG	531
Leu Ser His Ser Ala Phe Met Gly Ala Met Leu Gly Leu Ser Phe Gly	
160 165 170	
CTT GGC ACC AGC ATG CCG TTG TTT TTA ATG GGG ATT TTT TTA AGC AAA	579
Leu Gly Thr Ser Met Pro Leu Phe Leu Met Gly Ile Phe Leu Ser Lys	
175 180 185	
ATT TCC GTT TCT TAC AGG AAA TTT TTC AAT CTT TTG TCT AAA ATT TTA	627
Ile Ser Val Ser Tyr Arg Lys Phe Phe Asn Leu Leu Ser Lys Ile Leu	
190 195 200	
ATG GGG GTT TTT GGG CTT TAT ATC CTT TAT ATG GGG ATC ATG CTC ATT	675
Met Gly Val Phe Gly Leu Tyr Ile Leu Tyr Met Gly Ile Met Leu Ile	
205 210 215	
AAC CAC AAA ATG CCT CAT GCC ATG CAT CAT CAA AAC AAC ACC ACT CAG	723
Asn His Lys Met Pro His Ala Met His His Gln Asn Asn Thr Thr Gln	
220 225 230 235	
CAT GAT CAT AAA GGA GTG CAT TCG CAT GAA CAC TAACAAAGCC CTTTTTTTGG	776
His Asp His Lys Gly Val His Ser His Glu His	
240 245	

```

Asn Gln Val Ser Leu Lys Val Met Pro Lys Asp Lys Ile Ala Leu Ile
 210                215                220
Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Cys Lys Ile Leu Val Glu
225                230                235                240
Glu Leu Lys Pro Asp Lys Gly Val Val Lys Trp Gly Ala Thr Val Ser
                245                250                255
Lys Gly Tyr Phe Pro Gln Asn Val Ser Glu Glu Ile Ser Gly Glu Glu
                260                265                270
Thr Leu Tyr Gln Trp Leu Phe Asn Phe Asn Lys Lys Ile Glu Ser Ala
                275                280                285
Glu Val Arg Asn Ala Leu Gly Arg Met Leu Phe Asn Gly Glu Glu Gln
                290                295                300
Glu Lys Cys Val Asn Ala Leu Ser Gly Gly Glu Lys His Arg Met Val
305                310                315                320
Leu Ser Lys Leu Met Leu Glu Gly Gly Asn Phe Leu Val Leu Asp Glu
                325                330                335
Pro Thr Asn His Leu Asp Leu Glu Ala Ile Ile Ala Leu Gly Glu Ala
                340                345                350
Leu Phe Lys Phe Asp Gly Ala Leu Ile Cys Val Ser His Asp Arg Glu
                355                360                365
Leu Ile Asp Ala Tyr Ala Asn Arg Ile Ile Glu Leu Val Pro Ser Pro
                370                375                380
Lys Gly Ala Ser Ile Ile Asp Phe Lys Gly Ser Tyr Glu Glu Tyr Leu
385                390                395                400
Ala Ser Lys Lys

```

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...756
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

```

AAAAGCAGGG ATACTAGA ATG CAA ATG ATG CAC AAT TTG AGT TTT TTG GGC      51
          Met Gln Met Met His Asn Leu Ser Phe Leu Gly
              1              5              10

ATG TTT TTA GCC GCT TTG AGC ATG TCT TTA GGG CAT TGT GTG GGC ATG      99
Met Phe Leu Ala Ala Leu Ser Met Ser Leu Gly His Cys Val Gly Met
      15              20              25

TGT GGG GGG ATT GTG AGC GCG TTC AGT CAA ATA AGA TTT TCT AAA GTT     147

```

Asp Leu Glu Ala Ile Ile Ala Leu Gly Glu Ala Leu Phe Lys Phe Asp
 345 350 355
 GGG GCG CTG ATT TGC GTA AGC CAT GAC AGA GAG CTC ATT GAT GCG TAT 1160
 Gly Ala Leu Ile Cys Val Ser His Asp Arg Glu Leu Ile Asp Ala Tyr
 360 365 370
 GCT AAT AGG ATC ATT GAA TTA GTC CCA AGC CCT AAA GGC GCT TCA ATC 1208
 Ala Asn Arg Ile Ile Glu Leu Val Pro Ser Pro Lys Gly Ala Ser Ile
 375 380 385
 ATT GAT TTT AAA GGC AGT TAT GAA GAG TAT TTG GCG AGC AAA AAA TGAAA 1258
 Ile Asp Phe Lys Gly Ser Tyr Glu Glu Tyr Leu Ala Ser Lys Lys
 390 395 400
 CCGCAAGACA TTGAAATCGT TCAAAGCGTT TTAGAGATTA CAGGACC 1305

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

Met Tyr Glu Cys Glu Val Ala Ile Glu Lys Ile Leu Glu Asp Leu Gly
 1 5 10 15
 Ile Pro Ser Ser Lys His Asn Asp Leu Met Lys Thr Leu Pro Ser Ser
 20 25 30
 Asp Lys Phe Lys Ile Leu Leu Ala Gln Val Leu Phe Pro Lys Pro Asp
 35 40 45
 Ile Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Leu Asn Ala Ile
 50 55 60
 Glu Trp Leu Glu Asn Asn Leu Lys Arg His Glu Gly Thr Met Val Val
 65 70 75 80
 Ile Ser His Asp Arg His Phe Leu Asn Ala Val Cys Thr His Ile Leu
 85 90 95
 Asp Leu Asp Phe His Ser Val Arg Glu Phe Ser Gly Asn Tyr Asp Asp
 100 105 110
 Trp Tyr Ile Ala Ser Thr Leu Ile Ala Lys Gln Gln Glu Ala Glu Arg
 115 120 125
 Asn Lys Lys Leu Lys Glu Lys Glu Glu Leu Glu Lys Phe Ile Ala Arg
 130 135 140
 Phe Xaa Xaa Xaa Ala Ser Lys Ala Lys Gln Ala Thr Ser Arg Gln Lys
 145 150 155 160
 Gln Leu Asp Lys Leu Asp Ile Gln Ser Leu Ala Val Ser Ser Arg Arg
 165 170 175
 Asp Pro Ser Ile Ile Phe Lys Pro Lys Arg Thr Ile Gly Asn Glu Ala
 180 185 190
 Leu Glu Cys Glu Asn Ile Ser Lys Ser Tyr Asp Asp Gln Ile Val Leu
 195 200 205

120	125	130	
GAA AAA GAA GAG CTA GAA AAA TTC ATC GCG CGC TTT ARN NNN NAC GCT Glu Lys Glu Glu Leu Glu Lys Phe Ile Ala Arg Phe Xaa Xaa Xaa Ala 135 140 145			488
TCT AAA GCC AAG CAA GCC ACC AGC CGC CAA AAA CAA CTG GAT AAA TTA Ser Lys Ala Lys Gln Ala Thr Ser Arg Gln Lys Gln Leu Asp Lys Leu 150 155 160 165			536
GAC ATT CAA AGT TTA GCG GTA TCT AGC AGG AGG GAT CCT AGC ATT ATT Asp Ile Gln Ser Leu Ala Val Ser Ser Arg Arg Asp Pro Ser Ile Ile 170 175 180			584
TTT AAA CCC AAA CGC ACC ATT GGT AAT GAA GCC TTA GAG TGC GAA AAC Phe Lys Pro Lys Arg Thr Ile Gly Asn Glu Ala Leu Glu Cys Glu Asn 185 190 195			632
ATC TCT AAA AGT TAT GAC GAC CAA ATC GTT TTA AAT CAA GTG AGC TTG Ile Ser Lys Ser Tyr Asp Asp Gln Ile Val Leu Asn Gln Val Ser Leu 200 205 210			680
AAA GTG ATG CCT AAA GAC AAG ATC GCC CTC ATA GGG CCA AAC GGC GTG Lys Val Met Pro Lys Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Val 215 220 225			728
GGT AAA TCC ACG CTT TGT AAA ATT CTA GTA GAA GAA TTA AAG CCG GAT Gly Lys Ser Thr Leu Cys Lys Ile Leu Val Glu Glu Leu Lys Pro Asp 230 235 240 245			776
AAG GGC GTG GTG AAA TGG GGG GCG ACG GTT TCA AAA GGC TAT TTC CCT Lys Gly Val Val Lys Trp Gly Ala Thr Val Ser Lys Gly Tyr Phe Pro 250 255 260			824
CAA AAC GTG AGC GAA GAA ATT AGC GGG GAA GAG ACC TTG TAT CAA TGG Gln Asn Val Ser Glu Glu Ile Ser Gly Glu Glu Thr Leu Tyr Gln Trp 265 270 275			872
CTC TTT AAC TTC AAT AAA AAG ATT GAA AGC GCT GAG GTT AGG AAC GCT Leu Phe Asn Phe Asn Lys Lys Ile Glu Ser Ala Glu Val Arg Asn Ala 280 285 290			920
TTA GGG AGG ATG CTG TTT AAT GGC GAA GAG CAA GAA AAA TGC GTG AAC Leu Gly Arg Met Leu Phe Asn Gly Glu Glu Gln Glu Lys Cys Val Asn 295 300 305			968
GCT TTA AGT GGG GGC GAA AAA CAC CGA ATG GTT TTA TCC AAG CTC ATG Ala Leu Ser Gly Gly Glu Lys His Arg Met Val Leu Ser Lys Leu Met 310 315 320 325			1016
CTA GAG GGG GGG AAT TTT TTA GTC TTA GAT GAG CCA ACC AAC CAT TTG Leu Glu Gly Gly Asn Phe Leu Val Leu Asp Glu Pro Thr Asn His Leu 330 335 340			1064
GAT TTA GAA GCG ATT ATC GCT TTA GGC GAA GCG CTC TTT AAA TTT GAT			1112

290

295

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 42...1253
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GATTAGGGGA GTTAGAAACC ATTTGCGTGG AAGAAGATCC C ATG TAT GAA TGC GAA	56
Met Tyr Glu Cys Glu	
1 5	
GTG GCG ATT GAA AAA ATC CTA GAA GAT TTA GGC ATT CCT AGC TCT AAA	104
Val Ala Ile Glu Lys Ile Leu Glu Asp Leu Gly Ile Pro Ser Ser Lys	
10 15 20	
CAC AAC GAT TTG ATG AAA ACC CTG CCA AGC AGC GAT AAA TTT AAA ATC	152
His Asn Asp Leu Met Lys Thr Leu Pro Ser Ser Asp Lys Phe Lys Ile	
25 30 35	
CTT CTC GCT CAA GTC TTG TTC CCT AAA CCG GAT ATT TTG CTT TTA GAT	200
Leu Leu Ala Gln Val Leu Phe Pro Lys Pro Asp Ile Leu Leu Leu Asp	
40 45 50	
GAG CCG ACC AAC AAC CTG GAT TTA AAC GCC ATT GAA TGG CTA GAA AAC	248
Glu Pro Thr Asn Asn Leu Asp Leu Asn Ala Ile Glu Trp Leu Glu Asn	
55 60 65	
AAC CTC AAA CGC CAT GAA GGC ACG ATG GTC GTC ATT AGC CAT GAC AGG	296
Asn Leu Lys Arg His Glu Gly Thr Met Val Val Ile Ser His Asp Arg	
70 75 80 85	
CAT TTT TTA AAT GCG GTA TGC ACG CAT ATT TTG GAT TTG GAT TTC CAC	344
His Phe Leu Asn Ala Val Cys Thr His Ile Leu Asp Leu Asp Phe His	
90 95 100	
AGC GTG CGC GAA TTT AGC GGG AAT TAT GAC GAT TGG TAT ATC GCT TCC	392
Ser Val Arg Glu Phe Ser Gly Asn Tyr Asp Asp Trp Tyr Ile Ala Ser	
105 110 115	
ACT CTG ATC GCT AAA CAG CAA GAG GCC GAA CGC AAT AAA AAA CTC AAA	440
Thr Leu Ile Ala Lys Gln Gln Glu Ala Glu Arg Asn Lys Lys Leu Lys	

TAC CGA GAA AAA CTA CTG ACC TTC AAA CCT CTC CAA AAC AAG GAA TAACA 976
 Tyr Arg Glu Lys Leu Leu Thr Phe Lys Pro Leu Gln Asn Lys Glu
 285 290 295

TGAGTTACGA AACGATCGCA GAAAGCAATG AAAG 1010

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

Met	Phe	Cys	Phe	Glu	Asn	Leu	Asn	Ile	Gln	Asn	Xaa	Ile	Lys	Ser	Lys	1	5	10	15
Ser	Phe	Gly	Gly	Ile	Val	Lys	Ser	Ile	Ser	Met	Asn	Asp	Leu	Gln	Gln	20	25	30	
Ile	Thr	Ile	Pro	Ile	Pro	Pro	Leu	Glu	Ile	Gln	Gln	Glu	Ile	Val	Lys	35	40	45	
Ile	Leu	Asp	Ala	Phe	Thr	Glu	Leu	Asn	Thr	Glu	Leu	Asn	Thr	Glu	Leu	50	55	60	
Lys	Ala	Arg	Lys	Lys	Gln	Tyr	Glu	Tyr	Tyr	Gln	Asn	Met	Leu	Leu	Asp	65	70	75	80
Phe	Asn	Asp	Ile	Asn	Gln	Asn	His	Lys	Asp	Ala	Lys	Ile	Lys	Thr	Tyr	85	90	95	
Pro	Lys	Arg	Leu	Lys	Thr	Leu	Leu	His	Thr	Leu	Ala	Pro	Lys	Gly	Val	100	105	110	
Glu	Phe	Arg	Lys	Leu	Gly	Glu	Val	Cys	Glu	Ser	Thr	Asn	Lys	Lys	Thr	115	120	125	
Leu	Lys	Ile	Ser	Glu	Val	Ser	Glu	Val	Lys	Asn	Lys	Gly	Met	Tyr	Pro	130	135	140	
Val	Ile	Asn	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Tyr	Tyr	His	Asp	Phe	Asn	145	150	155	160
Asn	Asp	Gly	Glu	Asn	Ile	Thr	Ile	Ala	Ser	Arg	Gly	Glu	Tyr	Ala	Gly	165	170	175	
Phe	Ile	Asn	Tyr	Phe	Asn	Glu	Lys	Phe	Phe	Ala	Gly	Gly	Leu	Cys	Tyr	180	185	190	
Pro	Tyr	Lys	Val	Lys	Asp	Thr	Asn	Glu	Leu	Leu	Thr	Lys	Phe	Leu	Tyr	195	200	205	
Phe	Tyr	Leu	Lys	Thr	Asn	Glu	Ile	Gln	Ile	Met	Glu	Asn	Leu	Val	Phe	210	215	220	
Arg	Gly	Ser	Ile	Pro	Ala	Leu	Asn	Lys	Ala	Asp	Ile	Glu	Thr	Leu	Thr	225	230	235	240
Ile	Pro	Ile	Pro	Pro	Leu	Glu	Ile	Gln	Gln	Glu	Ile	Val	Lys	Ile	Leu	245	250	255	
Asp	Gln	Phe	Ser	Ala	Leu	Thr	Thr	Asp	Leu	Leu	Ala	Gly	Ile	Pro	Ala	260	265	270	
Glu	Ile	Lys	Ala	Arg	Lys	Lys	Gln	Tyr	Glu	Tyr	Tyr	Arg	Glu	Lys	Leu	275	280	285	
Leu	Thr	Phe	Lys	Pro	Leu	Gln	Asn	Lys	Glu										

Leu	Asn	Thr	Glu	Leu	Lys	Ala	Arg	Lys	Lys	Gln	Tyr	Glu	Tyr	Tyr	Gln	
60					65					70					75	
AAC	ATG	CTT	TTA	GAC	TTT	AAC	GAT	ATT	AAT	CAA	AAC	CAC	AAA	GAC	GCC	350
Asn	Met	Leu	Leu	Asp	Phe	Asn	Asp	Ile	Asn	Gln	Asn	His	Lys	Asp	Ala	
				80					85					90		
AAA	ATA	AAA	ACC	TAC	CCT	AAA	CGC	TTG	AAA	ACC	TTA	CTC	CAC	ACT	TTA	398
Lys	Ile	Lys	Thr	Tyr	Pro	Lys	Arg	Leu	Lys	Thr	Leu	Leu	His	Thr	Leu	
			95					100					105			
GCG	CCT	AAG	GGG	GTG	GAG	TTT	AGG	AAA	TTG	GGG	GAG	GTG	TGT	GAA	AGC	446
Ala	Pro	Lys	Gly	Val	Glu	Phe	Arg	Lys	Leu	Gly	Glu	Val	Cys	Glu	Ser	
		110					115					120				
ACA	AAT	AAA	AAA	ACA	CTC	AAA	ATA	AGC	GAA	GTA	AGT	GAA	GTA	AAA	AAT	494
Thr	Asn	Lys	Lys	Thr	Leu	Lys	Ile	Ser	Glu	Val	Ser	Glu	Val	Lys	Asn	
	125					130					135					
AAG	GGA	ATG	TAT	CCA	GTG	ATA	AAT	TCA	GGG	AGG	GAT	TTG	TAT	GGT	TAT	542
Lys	Gly	Met	Tyr	Pro	Val	Ile	Asn	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Tyr	
140					145				150					155		
TAC	CAT	GAT	TTT	AAC	AAT	GAT	GGA	GAA	AAT	ATA	ACT	ATT	GCA	TCT	AGG	590
Tyr	His	Asp	Phe	Asn	Asn	Asp	Gly	Glu	Asn	Ile	Thr	Ile	Ala	Ser	Arg	
				160					165					170		
GGA	GAA	TAT	GCA	GGA	TTT	ATA	AAC	TAT	TTC	AAT	GAA	AAA	TTT	TTT	GCA	638
Gly	Glu	Tyr	Ala	Gly	Phe	Ile	Asn	Tyr	Phe	Asn	Glu	Lys	Phe	Phe	Ala	
			175					180					185			
GGG	GGT	CTA	TGT	TAT	CCC	TAT	AAA	GTT	AAA	GAC	ACT	AAC	GAG	CTT	TTA	686
Gly	Gly	Leu	Cys	Tyr	Pro	Tyr	Lys	Val	Lys	Asp	Thr	Asn	Glu	Leu	Leu	
		190					195					200				
ACA	AAA	TTT	TTA	TAC	TTT	TAT	CTC	AAA	ACT	AAT	GAA	ATC	CAA	ATT	ATG	734
Thr	Lys	Phe	Leu	Tyr	Phe	Tyr	Leu	Lys	Thr	Asn	Glu	Ile	Gln	Ile	Met	
	205					210				215						
GAG	AAC	CTT	GTT	TTT	CGT	GGC	AGT	ATC	CCC	GCA	CTC	AAT	AAA	GCA	GAT	782
Glu	Asn	Leu	Val	Phe	Arg	Gly	Ser	Ile	Pro	Ala	Leu	Asn	Lys	Ala	Asp	
220					225				230					235		
ATT	GAA	ACT	TTA	ACA	ATC	CCC	ATC	CCA	CCT	CTA	GAG	ATC	CAA	CAA	GAG	830
Ile	Glu	Thr	Leu	Thr	Ile	Pro	Ile	Pro	Pro	Leu	Glu	Ile	Gln	Gln	Glu	
				240				245					250			
ATC	GTT	AAG	ATT	TTG	GAT	CAA	TTT	TCA	GCC	CTA	ACC	ACC	GAT	TTA	TTA	878
Ile	Val	Lys	Ile	Leu	Asp	Gln	Phe	Ser	Ala	Leu	Thr	Thr	Asp	Leu	Leu	
		255					260						265			
GCC	GGT	ATC	CCC	GCT	GAA	ATA	AAA	GCC	CGA	AAA	AAG	CAA	TAC	GAA	TAT	926
Ala	Gly	Ile	Pro	Ala	Glu	Ile	Lys	Ala	Arg	Lys	Lys	Gln	Tyr	Glu	Tyr	
		270					275					280				

145		150		155		160									
Ala	Ala	Gln	Lys	Tyr	Ser	Val	Ile	Ala	Val	Met	Thr	Gly	Lys	Thr	Asp
		165		170		175									
Tyr	Val	Ser	Asp	Gly	Lys	Lys	Val	Leu	Ser	Ile	Thr	Gly	Gly	Ser	Glu
		180		185		190									
Tyr	Leu	Ala	Leu	Ile	Thr	Gly	Ala	Gly	Cys	Leu	His	Ala	Ala	Ala	Cys
	195		200		205										
Ala	Ser	Phe	Leu	Ser	Leu	Lys	Lys	Asp	Pro	Leu	Asp	Ser	Met	Ala	Gln
	210		215		220										
Leu	Cys	Ala	Leu	Tyr	Lys	Gln	Ala	Ala	Phe	Asn	Ala	Gln	Lys	Lys	Val
225			230		235										
Leu	Glu	Asn	Asn	Gly	Ser	Asn	Gly	Ser	Phe	Leu	Phe	Tyr	Phe	Leu	Asp
		245		250		255									
Ala	Leu	Ser	Leu	Pro	Ile	Glu	Leu	Glu	Asn	Ser	Leu	Ile	Lys	Glu	Glu
	260		265		270										

Trp

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 78...971
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

ATCCAAATAA TTGGGCGATT AAAGAGGGAA TTTATTCAAT CAAACCAAAT AAAAAAATAG	60
TATTTCCAAG ATTTTTA ATG TTT TGC TTT GAA AAT TTG AAT ATT CAA AAT	110
Met Phe Cys Phe Glu Asn Leu Asn Ile Gln Asn	
1 5 10	
GMT ATA AAA AGT AAA AGT TTT GGA GGA ATA GTT AAA AGT ATA TCA ATG	158
Xaa Ile Lys Ser Lys Ser Phe Gly Gly Ile Val Lys Ser Ile Ser Met	
15 20 25	
AAC GAT TTA CAA CAA ATA ACC ATC CCC ATC CCA CCC CTA GAG ATC CAA	206
Asn Asp Leu Gln Gln Ile Thr Ile Pro Ile Pro Pro Glu Ile Gln	
30 35 40	
CAA GAG ATC GTT AAG ATT TTG GAC GCT TTC ACA GAA TTA AAC ACA GAA	254
Gln Glu Ile Val Lys Ile Leu Asp Ala Phe Thr Glu Leu Asn Thr Glu	
45 50 55	
TTA AAC ACA GAA TTA AAA GCG CGC AAA AAG CAA TAT GAG TAT TAC CAA	302

180	185	190	
TTA GCG CTC ATT ACT GGG GCT GGG TGT TTG CAT GCC GCA GCA TGC GCG			684
Leu Ala Leu Ile Thr Gly Ala Gly Cys Leu His Ala Ala Ala Cys Ala			
195	200	205	
AGC TTT TTA AGT TTG AAA AAA GAC CCC TTA GAT TCT ATG GCG CAA CTT			732
Ser Phe Leu Ser Leu Lys Lys Asp Pro Leu Asp Ser Met Ala Gln Leu			
210	215	220	225
TGC GCG CTC TAT AAA CAA GCC GCT TTT AAC GCG CAA AAA AAG GTG TTG			780
Cys Ala Leu Tyr Lys Gln Ala Ala Phe Asn Ala Gln Lys Lys Val Leu			
	230	235	240
GAA AAT AAC GGC TCT AAT GGT TCG TTC TTG TTT TAT TTT TTA GAT GCT			828
Glu Asn Asn Gly Ser Asn Gly Ser Phe Leu Phe Tyr Phe Leu Asp Ala			
	245	250	255
CTA AGC TTG CCC ATA GAG TTA GAA AAC AGC CTT ATT AAG GAA GAG TGG T			877
Leu Ser Leu Pro Ile Glu Leu Glu Asn Ser Leu Ile Lys Glu Glu Trp			
	260	265	270
GAAAATTAC CCGCAAGTTT TAAGCATTGC TGGCAGCGAT AG			919

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

Met	Asp	Phe	Cys	Lys	Ile	Lys	Glu	Ile	Leu	Arg	Arg	Leu	Val	Val	Leu
1				5					10					15	
Lys	Glu	Leu	Arg	Gln	Lys	Arg	Pro	Leu	Val	His	Asn	Ile	Thr	Asn	Tyr
			20					25					30		
Val	Ala	Ala	Gln	Phe	Val	Ala	Asn	Gly	Leu	Leu	Ala	Leu	Gly	Ala	Ser
			35					40					45		
Pro	Leu	Met	Ser	Asp	Ala	Ile	Asp	Glu	Met	Arg	Asp	Leu	Ala	Lys	Ile
		50				55				60					
Ser	Asp	Ala	Leu	Ala	Ile	Asn	Ile	Gly	Thr	Leu	Asn	Asp	Arg	Ala	Ile
65					70					75				80	
Leu	Cys	Ala	Lys	Glu	Ala	Ile	Lys	His	Tyr	Lys	Ala	Leu	Asn	Lys	Pro
			85						90					95	
Ile	Val	Leu	Asp	Pro	Val	Gly	Cys	Ser	Ala	Ser	Ala	Leu	Arg	His	Asp
			100					105					110		
Thr	Ser	Leu	Glu	Leu	Leu	Lys	Ser	Gly	Gly	Ile	Ser	Ala	Leu	Arg	Gly
		115				120						125			
Asn	Ala	Ala	Glu	Leu	Gly	Ser	Leu	Val	Gly	Ile	Ser	Cys	Glu	Ser	Lys
		130				135						140			
Gly	Leu	Asp	Ser	Asn	Asp	Ala	Ala	Thr	Pro	Val	Glu	Ile	Ile	Lys	Leu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

TAATGAAAAA TAGTTCATGA ACGCTTTTGC ATTAAGGCTC AAAAAAAGCG CCGTTTA ATG	60
	Met
	1
GAT TTT TGT AAA ATA AAA GAA ATT TTA AGG AGG CTT GTG GTG TTG AAA	108
Asp Phe Cys Lys Ile Lys Glu Ile Leu Arg Arg Leu Val Val Leu Lys	
5 10 15	
GAA TTA CGC CAA AAA CGC CCT TTA GTG CAT AAT ATC ACC AAT TAT GTG	156
Glu Leu Arg Gln Lys Arg Pro Leu Val His Asn Ile Thr Asn Tyr Val	
20 25 30	
GCG GCG CAA TTT GTG GCT AAT GGT TTG TTA GCT TTA GGG GCA TCG CCT	204
Ala Ala Gln Phe Val Ala Asn Gly Leu Leu Ala Leu Gly Ala Ser Pro	
35 40 45	
TTA ATG AGC GAT GCG ATT GAT GAA ATG CGA GAT TTA GCG AAA ATT TCT	252
Leu Met Ser Asp Ala Ile Asp Glu Met Arg Asp Leu Ala Lys Ile Ser	
50 55 60 65	
GAC GCG CTC GCT ATC AAT ATT GGC ACC CTT AAT GAT CGC GCT ATT TTA	300
Asp Ala Leu Ala Ile Asn Ile Gly Thr Leu Asn Asp Arg Ala Ile Leu	
70 75 80	
TGC GCT AAA GAG GCT ATC AAG CAT TAC AAG GCT TTG AAC AAA CCC ATT	348
Cys Ala Lys Glu Ala Ile Lys His Tyr Lys Ala Leu Asn Lys Pro Ile	
85 90 95	
GTG TTA GAT CCT GTG GGG TGT TCA GCG AGC GCT TTG CGT CAT GAC ACC	396
Val Leu Asp Pro Val Gly Cys Ser Ala Ser Ala Leu Arg His Asp Thr	
100 105 110	
AGT TTA GAG CTT TTG AAA AGT GGT GGG ATT AGC GCG CTT AGG GGT AAT	444
Ser Leu Glu Leu Leu Lys Ser Gly Gly Ile Ser Ala Leu Arg Gly Asn	
115 120 125	
GCT GCA GAA TTA GGC TCT TTA GTG GGG ATT TCT TGC GAA AGT AAG GGG	492
Ala Ala Glu Leu Gly Ser Leu Val Gly Ile Ser Cys Glu Ser Lys Gly	
130 135 140 145	
CTA GAC TCT AAT GAT GCC GCC ACG CCT GTA GAA ATA ATC AAA TTA GCG	540
Leu Asp Ser Asn Asp Ala Ala Thr Pro Val Glu Ile Ile Lys Leu Ala	
150 155 160	
GCT CAA AAA TAT TCT GTG ATA GCG GTA ATG ACG GGT AAA ACA GAT TAC	588
Ala Gln Lys Tyr Ser Val Ile Ala Val Met Thr Gly Lys Thr Asp Tyr	
165 170 175	
GTG AGC GAT GGG AAA AAG GTT TTG AGT ATT ACT GGG GGG AGC GAG TAT	636
Val Ser Asp Gly Lys Lys Val Leu Ser Ile Thr Gly Gly Ser Glu Tyr	

```

Lys Ile Glu Lys Leu Pro Ile Val Asp Lys Asp Asn Val Leu Lys Gly
      180      185      190
Leu Ile Thr Ile Lys Asp Ile Gln Lys Arg Ile Glu Tyr Pro Glu Ala
      195      200      205
Asn Lys Asp Asp Phe Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Val
      210      215      220
Gly Gln Leu Asp Arg Ala Glu Met Leu Val Lys Ala Gly Val Asp Ala
      225      230      235      240
Leu Val Leu Asp Ser Ala His Gly His Ser Ala Asn Ile Leu His Thr
      245      250      255
Leu Glu Glu Ile Lys Lys Ser Leu Val Val Asp Val Ile Val Gly Asn
      260      265      270
Val Val Thr Lys Glu Ala Thr Ser Asp Leu Ile Ser Ala Gly Ala Asp
      275      280      285
Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile
      290      295      300
Val Ala Gly Val Gly Met Pro Gln Val Ser Ala Ile Asp Asn Cys Val
      305      310      315      320
Glu Val Ala Ser Lys Phe Asp Ile Pro Val Ile Ala Asp Gly Gly Ile
      325      330      335
Arg Tyr Ser Gly Asp Val Ala Lys Ala Leu Ala Leu Gly Ala Ser Ser
      340      345      350
Val Met Ile Gly Ser Leu Leu Ala Gly Thr Glu Glu Ser Pro Gly Asp
      355      360      365
Phe Met Ile Tyr Gln Gly Arg Gln Tyr Lys Ser Tyr Arg Gly Met Gly
      370      375      380
Ser Ile Gly Ala Met Thr Lys Gly Ser Ser Asp Arg Tyr Phe Gln Glu
      385      390      395      400
Gly Val Ala Ser Glu Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val
      405      410      415
Pro Tyr Arg Gly Lys Val Ser Asp Met Ile Phe Gln Leu Val Gly Gly
      420      425      430
Val Arg Ser Ser Met Gly Tyr Gln Gly Ala Lys Asn Ile Leu Glu Leu
      435      440      445
Tyr Gln Asn Ala Glu Phe Val Glu Ile Thr Ser Ala Gly Leu Lys Glu
      450      455      460
Ser His Val His Gly Val Asp Ile Thr Lys Glu Ala Pro Asn Tyr Tyr
      465      470      475      480
Gly

```

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...876
- (D) OTHER INFORMATION:

```

Pro Glu Gly Ile Glu Gly Arg Val Pro Tyr Arg Gly Lys Val Ser Asp
  410                      415                      420

ATG ATT TTC CAA TTA GTA GGG GGC GTG CGC TCT TCT ATG GGG TAT CAG      1350
Met Ile Phe Gln Leu Val Gly Gly Val Arg Ser Ser Met Gly Tyr Gln
425                      430                      435                      440

GGG GCG AAA AAT ATT TTG GAA TTG TAT CAA AAC GCT GAA TTT GTA GAA      1398
Gly Ala Lys Asn Ile Leu Glu Leu Tyr Gln Asn Ala Glu Phe Val Glu
                      445                      450                      455

ATC ACT AGC GCG GGG TTA AAA GAA AGC CAT GTG CAT GGC GTG GAT ATT      1446
Ile Thr Ser Ala Gly Leu Lys Glu Ser His Val His Gly Val Asp Ile
                      460                      465                      470

ACT AAA GAA GCC CCT AAT TAT TAT GGG TGAATTGTAA AAGAAAACAA GACAAAT      1500
Thr Lys Glu Ala Pro Asn Tyr Tyr Gly
                      475                      480

CGTTAAAAAA CTCGTTAAAA AGCTTGTTTT AATGAGTTTT TAAAACTTAA TTGCTACA      1558

```

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

```

Met Arg Ile Leu Gln Arg Ala Leu Thr Phe Glu Asp Val Leu Met Val
  1                      5                      10                      15
Pro Arg Lys Ser Ser Val Leu Pro Lys Asp Val Ser Leu Lys Ser Arg
                      20                      25                      30
Leu Thr Lys Asn Ile Arg Leu Asn Ile Pro Phe Ile Ser Ala Ala Met
                      35                      40                      45
Asp Thr Val Thr Glu His Lys Thr Ala Ile Ala Met Ala Arg Leu Gly
                      50                      55                      60
Gly Ile Gly Ile Val His Lys Asn Met Asp Ile Gln Thr Gln Val Lys
65                      70                      75                      80
Glu Ile Thr Lys Val Lys Lys Ser Glu Ser Gly Val Ile Asn Asp Pro
                      85                      90                      95
Ile Phe Ile His Ala His Arg Thr Leu Ala Asp Ala Lys Val Ile Thr
                      100                     105                     110
Asp Asn Tyr Lys Ile Ser Gly Val Pro Val Val Asp Asp Lys Gly Leu
                      115                     120                     125
Leu Ile Gly Ile Leu Thr Asn Arg Asp Val Arg Phe Glu Thr Asp Leu
                      130                     135                     140
Ser Lys Lys Val Gly Asp Val Met Thr Lys Met Pro Leu Val Thr Ala
145                      150                      155                      160
His Val Gly Ile Ser Leu Asp Glu Ala Ser Asp Leu Met His Lys His
                      165                      170                      175

```

185	190	195	200	
AAA CGC ATT GAA TAC CCT GAG GCC AAT AAA GAT GAT TTT GGG AGG TTG				678
Lys Arg Ile Glu Tyr Pro Glu Ala Asn Lys Asp Asp Phe Gly Arg Leu	205	210	215	
AGA GTG GGG GCG GCT ATT GGA GTG GGG CAG TTG GAT AGG GCT GAG ATG				726
Arg Val Gly Ala Ala Ile Gly Val Gly Gln Leu Asp Arg Ala Glu Met	220	225	230	
TTA GTT AAA GCG GGG GTG GAT GCA CTG GTG CTA GAC AGC GCA CAT GGG				774
Leu Val Lys Ala Gly Val Asp Ala Leu Val Leu Asp Ser Ala His Gly	235	240	245	
CAT TCA GCC AAT ATC TTA CAC ACT TTA GAA GAG ATT AAA AAA AGC TTG				822
His Ser Ala Asn Ile Leu His Thr Leu Glu Glu Ile Lys Lys Ser Leu	250	255	260	
GTA GTG GAT GTG ATT GTG GGG AAT GTG GTT ACT AAA GAA GCC ACA AGC				870
Val Val Asp Val Ile Val Gly Asn Val Val Thr Lys Glu Ala Thr Ser	265	270	275	280
GAT TTG ATT AGC GCG GGA GCA GAC GCT ATT AAA GTG GGT ATT GGG CCA				918
Asp Leu Ile Ser Ala Gly Ala Asp Ala Ile Lys Val Gly Ile Gly Pro	285	290	295	
GGA AGC ATT TGC ACC ACT AGG ATT GTG GCT GGG GTG GGA ATG CCC CAA				966
Gly Ser Ile Cys Thr Thr Arg Ile Val Ala Gly Val Gly Met Pro Gln	300	305	310	
GTG AGC GCG ATT GAT AAT TGC GTA GAA GTG GCG TCT AAA TTT GAT ATT				1014
Val Ser Ala Ile Asp Asn Cys Val Glu Val Ala Ser Lys Phe Asp Ile	315	320	325	
CCT GTG ATT GCA GAT GGA GGG ATC CGC TAT TCA GGC GAT GTG GCT AAG				1062
Pro Val Ile Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Val Ala Lys	330	335	340	
GCT TTG GCT TTG GGG GCA TCA AGC GTG ATG ATA GGC TCT TTA CTC GCT				1110
Ala Leu Ala Leu Gly Ala Ser Ser Val Met Ile Gly Ser Leu Leu Ala	345	350	355	360
GGC ACA GAA GAA TCT CCT GGG GAT TTT ATG ATC TAT CAA GGG AGG CAA				1158
Gly Thr Glu Glu Ser Pro Gly Asp Phe Met Ile Tyr Gln Gly Arg Gln	365	370	375	
TAT AAA AGC TAT AGG GGC ATG GGC AGC ATT GGG GCT ATG ACT AAA GGG				1206
Tyr Lys Ser Tyr Arg Gly Met Gly Ser Ile Gly Ala Met Thr Lys Gly	380	385	390	
AGC TCT GAT AGG TAT TTT CAA GAG GGC GTA GCG AGT GAA AAG TTA GTC				1254
Ser Ser Asp Arg Tyr Phe Gln Glu Gly Val Ala Ser Glu Lys Leu Val	395	400	405	
CCA GAA GGC ATT GAA GGG CGT GTG CCT TAT CGT GGT AAG GTT TCG GAT				1302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

TTAGATTAA AATTAGATTA AGGATAGAAA	ATG AGA ATT TTA CAA AGG GCT TTG	54
	Met Arg Ile Leu Gln Arg Ala Leu	
	1 5	
ACT TTT GAA GAT GTG TTG ATG GTG CCT AGA AAG TCT AGC GTT TTA CCT	102	
Thr Phe Glu Asp Val Leu Met Val Pro Arg Lys Ser Ser Val Leu Pro		
10 15 20		
AAA GAT GTG AGC TTA AAG TCT CGC TTA ACT AAA AAC ATT CGT TTG AAT	150	
Lys Asp Val Ser Leu Lys Ser Arg Leu Thr Lys Asn Ile Arg Leu Asn		
25 30 35 40		
ATC CCC TTT ATC AGT GCG GCT ATG GAT ACG GTT ACA GAG CAT AAA ACC	198	
Ile Pro Phe Ile Ser Ala Ala Met Asp Thr Val Thr Glu His Lys Thr		
45 50 55		
GCT ATC GCT ATG GCG CGC CTT GGG GGT ATT GGC ATC GTG CAT AAA AAC	246	
Ala Ile Ala Met Ala Arg Leu Gly Gly Ile Gly Ile Val His Lys Asn		
60 65 70		
ATG GAT ATT CAA ACG CAA GTT AAA GAA ATC ACT AAG GTT AAA AAA AGC	294	
Met Asp Ile Gln Thr Gln Val Lys Glu Ile Thr Lys Val Lys Lys Ser		
75 80 85		
GAG AGC GGG GTG ATT AAT GAT CCT ATT TTT ATC CAT GCG CAC AGG ACG	342	
Glu Ser Gly Val Ile Asn Asp Pro Ile Phe Ile His Ala His Arg Thr		
90 95 100		
CTA GCG GAC GCT AAA GTC ATA ACG GAT AAT TAC AAG ATT TCA GGC GTG	390	
Leu Ala Asp Ala Lys Val Ile Thr Asp Asn Tyr Lys Ile Ser Gly Val		
105 110 115 120		
CCT GTG GTA GAT GAT AAG GGG TTG TTG ATT GGG ATT TTA ACC AAC AGA	438	
Pro Val Val Asp Asp Lys Gly Leu Leu Ile Gly Ile Leu Thr Asn Arg		
125 130 135		
GAT GTG CGC TTT GAA ACC GAT TTG AGT AAA AAA GTG GGC GAT GTG ATG	486	
Asp Val Arg Phe Glu Thr Asp Leu Ser Lys Lys Val Gly Asp Val Met		
140 145 150		
ACT AAA ATG CCT TTA GTT ACC GCT CAT GTG GGT ATC AGT TTG GAT GAA	534	
Thr Lys Met Pro Leu Val Thr Ala His Val Gly Ile Ser Leu Asp Glu		
155 160 165		
GCG AGC GAT TTG ATG CAC AAG CAT AAG ATT GAA AAA TTG CCC ATT GTG	582	
Ala Ser Asp Leu Met His Lys His Lys Ile Glu Lys Leu Pro Ile Val		
170 175 180		
GAT AAA GAT AAT GTC TTA AAA GGC TTG ATC ACG ATC AAA GAT ATT CAA	630	
Asp Lys Asp Asn Val Leu Lys Gly Leu Ile Thr Ile Lys Asp Ile Gln		

```

AAA CCT AAA GGT TTT GGC TTT GTA GAA ATG CAA GAA GAG AGC GTT AGT      240
Lys Pro Lys Gly Phe Gly Phe Val Glu Met Gln Glu Glu Ser Val Ser
65                               70                               75                               80

GAA GCG ATC GCT AAA TTA GAC AAT ACG GAT TTT ATG GGC AGA ACG ATT      288
Glu Ala Ile Ala Lys Leu Asp Asn Thr Asp Phe Met Gly Arg Thr Ile
                        85                               90                               95

AGG GTA ACC GAA GCT AAT CCT AAA AAG TCT TAGTAACATT AGAAAATAAT TTT    341
Arg Val Thr Glu Ala Asn Pro Lys Lys Ser
                100                               105

CTAATGCGCT T                                                              352

```

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

```

Lys Cys Tyr Phe Phe Ile Thr Phe Ser Tyr Ser Tyr Gly Tyr Val Val
1           5           10           15
Ile Phe Leu Pro Glu Asn Phe Ile Leu Arg Asn Ile Tyr Val Gly Asn
20           25           30
Leu Val Tyr Ser Ala Thr Ser Glu Gln Val Lys Glu Leu Phe Ser Gln
35           40           45
Phe Gly Lys Val Phe Asn Val Lys Leu Ile Tyr Asp Arg Glu Thr Lys
50           55           60
Lys Pro Lys Gly Phe Gly Phe Val Glu Met Gln Glu Glu Ser Val Ser
65           70           75           80
Glu Ala Ile Ala Lys Leu Asp Asn Thr Asp Phe Met Gly Arg Thr Ile
85           90           95
Arg Val Thr Glu Ala Asn Pro Lys Lys Ser
100           105

```

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1473
- (D) OTHER INFORMATION:


```

      1           5           10           15
Lys Leu Glu Thr Leu Leu Lys Leu Lys Lys Leu Lys Val Phe Met Pro
      20           25           30
Leu Ser Leu Gln Glu Asn Leu Leu Phe Ile Phe Ile Lys Asp Ser Lys
      35           40           45
Leu Leu Phe Ala Phe Lys Asp Ile Trp Ala Ser Lys Glu Phe Asn Gln
      50           55           60
Arg Phe Ala Lys Glu Ile Ser His Phe Leu Asn Thr Gln Gly His Ala
      65           70           75           80
Tyr Gly Phe Asp Gly Leu Asn Gly Leu Glu Ile Leu Gly Tyr Val Pro
      85           90           95
Lys Asp Ala Leu Lys Lys Ser Asn Phe Tyr Ala Pro Ile Lys Lys Gln
      100          105          110
Ala Arg Phe Phe Arg Pro Ser Ala Leu Gly Leu Phe His Asn Pro Ile
      115          120          125
Lys Asp Ala Arg Leu His Glu Cys Phe Glu Lys Ala Arg Ala Leu Ile
      130          135          140
His Tyr Gln Arg Ser Phe Phe Glu Glu
      145          150

```

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...318
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

```

AAG TGT TAC TTT TTT ATA ACT TTT TCA TAT TCT TAT GGG TAT GTT GTC      48
Lys Cys Tyr Phe Phe Ile Thr Phe Ser Tyr Ser Tyr Gly Tyr Val Val
  1           5           10           15

ATT TTT TTA CCG GAG AAT TTT ATC TTG AGA AAC ATT TAT GTA GGG AAT      96
Ile Phe Leu Pro Glu Asn Phe Ile Leu Arg Asn Ile Tyr Val Gly Asn
      20           25           30

TTG GTT TAT AGC GCT ACC AGT GAG CAA GTC AAG GAG CTT TTC AGT CAA      144
Leu Val Tyr Ser Ala Thr Ser Glu Gln Val Lys Glu Leu Phe Ser Gln
      35           40           45

TTT GGC AAA GTT TTT AAT GTC AAG CTG ATT TAT GAC AGA GAA ACG AAG      192
Phe Gly Lys Val Phe Asn Val Lys Leu Ile Tyr Asp Arg Glu Thr Lys
      50           55           60

```

Met	Glu	Gln	Asn	Ile	Phe	Ser	Leu	Leu	Ile	Gln	Lys	
1				5						10		
AAG TCT TAT AAA AAG CTT GAA ACC CTT TTG AAA CTC AAA AAG CTT AAG												99
Lys Ser Tyr Lys Lys Leu Glu Thr Leu Leu Lys Leu Lys Lys Leu Lys												
15				20						25		
GTT TTT ATG CCT TTA AGT TTA CAA GAA AAT TTG CTT TTT ATC TTC ATA												147
Val Phe Met Pro Leu Ser Leu Gln Glu Asn Leu Leu Phe Ile Phe Ile												
30				35						40		
AAA GAC TCT AAA TTG CTT TTT GCG TTT AAA GAC ATT TGG GCT TCT AAA												195
Lys Asp Ser Lys Leu Leu Phe Ala Phe Lys Asp Ile Trp Ala Ser Lys												
45				50						55		60
GAA TTT AAC CAA CGA TTC GCT AAA GAA ATC AGC CAT TTT TTA AAC ACG												243
Glu Phe Asn Gln Arg Phe Ala Lys Glu Ile Ser His Phe Leu Asn Thr												
				65						70		75
CAA GGG CAT GCT TAT GGG TTT GAC GGG TTG AAT GGG TTA GAA ATT TTA												291
Gln Gly His Ala Tyr Gly Phe Asp Gly Leu Asn Gly Leu Glu Ile Leu												
				80						85		90
GGT TAT GTG CCT AAA GAC GCG CTA AAA AAA TCC AAT TTT TAT GCC CCC												339
Gly Tyr Val Pro Lys Asp Ala Leu Lys Lys Ser Asn Phe Tyr Ala Pro												
				95						100		105
ATT AAA AAA CAA GCC CGT TTT TTT CGC CCT AGT GCT TTA GGG TTG TTC												387
Ile Lys Lys Gln Ala Arg Phe Phe Arg Pro Ser Ala Leu Gly Leu Phe												
				110						115		120
CAT AAC CCC ATT AAA GAC GCT CGT TTG CAT GAA TGT TTT GAA AAA GCG												435
His Asn Pro Ile Lys Asp Ala Arg Leu His Glu Cys Phe Glu Lys Ala												
				125						130		135
CGC GCT TTG ATC CAC TAC CAA CGA AGT TTT TTT GAG GAA TGAATGGCTG AT												486
Arg Ala Leu Ile His Tyr Gln Arg Ser Phe Phe Glu Glu												
				145						150		
TTATTGTCCA GTTTAAAAA CCTTCCTAAC AGCAGTGGCG TGTATCAATA TTTTGATAAA												546
AAC												549

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

Met Glu Gln Asn Ile Phe Ser Leu Leu Ile Gln Lys Lys Ser Tyr Lys

```

Met Ala Lys Lys Asn Xaa Pro Thr Glu Cys Pro Ala Gly Glu Lys Trp
 1          5          10          15
Ala Val Pro Tyr Ala Asp Phe Leu Ser Leu Leu Leu Ala Leu Phe Ile
 20          25          30
Ala Leu Tyr Ala Ile Ser Ala Val Asn Lys Ser Lys Val Glu Ala Leu
 35          40          45
Lys Thr Glu Phe Ile Lys Ile Phe Asn Tyr Ala Pro Lys Pro Glu Ala
 50          55          60
Met Gln Pro Val Val Val Ile Pro Pro Asp Ser Gly Lys Glu Glu Glu
 65          70          75          80
Gln Met Ala Ser Glu Ser Ser Lys Pro Ala Ser Gln Asn Thr Glu Thr
 85          90          95
Lys Ala Thr Ile Ala Arg Lys Gly Glu Gly Ser Val Leu Glu Gln Ile
100          105          110
Asp Gln Gly Ser Ile Leu Lys Leu Pro Ser Asn Leu Leu Phe Glu Asn
115          120          125
Ala Thr Ser Asp Ala Ile Asn Gln Asp Met Met Leu Tyr Ile Glu Arg
130          135          140
Ile Ala Lys Ile Ile Gln Lys Leu Pro Lys Arg Val His Ile Asn Val
145          150          155          160
Arg Gly Phe Thr Asp Asp Thr Pro Leu Val Lys Thr Arg Phe Lys Ser
165          170          175
His Tyr Glu Leu Ala Ala Asn Arg Ala Tyr Arg Val Met Lys Val Leu
180          185          190
Ile Gln Tyr Gly Val Asn Pro Asn Gln Leu Ser Phe Ser Ser Tyr Gly
195          200          205
Ser Thr Asn Pro Ile Ala Pro Asn Asp Ser Leu Glu Asn Arg Met Lys
210          215          220
Asn Asn Arg Val Glu Ile Phe Phe Ser Thr Asp Ala Asn Asp Leu Ser
225          230          235          240
Lys Ile His Ser Ile Leu Asp Asn Glu Phe Asn Pro His Lys Gln Gln
245          250          255
Glu

```

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...474
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

TGTTAAGATC AGTTT ATG GAA CAA AAT ATT TTC TCC TTA CTC ATT CAA AAA

51

95	100	105	
GAG CAA ATT GAT CAA GGC TCT ATC TTA AAG CTC CCC TCT AAT TTG CTG			387
Glu Gln Ile Asp Gln Gly Ser Ile Leu Lys Leu Pro Ser Asn Leu Leu			
110	115	120	125
TTT GAA AAC GCT ACT TCA GAC GCT ATC AAT CAA GAC ATG ATG CTT TAT			435
Phe Glu Asn Ala Thr Ser Asp Ala Ile Asn Gln Asp Met Met Leu Tyr			
	130	135	140
ATT GAA CGG ATC GCT AAA ATC ATT CAA AAA CTC CCT AAA AGG GTG CAT			483
Ile Glu Arg Ile Ala Lys Ile Ile Gln Lys Leu Pro Lys Arg Val His			
	145	150	155
ATT AAT GTG AGA GGC TTT ACG GAT GAT ACG CCT TTA GTT AAA ACC CGT			531
Ile Asn Val Arg Gly Phe Thr Asp Asp Thr Pro Leu Val Lys Thr Arg			
	160	165	170
TTT AAA AGC CAT TAT GAA TTA GCC GCC AAT CGC GCT TAT AGG GTG ATG			579
Phe Lys Ser His Tyr Glu Leu Ala Ala Asn Arg Ala Tyr Arg Val Met			
	175	180	185
AAA GTC CTT ATA CAA TAC GGC GTA AAT CCT AAC CAA TTG TCT TTT TCT			627
Lys Val Leu Ile Gln Tyr Gly Val Asn Pro Asn Gln Leu Ser Phe Ser			
	190	195	200
TCT TAC GGC TCT ACC AAC CCT ATC GCG CCT AAC GAC TCC CTA GAG AAC			675
Ser Tyr Gly Ser Thr Asn Pro Ile Ala Pro Asn Asp Ser Leu Glu Asn			
	210	215	220
AGA ATG AAA AAC AAT CGT GTG GAA ATC TTT TTT TCA ACC GAT GCG AAC			723
Arg Met Lys Asn Asn Arg Val Glu Ile Phe Phe Ser Thr Asp Ala Asn			
	225	230	235
GAT TTG AGT AAA ATT CAT TCT ATT TTA GAT AAT GAG TTC AAT CCC CAC			771
Asp Leu Ser Lys Ile His Ser Ile Leu Asp Asn Glu Phe Asn Pro His			
	240	245	250
AAA CAG CAA GAA TGAATCGCAT GAATAAAAAT TATCTTT			810
Lys Gln Gln Glu			
255			

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

```

145          150          155          160
Lys Ala Lys Ser Lys Asp Ile Ile Lys Glu Lys Thr Val Leu Leu Glu
          165          170          175
Gly Ile Leu Gly Ile Ala Asn Gly Glu Asn Pro Arg Asp Leu Glu Asn
          180          185          190
Lys Leu Leu Asn Tyr Ile Ala Pro Gly Glu Pro Lys Lys Ser Gln Phe
          195          200          205
Glu Gly
          210

```

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...783
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

```

TGAGGGCTAA AG ATG GCT AAG AAA AAC AMA CCC ACC GAA TGC CCC GCC GGT      51
      Met Ala Lys Lys Asn Xaa Pro Thr Glu Cys Pro Ala Gly
          1          5          10

GAA AAA TGG GCG GTT CCT TAT GCG GAC TTT TTG TCG TTG TTG CTC GCG      99
Glu Lys Trp Ala Val Pro Tyr Ala Asp Phe Leu Ser Leu Leu Leu Ala
          15          20          25

CTT TTT ATC GCT CTT TAT GCC ATT TCA GCG GTC AAC AAA TCC AAA GTG      147
Leu Phe Ile Ala Leu Tyr Ala Ile Ser Ala Val Asn Lys Ser Lys Val
          30          35          40          45

GAA GCC TTA AAA ACC GAA TTT ATT AAG ATT TTT AAT TAC GCT CCC AAG      195
Glu Ala Leu Lys Thr Glu Phe Ile Lys Ile Phe Asn Tyr Ala Pro Lys
          50          55          60

CCA GAG GCG ATG CAG CCG GTT GTA GTG ATC CCG CCT GAT TCA GGG AAA      243
Pro Glu Ala Met Gln Pro Val Val Val Ile Pro Pro Asp Ser Gly Lys
          65          70          75

GAA GAA GAA CAA ATG GCG AGC GAA AGC TCC AAA CCG GCT TCG CAA AAT      291
Glu Glu Glu Gln Met Ala Ser Glu Ser Ser Lys Pro Ala Ser Gln Asn
          80          85          90

ACC GAA ACA AAA GCC ACT ATC GCT CGC AAA GGC GAA GGC AGT GTT TTA      339
Thr Glu Thr Lys Ala Thr Ile Ala Arg Lys Gly Glu Gly Ser Val Leu

```

125										130					135					
GCT	TTT	ACG	GCT	ACT	GTT	ACA	GGG	ATT	ATG	TGT	TCT	TAT	GCG	ATT	TTT	484				
Ala	Phe	Thr	Ala	Thr	Val	Thr	Gly	Ile	Met	Cys	Ser	Tyr	Ala	Ile	Phe					
140					145					150										
GGC	CCT	TTT	GGG	CAT	AAG	CTC	AAA	GCT	AAG	TCT	AAA	GAC	ATT	ATC	AAA	532				
Gly	Pro	Phe	Gly	His	Lys	Leu	Lys	Ala	Lys	Ser	Lys	Asp	Ile	Ile	Lys					
155					160					165										
GAA	AAA	ACC	GTT	CTT	TTA	GAG	GGG	ATT	TTA	GGC	ATC	GCT	AAT	GGG	GAA	580				
Glu	Lys	Thr	Val	Leu	Leu	Glu	Gly	Ile	Leu	Gly	Ile	Ala	Asn	Gly	Glu					
170					175					180					185					
AAC	CCA	AGG	GAT	TTA	GAA	AAC	AAA	CTC	TTA	AAC	TAC	ATC	GCT	CCC	GGT	628				
Asn	Pro	Arg	Asp	Leu	Glu	Asn	Lys	Leu	Leu	Asn	Tyr	Ile	Ala	Pro	Gly					
190					195					200										
GAA	CCT	AAA	AAA	TCT	CAA	TTT	GAG	GGC	TAAAGATGGC	TAAGAAAAAC	AMACCCA	682								
Glu	Pro	Lys	Lys	Ser	Gln	Phe	Glu	Gly												
205					210															
CCGAATGCCC CGC															695					

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

Met	Thr	Gly	Thr	His	Ala	Arg	Tyr	Val	Lys	Ala	Ala	Tyr	Lys	Glu	Ile
1				5					10					15	
Lys	Ile	Val	Phe	Leu	Asn	Pro	Lys	Ile	Asn	Leu	Asn	Glu	Thr	Ile	Lys
			20					25					30		
Asn	Leu	Val	Glu	Leu	Ala	Thr	Leu	Ala	Arg	Lys	Asp	Gly	Val	Leu	Ser
		35					40					45			
Leu	Glu	Gly	Arg	Val	Ala	Gln	Ile	Glu	Asp	Asp	Phe	Thr	Arg	Asn	Gly
	50					55				60					
Leu	Ser	Met	Ile	Ile	Asp	Gly	Lys	Asp	Leu	Lys	Ser	Val	Lys	Glu	Ser
65					70					75				80	
Leu	Glu	Ile	Ser	Ile	Glu	Glu	Met	Glu	Glu	Tyr	Tyr	His	Gly	Ala	Ala
			85					90					95		
His	Tyr	Trp	Glu	Thr	Ala	Gly	Glu	Thr	Ala	Pro	Thr	Met	Gly	Leu	Val
		100					105						110		
Gly	Ala	Val	Met	Gly	Leu	Met	Leu	Ala	Leu	Gln	Lys	Leu	Asp	Asn	Pro
		115				120					125				
Ala	Glu	Met	Ala	Ala	Gly	Ile	Ala	Gly	Ala	Phe	Thr	Ala	Thr	Val	Thr
	130					135					140				
Gly	Ile	Met	Cys	Ser	Tyr	Ala	Ile	Phe	Gly	Pro	Phe	Gly	His	Lys	Leu

195

200

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...655
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

CGTGCCTACT TCGCTTTTTTG CCGCC ATG ACA GGC ACA CAT GCG CGT TAC GTG	52
Met Thr Gly Thr His Ala Arg Tyr Val	
1 5	
AAA GCC GCT TAC AAA GAG ATA AAA ATT GTT TTT TTA AAC CCT AAA ATC	100
Lys Ala Ala Tyr Lys Glu Ile Lys Ile Val Phe Leu Asn Pro Lys Ile	
10 15 20 25	
AAT TTA AAC GAA ACC ATC AAA AAT TTA GTG GAA TTA GCC ACT CTG GCT	148
Asn Leu Asn Glu Thr Ile Lys Asn Leu Val Glu Leu Ala Thr Leu Ala	
30 35 40	
AGA AAA GAT GGG GTG TTG AGT TTA GAG GGG CGA GTG GCG CAA ATT GAA	196
Arg Lys Asp Gly Val Leu Ser Leu Glu Gly Arg Val Ala Gln Ile Glu	
45 50 55	
GAC GAT TTC ACC CGT AAT GGC TTG TCT ATG ATC ATA GAT GGC AAG GAT	244
Asp Asp Phe Thr Arg Asn Gly Leu Ser Met Ile Ile Asp Gly Lys Asp	
60 65 70	
TTA AAA TCC GTT AAG GAA AGC TTA GAA ATC AGC ATT GAA GAA ATG GAA	292
Leu Lys Ser Val Lys Glu Ser Leu Glu Ile Ser Ile Glu Glu Met Glu	
75 80 85	
GAG TAT TAC CAC GGC GCC GCT CAT TAT TGG GAG ACG GCC GGT GAG ACC	340
Glu Tyr Tyr His Gly Ala Ala His Tyr Trp Glu Thr Ala Gly Glu Thr	
90 95 100 105	
GCT CCT ACT ATG GGG TTA GTG GGG GCG GTT ATG GGG CTT ATG TTA GCC	388
Ala Pro Thr Met Gly Leu Val Gly Ala Val Met Gly Leu Met Leu Ala	
110 115 120	
TTG CAA AAA CTA GAC AAC CCG GCT GAA ATG GCA GCA GGG ATC GCT GGG	436
Leu Gln Lys Leu Asp Asn Pro Ala Glu Met Ala Ala Gly Ile Ala Gly	

GAA ACA AGT GGG TTT TTA GGG ATT TAT GAA AAG TGT TTT CAA GCT TTA	486
Glu Thr Ser Gly Phe Leu Gly Ile Tyr Glu Lys Cys Phe Gln Ala Leu	
140 145 150	
GAA AGG TTA TTG AAA CGC TTT AAT CCA AAA AAT CTT TTA GTG GTT TTT	534
Glu Arg Leu Leu Lys Arg Phe Asn Pro Lys Asn Leu Leu Val Val Phe	
155 160 165	
GAG CAT GAA AGC ATG CAT GAA ATG CCT AAA AGT CTT GTA ACT TTA GCT	582
Glu His Glu Ser Met His Glu Met Pro Lys Ser Leu Val Thr Leu Ala	
170 175 180	
ATA ATC AAA CAA AAA AAA TTT GGA AAA ACC ACT TTA ACT TAT TTT CAA T	631
Ile Ile Lys Gln Lys Lys Phe Gly Lys Thr Thr Leu Thr Tyr Phe Gln	
185 190 195 200	
AGGAATAGGC ATGGCAGAAG AACAAGAA	659

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

Met	Pro	Asn	His	Gln	Pro	Val	Lys	Lys	Phe	Lys	Ile	Ile	Gly	Gly	Ala
1				5					10					15	
Cys	Lys	Gly	Leu	Gly	Leu	Asn	Leu	Pro	Asn	Ile	Ser	Ser	Thr	Arg	Pro
			20					25					30		
Thr	Lys	Ala	Ile	Val	Arg	Glu	Ser	Phe	Phe	Asn	Thr	Leu	Gln	Ala	Glu
		35				40						45			
Ile	Asn	Gly	Ala	His	Phe	Ile	Glu	Val	Phe	Ser	Gly	Ser	Ala	Ser	Met
	50					55					60				
Gly	Leu	Glu	Ala	Leu	Ser	Arg	Gly	Ala	Lys	Ser	Ala	Val	Phe	Phe	Glu
	65				70				75					80	
Gln	Asn	Lys	Ser	Ala	Tyr	Lys	Thr	Leu	Leu	Glu	Asn	Ile	Ser	Leu	Phe
			85					90					95		
Lys	Asn	Arg	Leu	Lys	Lys	Glu	Met	Glu	Ile	Gln	Thr	Phe	Leu	Asp	Asp
			100					105					110		
Ala	Phe	Lys	Leu	Leu	Pro	Thr	Leu	Cys	Leu	Lys	Asn	Gly	Val	Leu	Asn
		115					120					125			
Ile	Ile	Tyr	Leu	Asp	Pro	Pro	Phe	Glu	Thr	Ser	Gly	Phe	Leu	Gly	Ile
	130					135					140				
Tyr	Glu	Lys	Cys	Phe	Gln	Ala	Leu	Glu	Arg	Leu	Leu	Lys	Arg	Phe	Asn
	145				150				155					160	
Pro	Lys	Asn	Leu	Leu	Val	Val	Phe	Glu	His	Glu	Ser	Met	His	Glu	Met
			165					170					175		
Pro	Lys	Ser	Leu	Val	Thr	Leu	Ala	Ile	Ile	Lys	Gln	Lys	Lys	Phe	Gly
			180					185					190		
Lys	Thr	Thr	Leu	Thr	Tyr	Phe	Gln								

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...630
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

GCAATTACTA GAAGAATACA CCCACAAATT	ATG CCA AAT CAT CAG CCA GTA AAA	54
	Met Pro Asn His Gln Pro Val Lys	
	1 5	
AAA TTT AAG ATT ATT GGG GGG GCT TGT AAG GGA TTA GGC TTG AAT TTG		102
Lys Phe Lys Ile Ile Gly Gly Ala Cys Lys Gly Leu Gly Leu Asn Leu		
10 15 20		
CCT AAC ATT TCT AGC ACG CGC CCC ACC AAA GCG ATC GTA AGA GAG TCG		150
Pro Asn Ile Ser Ser Thr Arg Pro Thr Lys Ala Ile Val Arg Glu Ser		
25 30 35 40		
TTT TTT AAC ACC TTG CAA GCA GAA ATT AAT GGA GCG CAT TTT ATA GAA		198
Phe Phe Asn Thr Leu Gln Ala Glu Ile Asn Gly Ala His Phe Ile Glu		
45 50 55		
GTG TTT TCA GGC AGC GCT TCT ATG GGT TTA GAG GCT TTG AGT AGG GGG		246
Val Phe Ser Gly Ser Ala Ser Met Gly Leu Glu Ala Leu Ser Arg Gly		
60 65 70		
GCT AAA AGT GCG GTG TTT TTT GAA CAA AAC AAA AGC GCT TAT AAG ACG		294
Ala Lys Ser Ala Val Phe Phe Glu Gln Asn Lys Ser Ala Tyr Lys Thr		
75 80 85		
CTT TTA GAA AAT ATT TCC CTT TTT AAA AAC CGC TTG AAA AAA GAA ATG		342
Leu Leu Glu Asn Ile Ser Leu Phe Lys Asn Arg Leu Lys Lys Glu Met		
90 95 100		
GAA ATT CAA ACC TTT TTA GAT GAC GCT TTC AAG CTT TTG CCC ACG CTG		390
Glu Ile Gln Thr Phe Leu Asp Asp Ala Phe Lys Leu Leu Pro Thr Leu		
105 110 115 120		
TGT TTA AAA AAT GGC GTT TTG AAT ATT ATT TAT TTG GAT CCT CCT TTT		438
Cys Leu Lys Asn Gly Val Leu Asn Ile Ile Tyr Leu Asp Pro Pro Phe		
125 130 135		

(2) INFORMATION FOR SEO ID NO:856:

(A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

- 1281 -

```

      115              120              125
Val Lys Ala Ile Asp Lys Ser Met Thr Ile Ser Gly Val Met Leu Glu
      130              135              140
His Lys Ser Gly Gly Lys Ser Gly Asp Tyr Asn Ala Lys Lys
      145              150              155

```

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...552
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

```

CTTTTAGCTT AAAAAGGAGT TCAA ATG CAA ACG ATT CAT ATA GGC GTT TTG      51
      Met Gln Thr Ile His Ile Gly Val Leu
      1              5

AGC GCG AGC GAT AGA GCG TCA AAA GGG ATT TAT GAA GAT TTA AGC GGT      99
Ser Ala Ser Asp Arg Ala Ser Lys Gly Ile Tyr Glu Asp Leu Ser Gly
      10              15              20              25

AAG GCG ATA CAA GAA GTG TTG AGC GAA TAC TTG CTC AAT CCT TTA GAA      147
Lys Ala Ile Gln Glu Val Leu Ser Glu Tyr Leu Leu Asn Pro Leu Glu
      30              35              40

TTT TAT TAC GAA ATT GTC GCT GAT GAA AGG GAT TTA ATT GAA AAA TCA      195
Phe Tyr Tyr Glu Ile Val Ala Asp Glu Arg Asp Leu Ile Glu Lys Ser
      45              50              55

CTG ATT AAA ATG TGC GAT GAA TAC CAA TGC GAT CTA GTC GTT ACT ACA      243
Leu Ile Lys Met Cys Asp Glu Tyr Gln Cys Asp Leu Val Val Thr Thr
      60              65              70

GGA GGC ACA GGC CCT GCT TTA AGA GAT ATA ACC CCA GAA GCC ACA GAA      291
Gly Gly Thr Gly Pro Ala Leu Arg Asp Ile Thr Pro Glu Ala Thr Glu
      75              80              85

AAA GTG TGC CAA AAA ATG CTT CCT GGT TTT GGA GAG CTT ATG CGA ATG      339
Lys Val Cys Gln Lys Met Leu Pro Gly Phe Gly Glu Leu Met Arg Met
      90              95              100              105

ACT AGT TTA AAA TAT GTG CCT ACA GCG ATC CTG TCG CGC CAG AGC GCT      387
Thr Ser Leu Lys Tyr Val Pro Thr Ala Ile Leu Ser Arg Gln Ser Ala

```

60	65	70	
TGC CAT CCA ATC ATG	CTC AAT GGG GTG GAT	ATT GAT ATT TTA GAA GAA	291
Cys His Pro Ile Met	Leu Asn Gly Val Asp	Ile Asp Ile Leu Glu Glu	
75	80	85 90	
AAA GAG ACT TGT AGT	TTT AAA CTC TAT GCG	AGA GTC AAA ACT CAA GCT	339
Lys Glu Thr Cys Ser	Phe Lys Leu Tyr Ala	Arg Val Lys Thr Gln Ala	
95	100	105	
AAA ACG GGC GTA GAA	ATG GAA GCG CTA ATG	AGT GTG AGC ATA GGG CTT	387
Lys Thr Gly Val Glu	Met Glu Ala Leu Met	Ser Val Ser Ile Gly Leu	
110	115	120	
TTA ACC ATT TAT GAC	ATG GTG AAA GCC ATT	GAC AAG AGC ATG ACA ATT	435
Leu Thr Ile Tyr Asp	Met Val Lys Ala Ile	Asp Lys Ser Met Thr Ile	
125	130	135	
AGC GGT GTG ATG TTG	GAG CAT AAA AGT GGA	GGC AAA AGT GGG GAT TAT	483
Ser Gly Val Met Leu	Glu His Lys Ser Gly	Gly Lys Ser Gly Asp Tyr	
140	145	150	
AAC GCT AAA AAA	TAGAAAAAGA CCAATAATCT AAAGATGTTA GGGTAAAATA ACATT		540
Asn Ala Lys Lys			
155			
TTGACAACAA AAGCGTGTG	GTTG		564

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

Met	Pro	Leu	Thr	His	Leu	Asn	Glu	Glu	Asn	Gln	Pro	Lys	Met	Val	Asp
1				5					10					15	
Ile	Gly	Asp	Lys	Glu	Thr	Thr	Glu	Arg	Ile	Ala	Leu	Ala	Ser	Gly	Arg
		20						25					30		
Ile	Ser	Met	Asn	Lys	Glu	Ala	Tyr	Asp	Ala	Ile	Ile	Asn	His	Cys	Val
		35					40					45			
Lys	Lys	Gly	Pro	Val	Leu	Gln	Thr	Ala	Ile	Ile	Ala	Gly	Ile	Met	Gly
	50					55					60				
Ala	Lys	Lys	Thr	Ser	Glu	Leu	Ile	Pro	Met	Cys	His	Pro	Ile	Met	Leu
65					70					75				80	
Asn	Gly	Val	Asp	Ile	Asp	Ile	Leu	Glu	Glu	Lys	Glu	Thr	Cys	Ser	Phe
			85					90					95		
Lys	Leu	Tyr	Ala	Arg	Val	Lys	Thr	Gln	Ala	Lys	Thr	Gly	Val	Glu	Met
			100					105					110		
Glu	Ala	Leu	Met	Ser	Val	Ser	Ile	Gly	Leu	Leu	Thr	Ile	Tyr	Asp	Met

```

      35              40              45
Ala Ile Gln Val Gly Leu Pro Leu Arg Met Leu Ile Ile Asn Leu Pro
      50              55              60
Gln Glu Asp Gly Val Gln His Lys Glu Asp Cys Leu Glu Ile Ile Asn
65              70              75              80
Pro Lys Phe Ile Glu Thr Gly Gly Ser Met Met Tyr Arg Glu Gly Cys
      85              90              95
Leu Ser Val Pro Gly Phe Tyr Glu Glu Val Glu Arg Phe Glu Lys Val
      100             105             110
Lys Ile Glu Tyr Gln Asn Arg Phe Ala Glu Val Lys Val Leu Glu Ala
      115             120             125
Ser Glu Leu Leu Ala Val Ala Ile Gln His Glu Ile Asp His Leu Asn
      130             135             140
Gly Val Leu Phe Val Asp Lys Leu Ser Ile Leu Lys Arg Lys Lys Phe
145             150             155             160
Glu Lys Glu Leu Lys Glu Leu Gln Lys Lys Gln Lys His Glu
      165             170

```

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...495
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

```

CCCCAAACAA TAGGATAAAA A ATG CCG CTC ACT CAT TTG AAT GAA GAA AAT      51
                      Met Pro Leu Thr His Leu Asn Glu Glu Asn
                      1              5              10

CAG CCT AAA ATG GTG GAT ATA GGG GAT AAA GAA ACC ACT GAA AGA ATC      99
Gln Pro Lys Met Val Asp Ile Gly Asp Lys Glu Thr Thr Glu Arg Ile
                      15              20              25

GCT TTA GCA AGC GGT CGT ATC AGC ATG AAT AAA GAG GCT TAT GAC GCT     147
Ala Leu Ala Ser Gly Arg Ile Ser Met Asn Lys Glu Ala Tyr Asp Ala
                      30              35              40

ATT ATC AAT CAT TGC GTC AAA AAG GGT CCG GTG TTA CAG ACT GCT ATT     195
Ile Ile Asn His Cys Val Lys Lys Gly Pro Val Leu Gln Thr Ala Ile
                      45              50              55

ATT GCT GGA ATT ATG GGG GCT AAA AAG ACA AGC GAG CTC ATT CCC ATG     243
Ile Ala Gly Ile Met Gly Ala Lys Lys Thr Ser Glu Leu Ile Pro Met

```

```

AGT GAG GGG ATA GGG TTA GCC GCT ATT CAA GTG GGT TTG CCT TTA AGA      196
Ser Glu Gly Ile Gly Leu Ala Ala Ile Gln Val Gly Leu Pro Leu Arg
      45                      50                      55

ATG CTC ATC ATC AAC CTC CCG CAA GAA GAC GGC GTG CAA CAC AAA GAA      244
Met Leu Ile Ile Asn Leu Pro Gln Glu Asp Gly Val Gln His Lys Glu
      60                      65                      70

GAC TGC TTG GAA ATC ATT AAC CCT AAG TTT ATA GAA ACT GGG GGA TCA      292
Asp Cys Leu Glu Ile Ile Asn Pro Lys Phe Ile Glu Thr Gly Gly Ser
      75                      80                      85

ATG ATG TAT AGA GAA GGG TGC TTG TCT GTG CCG GGA TTT TAC GAA GAA      340
Met Met Tyr Arg Glu Gly Cys Leu Ser Val Pro Gly Phe Tyr Glu Glu
      90                      95                      100                      105

GTG GAG CGT TTT GAA AAG GTT AAG ATA GAG TAT CAA AAC CGC TTC GCT      388
Val Glu Arg Phe Glu Lys Val Lys Ile Glu Tyr Gln Asn Arg Phe Ala
      110                      115                      120

GAA GTG AAA GTT TTA GAA GCG AGC GAG CTT TTA GCG GTA GCC ATT CAG      436
Glu Val Lys Val Leu Glu Ala Ser Glu Leu Leu Ala Val Ala Ile Gln
      125                      130                      135

CAT GAG ATC GAT CAC CTC AAT GGC GTG TTA TTC GTG GAT AAA TTA TCC      484
His Glu Ile Asp His Leu Asn Gly Val Leu Phe Val Asp Lys Leu Ser
      140                      145                      150

ATT TTG AAG CGT AAG AAA TTT GAA AAA GAA CTC AAA GAG CTG CAA AAA      532
Ile Leu Lys Arg Lys Lys Phe Glu Lys Glu Leu Lys Glu Leu Gln Lys
      155                      160                      165

AAA CAA AAA CAC GAG TAACAACCAT GATTAACACG ATGTTTTGCG CGACCATGCA A      588
Lys Gln Lys His Glu
      170

AGGGGAGTGG CGGAAAT      605

```

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

```

Met Ala Leu Leu Glu Ile Ile His Tyr Pro Ser Lys Ile Leu Arg Thr
  1             5             10             15
Ile Ser Lys Glu Val Val Ser Phe Asp Ser Lys Leu His Gln Gln Leu
      20             25             30
Asp Asp Met His Glu Thr Met Ile Ala Ser Glu Gly Ile Gly Leu Ala

```

BNSDOCID: <WO 9843478A1 | >

CAAGAATACC ACATTCATAA TTTGGATTGC CC

1631

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

```

Met Ile Asn Thr Met Phe Cys Ala Thr Met Gln Arg Gly Val Ala Glu
 1           5           10           15
Ile Val Ala Val Glu Ala Thr Phe Thr Arg Ala Leu Pro Ala Phe Val
          20           25           30
Ile Ser Gly Leu Ala Asn Ser Ser Ile Gln Glu Ala Lys Gln Arg Val
          35           40           45
Gln Ser Ala Leu Gln Asn Asn Asp Phe Thr Phe Pro Pro Leu Lys Ile
          50           55           60
Thr Ile Asn Leu Ser Pro Ser Asp Leu Pro Lys Ser Gly Ser His Phe
65           70           75           80
Asp Leu Pro Ile Ala Leu Leu Ile Ala Leu Gln Lys Gln Glu Leu Ala
          85           90           95
Phe Lys Glu Trp Phe Ala Phe Gly Glu Leu Gly Leu Asp Gly Lys Ile
          100          105          110
Lys Pro Asn Pro Asn Ile Phe Pro Met Leu Leu Asp Ile Ala Ile Lys
          115          120          125
His Pro His Ala Lys Ile Ile Ala Pro Lys Ala Asn Glu Glu Leu Phe
          130          135          140
Ser Leu Ile Pro Asn Leu Gln Cys Phe Phe Val Gly His Phe Lys Glu
145          150          155          160
Ala Leu Glu Ile Leu Gln Asn Pro Glu Thr Lys Ala Asp Thr His Thr
          165          170          175
Lys Lys Leu Pro Phe Lys Thr Ile Glu Leu Asn Asp Lys Glu Tyr Tyr
          180          185          190
Phe Ser Asp Ala Tyr Ala Leu Asp Phe Lys Glu Val Lys Gly Gln Ala
          195          200          205
Val Ala Lys Glu Ala Ala Leu Ile Ala Ser Ala Gly Phe His Asn Leu
          210          215          220
Ile Leu Glu Gly Ser Pro Gly Cys Gly Lys Ser Met Ile Ile Asn Arg
225          230          235          240
Met Arg Tyr Ile Leu Pro Pro Leu Ser Leu Asn Glu Ile Leu Glu Ala
          245          250          255
Thr Lys Leu Arg Ile Leu Ser Glu Gln Asp Ser Ala Tyr Tyr Pro Leu
          260          265          270
Arg Ser Phe Arg Asn Pro His Gln Ser Ala Ser Lys Ser Ser Ile Leu
          275          280          285
Gly Ser Ser Ser Leu Arg Glu Pro Lys Pro Gly Glu Ile Ala Leu Ala
          290          295          300
His Asn Gly Met Leu Phe Phe Asp Glu Leu Pro His Phe Lys Lys Asp
305          310          315          320
Ile Leu Glu Ala Leu Arg Glu Pro Leu Glu Asn Asn Lys Leu Val Val

```


AGC TCT CTA AGA GAG CCA AAA CCT GGC GAA ATC GCG CTA GCG CAT AAC	969
Ser Ser Leu Arg Glu Pro Lys Pro Gly Glu Ile Ala Leu Ala His Asn	
295 300 305	
GGC ATG CTT TTT TTT GAT GAA TTG CCT CAT TTT AAA AAG GAT ATT TTG	1017
Gly Met Leu Phe Phe Asp Glu Leu Pro His Phe Lys Lys Asp Ile Leu	
310 315 320	
GAA GCT TTA AGA GAG CCT TTA GAA AAC AAT AAA TTG GTG GTT TCA AGA	1065
Glu Ala Leu Arg Glu Pro Leu Glu Asn Asn Lys Leu Val Val Ser Arg	
325 330 335	
GTG CAT AGC AAA ATT GAA TAC GAA ACC TCT TTT TTA TTT GTA GGG GCT	1113
Val His Ser Lys Ile Glu Tyr Glu Thr Ser Phe Leu Phe Val Gly Ala	
340 345 350	
CAA AAC CCT TGC TTG TGC GGG AAT TTA CTC AGC GCG ACC AAA GCA TGC	1161
Gln Asn Pro Cys Leu Cys Gly Asn Leu Leu Ser Ala Thr Lys Ala Cys	
355 360 365 370	
CGT TGC CAA GAC AGA GAA ATC ACG CAG TAT AAA AAC CGC TTG AGC GAG	1209
Arg Cys Gln Asp Arg Glu Ile Thr Gln Tyr Lys Asn Arg Leu Ser Glu	
375 380 385	
CCT TTT TTG GAT AGG ATT GAT TTG TTT GTG CAA ATG GAA GAG GGG AAT	1257
Pro Phe Leu Asp Arg Ile Asp Leu Phe Val Gln Met Glu Glu Gly Asn	
390 395 400	
TAT AAA GAC ACG CCG TCG CAT TCT TGG ACT TCA AAA GAG ATG CAT GAA	1305
Tyr Lys Asp Thr Pro Ser His Ser Trp Thr Ser Lys Glu Met His Glu	
405 410 415	
TTG GTG TTA TTA GCT TTC AAG CAG CAA AAG TTA AGG AAA CAG AGC GTT	1353
Leu Val Leu Leu Ala Phe Lys Gln Gln Lys Leu Arg Lys Gln Ser Val	
420 425 430	
TTT AAT GGT AAG CTT AAT GAA GAG CAG ATA GAA CGA TTT TGC CCC TTA	1401
Phe Asn Gly Lys Leu Asn Glu Glu Gln Ile Glu Arg Phe Cys Pro Leu	
435 440 445 450	
AAC GCT GAA GCA AAA AAG TTG TTG GAG CAG GCG GTT GAA AGG TTT AAT	1449
Asn Ala Glu Ala Lys Lys Leu Leu Glu Gln Ala Val Glu Arg Phe Asn	
455 460 465	
CTC TCC ATG CGC TCT ATT AAT AAG GTC AAA AAA GTC GCT AGG ACG ATT	1497
Leu Ser Met Arg Ser Ile Asn Lys Val Lys Lys Val Ala Arg Thr Ile	
470 475 480	
GCG GAT TTA AAC GCT TGC GAG GAT ATA GAA AAA TCT CAC ATG CTT AAA	1545
Ala Asp Leu Asn Ala Cys Glu Asp Ile Glu Lys Ser His Met Leu Lys	
485 490 495	
GCG CTG AGT TTT AGA AAG ATT TCT TAAAAGGATT TTTATAAGGG AGAAAAAATG	1599
Ala Leu Ser Phe Arg Lys Ile Ser	
500 505	

AAC CTT TCC CCC TCA GAT TTG CCT AAA TCC GGG AGT CAT TTT GAT TTG	297
Asn Leu Ser Pro Ser Asp Leu Pro Lys Ser Gly Ser His Phe Asp Leu	
70 75 80	
CCT ATC GCT CTT TTA ATC GCT TTG CAA AAA CAA GAG TTG GCT TTT AAA	345
Pro Ile Ala Leu Leu Ile Ala Leu Gln Lys Gln Glu Leu Ala Phe Lys	
85 90 95	
GAG TGG TTT GCT TTT GGG GAG TTA GGG CTT GAT GGC AAG ATC AAA CCC	393
Glu Trp Phe Ala Phe Gly Glu Leu Gly Leu Asp Gly Lys Ile Lys Pro	
100 105 110	
AAT CCT AAC ATT TTC CCC ATG CTT TTA GAC ATT GCC ATT AAA CAC CCC	441
Asn Pro Asn Ile Phe Pro Met Leu Leu Asp Ile Ala Ile Lys His Pro	
115 120 125 130	
CAT GCT AAG ATC ATT GCG CCT AAG GCC AAT GAA GAG CTT TTT TCG CTT	489
His Ala Lys Ile Ile Ala Pro Lys Ala Asn Glu Glu Leu Phe Ser Leu	
135 140 145	
ATC CCT AAT TTG CAA TGC TTT TTT GTG GGG CAT TTT AAA GAA GCG TTA	537
Ile Pro Asn Leu Gln Cys Phe Phe Val Gly His Phe Lys Glu Ala Leu	
150 155 160	
GAA ATC TTG CAA AAC CCT GAA ACC AAA GCA GAC ACC CAC ACG AAA AAA	585
Glu Ile Leu Gln Asn Pro Glu Thr Lys Ala Asp Thr His Thr Lys Lys	
165 170 175	
CTA CCC TTT AAA ACG ATA GAA TTG AAC GAT AAA GAG TAT TAT TTT TCA	633
Leu Pro Phe Lys Thr Ile Glu Leu Asn Asp Lys Glu Tyr Tyr Phe Ser	
180 185 190	
GAC GCC TAT GCC TTA GAT TTT AAA GAA GTT AAG GGG CAA GCT GTC GCT	681
Asp Ala Tyr Ala Leu Asp Phe Lys Glu Val Lys Gly Gln Ala Val Ala	
195 200 205 210	
AAA GAG GCC GCT TTG ATC GCT AGC GCT GGG TTT CAT AAC TTG ATT TTA	729
Lys Glu Ala Ala Leu Ile Ala Ser Ala Gly Phe His Asn Leu Ile Leu	
215 220 225	
GAG GGA AGT CCA GGG TGT GGG AAA AGC ATG ATC ATT AAT CGC ATG CGT	777
Glu Gly Ser Pro Gly Cys Gly Lys Ser Met Ile Ile Asn Arg Met Arg	
230 235 240	
TAT ATC TTG CCT CCA TTA AGC CTG AAT GAA ATC CTA GAA GCG ACA AAA	825
Tyr Ile Leu Pro Pro Leu Ser Leu Asn Glu Ile Leu Glu Ala Thr Lys	
245 250 255	
TTA CGC ATT TTA AGC GAG CAA GAC AGT GCC TAT TAC CCC TTA AGG AGT	873
Leu Arg Ile Leu Ser Glu Gln Asp Ser Ala Tyr Tyr Pro Leu Arg Ser	
260 265 270	
TTT AGA AAC CCT CAC CAA AGC GCT TCA AAA TCC AGT ATT TTA GGC TCA	921
Phe Arg Asn Pro His Gln Ser Ala Ser Lys Ser Ser Ile Leu Gly Ser	
275 280 285 290	

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

```

Val Ala Val Lys Lys Ile Val Val Ser Trp Cys Val Ala Leu Ala Phe
 1           5           10           15
Leu Ser Ala Asp Ser Ala Gln Ala Asn Lys Ala Ile Ser Asn Ala Asp
 20           25           30
Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala Gln Asn
 35           40           45
Thr Glu Ile Asn Asn Leu Arg Lys Val Gln Glu Val Leu Ser Gly Gln
 50           55           60
Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr Cys Ile
 65           70           75           80
Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg
           85           90

```

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1569
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

```

TGAAAAAGAA CTCAAAGAGC TGCAAAAAAA ACAAAAACAC GAGTAACAAC C ATG ATT      57
                                   Met Ile
                                   1

AAC ACG ATG TTT TGC GCG ACC ATG CAA AGG GGA GTG GCG GAA ATC GTG      105
Asn Thr Met Phe Cys Ala Thr Met Gln Arg Gly Val Ala Glu Ile Val
 5           10           15

GCT GTG GAA GCG ACT TTC ACA AGG GCT TTG CCG GCG TTT GTG ATT TCA      153
Ala Val Glu Ala Thr Phe Thr Arg Ala Leu Pro Ala Phe Val Ile Ser
 20           25           30

GGG TTA GCT AAT AGC TCT ATC CAA GAA GCC AAA CAG CGG GTT CAA TCG      201
Gly Leu Ala Asn Ser Ser Ile Gln Glu Ala Lys Gln Arg Val Gln Ser
 35           40           45           50

GCT TTA CAA AAT AAC GAT TTC ACT TTC CCG CCT TTA AAA ATC ACC ATC      249
Ala Leu Gln Asn Asn Asp Phe Thr Phe Pro Pro Leu Lys Ile Thr Ile
           55           60           65

```

Leu Asp Asp Ala Tyr Glu Ser
770 775

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 10...279
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

AAAAGGAGA GTG GCG GTG AAA AAA ATC GTT GTG AGT TGG TGT GTG GCG TTG	51
Val Ala Val Lys Lys Ile Val Val Ser Trp Cys Val Ala Leu	
1 5 10	
GCT TTT TTA AGC GCG GAT TCA GCA CAA GCC AAT AAA GCG ATC AGT AAT	99
Ala Phe Leu Ser Ala Asp Ser Ala Gln Ala Asn Lys Ala Ile Ser Asn	
15 20 25 30	
GCG GAT TTG ATT AAA GAG ATA AGG GAT TTA AAA AAA ATC ATC AGC GCG	147
Ala Asp Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala	
35 40 45	
CAA AAC ACT GAG ATT AAC AAC TTA AGA AAA GTG CAA GAA GTG TTG TCT	195
Gln Asn Thr Glu Ile Asn Asn Leu Arg Lys Val Gln Glu Val Leu Ser	
50 55 60	
GGG CAA TTA GGG GAC ATG CGT AAG GAT ATA TTA AGC ACT AGA GAT TAT	243
Gly Gln Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr	
65 70 75	
TGC ATT AGC TTA AGG CCT TAT ATC TAT AAT TGG CGC TAGGGGATAA TCCAAA	295
Cys Ile Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg	
80 85 90	
AAATGAAAGC ATGCG	310

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

				325					330				335				
Ile	His	Thr	Thr	Ile	Phe	Asp	Glu	Ser	Ser	Val	Tyr	Glu	Val	Gln	Ile		
			340					345					350				
Arg	Thr	Phe	Asp	Met	His	Met	Gly	Ala	Glu	Tyr	Gly	Asn	Ser	Ala	His		
		355					360					365					
Trp	Lys	Tyr	Lys	Ala	Gly	Gly	Val	Asp	His	Glu	Asp	His	His	Glu	Gly		
	370					375					380						
Met	Arg	Trp	Leu	Gln	Asn	Phe	Lys	Tyr	His	Asp	Ser	Asp	Leu	Lys	Asn		
385					390					395					400		
Asp	Pro	Lys	Glu	Phe	Tyr	Glu	Leu	Ala	Lys	Asn	Asp	Leu	Tyr	Arg	Glu		
			405						410					415			
Asp	Ile	Val	Val	Phe	Ser	Pro	His	Gly	Asp	Thr	Tyr	Thr	Leu	Pro	Val		
		420						425					430				
Gly	Ala	Ile	Ala	Leu	Asp	Phe	Ala	Tyr	Met	Val	His	Ser	Asp	Leu	Gly		
		435					440					445					
Asp	Lys	Ala	Thr	Asp	Ala	Tyr	Ile	Asn	Ser	Lys	Lys	Ala	Leu	Leu	Asn		
	450					455				460							
Gln	Glu	Leu	Arg	Ser	Gly	Asp	Val	Val	Lys	Ile	Ile	Lys	Gly	Asp	Lys		
465					470					475					480		
Ile	Ile	Pro	Arg	Phe	Ile	Trp	Met	Asp	Gln	Leu	Lys	Thr	Ser	Lys	Ala		
				485				490						495			
Lys	Asn	His	Leu	Arg	Ile	Gln	Arg	Arg	Asn	Arg	Leu	Lys	Glu	Val	Asp		
		500					505						510				
Thr	Lys	Ser	Met	Ile	Asn	Ile	Leu	Ala	Thr	Phe	Phe	Gly	Arg	Ser	Val		
		515				520						525					
Phe	Glu	Asp	Met	Asp	Leu	Lys	Asp	Tyr	Lys	Asn	Phe	Glu	Glu	Arg	Leu		
	530					535				540							
Thr	Asp	Cys	Gly	Val	Glu	Thr	Thr	Leu	Thr	Glu	Ala	Met	Lys	Ser	Phe		
545					550					555					560		
Glu	Asn	Leu	Ala	Lys	Leu	Thr	Glu	Glu	Ile	Glu	Asn	Lys	Val	Phe	Ser		
			565					570						575			
Leu	Lys	Glu	Asp	Ala	Ile	Leu	Glu	Tyr	Gln	Glu	Met	Ser	Leu	Trp	Thr		
		580					585						590				
Arg	Gly	Leu	Arg	Tyr	Leu	Gly	Phe	Lys	Thr	Asn	Val	Leu	Asn	Phe	Leu		
	595					600						605					
Ala	Pro	Asn	Arg	Gln	Trp	Gln	Cys	Lys	Glu	Leu	Glu	His	Phe	Ser	Val		
	610					615						620					
Cys	Ser	Ser	Asn	Ala	Leu	Glu	Ile	Lys	Gln	Val	Leu	Leu	Asn	Asp	Cys		
625				630						635					640		
Cys	Tyr	Pro	Lys	Tyr	Gly	Asp	Glu	Ile	Ile	Ala	Ile	Val	Thr	Asp	Leu		
			645					650						655			
Lys	Asp	Pro	Lys	Ala	Ile	Ala	His	His	Lys	Phe	Cys	Lys	Lys	Ala	Met		
		660					665						670				
Ala	Glu	Val	Asp	Ala	Lys	Val	Pro	Met	Val	Tyr	Ile	Glu	Trp	His	Lys		
	675					680						685					
Arg	Asp	Arg	Thr	Ile	Tyr	Lys	Met	Met	Phe	Tyr	Leu	Gly	Glu	Lys	Lys		
	690					695					700						
Ser	Val	Leu	Ala	Gly	Leu	Leu	Thr	Phe	Leu	Asn	Arg	Asn	Glu	Cys	Asn		
705				710						715					720		
Ile	Val	Gly	Val	Ser	Tyr	Leu	Gly	Tyr	Lys	Asp	Lys	Tyr	Ser	Ser	His		
			725					730						735			
Cys	Glu	Val	Ser	Phe	Glu	Ile	Ala	Thr	Asp	Lys	Ala	Asp	Trp	Ile	Arg		
		740						745					750				
Ala	Leu	Ile	Asn	Arg	Lys	Tyr	Gln	Asp	Arg	Ile	Val	Glu	Leu	Ser	Ser		
	755						760						765				

AACATGGAAC AAA

2373

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

```

Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu
 1           5           10           15
Asp Val Ile Lys Lys Val Thr Thr Pro Lys Gly Gly Ile Glu Ile Leu
          20           25           30
Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
          35           40           45
Ala Ala Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
          50           55           60
Ile Val His Pro Ile Cys Val Ala Ser Leu Val Ala Phe Cys Gly Gly
65           70           75           80
Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
          85           90           95
Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln Glu Phe Gly Gln Asp Val
          100          105          110
Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu
          115          120          125
Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu
          130          135          140
Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu
145          150          155          160
Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr Leu Asp Ala
          165          170          175
Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr Leu Ala Val
          180          185          190
Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile Lys Asn Glu
          195          200          205
Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu Tyr Lys Asn
          210          215          220
Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu Leu Lys Leu
225          230          235          240
Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp Ser Gly Phe
          245          250          255
Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg Pro Tyr Ser
          260          265          270
Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile Asp Glu Ile
          275          280          285
Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro Ile Asp Cys
          290          295          300
Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro Ile Val Ser
305          310          315          320
Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly Tyr Lys Thr

```

AAA AGT TTT GAA AAT TTA GCC AAA CTC ACT GAA GAA ATT GAA AAT AAG	1731
Lys Ser Phe Glu Asn Leu Ala Lys Leu Thr Glu Glu Ile Glu Asn Lys	
560 565 570	
GTG TTT TCT TTA AAA GAA GAT GCG ATT TTA GAA TAC CAA GAG ATG AGT	1779
Val Phe Ser Leu Lys Glu Asp Ala Ile Leu Glu Tyr Gln Glu Met Ser	
575 580 585	
TTA TGG ACT CGA GGT TTA AGG TAT TTG GGC TTT AAA ACC AAT GTC TTG	1827
Leu Trp Thr Arg Gly Leu Arg Tyr Leu Gly Phe Lys Thr Asn Val Leu	
590 595 600 605	
AAT TTT TTA GCC CCC AAT CGG CAG TGG CAG TGT AAG GAA TTA GAA CAT	1875
Asn Phe Leu Ala Pro Asn Arg Gln Trp Gln Cys Lys Glu Leu Glu His	
610 615 620	
TTT AGC GTT TGT TCA AGC AAC GCT TTA GAA ATC AAA CAG GTG TTG TTG	1923
Phe Ser Val Cys Ser Ser Asn Ala Leu Glu Ile Lys Gln Val Leu Leu	
625 630 635	
AAT GAT TGT TGT TAC CCT AAA TAT GGC GAT GAA ATC ATT GCG ATT GTA	1971
Asn Asp Cys Cys Tyr Pro Lys Tyr Gly Asp Glu Ile Ile Ala Ile Val	
640 645 650	
ACG GAT TTA AAA GAT CCA AAA GCG ATT GCG CAC CAT AAA TTT TGC AAA	2019
Thr Asp Leu Lys Asp Pro Lys Ala Ile Ala His His Lys Phe Cys Lys	
655 660 665	
AAA GCG ATG GCG GAA GTA GAT GCT AAA GTG CCT ATG GTT TAT ATA GAA	2067
Lys Ala Met Ala Glu Val Asp Ala Lys Val Pro Met Val Tyr Ile Glu	
670 675 680 685	
TGG CAC AAG CGG GAT CGA ACG ATT TAT AAA ATG ATG TTT TAT TTG GGC	2115
Trp His Lys Arg Asp Arg Thr Ile Tyr Lys Met Met Phe Tyr Leu Gly	
690 695 700	
GAA AAA AAG TCG GTT TTA GCG GGT TTA TTA ACT TTT TTA AAC AGG AAT	2163
Glu Lys Lys Ser Val Leu Ala Gly Leu Leu Thr Phe Leu Asn Arg Asn	
705 710 715	
GAA TGC AAC ATT GTG GGC GTG TCT TAT TTG GGC TAT AAA GAC AAG TAT	2211
Glu Cys Asn Ile Val Gly Val Ser Tyr Leu Gly Tyr Lys Asp Lys Tyr	
720 725 730	
TCT AGC CAT TGT GAA GTG AGT TTT GAA ATA GCC ACA GAT AAG GCG GAT	2259
Ser Ser His Cys Glu Val Ser Phe Glu Ile Ala Thr Asp Lys Ala Asp	
735 740 745	
TGG ATC AGA GCC TTA ATC AAT CGC AAA TAT CAG GAT AGG ATT GTA GAA	2307
Trp Ile Arg Ala Leu Ile Asn Arg Lys Tyr Gln Asp Arg Ile Val Glu	
750 755 760 765	
TTA TCC AGT CTG GAT GAC GCT TAT GAA TCA TAATAAGCCC TAATTAAGGA ATG	2360
Leu Ser Ser Leu Asp Asp Ala Tyr Glu Ser	
770 775	

TAT AAG ACG ATA CAC ACG ACC ATT TTT GAT GAA TCT TCT GTT TAT GAA	1059
Tyr Lys Thr Ile His Thr Thr Ile Phe Asp Glu Ser Ser Val Tyr Glu	
335 340 345	
GTG CAG ATC CGC ACC TTT GAT ATG CAT ATG GGG GCG GAG TAT GGT AAT	1107
Val Gln Ile Arg Thr Phe Asp Met His Met Gly Ala Glu Tyr Gly Asn	
350 355 360 365	
TCA GCC CAC TGG AAG TAT AAA GCC GGG GGC GTG GAT CAT GAA GAT CAT	1155
Ser Ala His Trp Lys Tyr Lys Ala Gly Gly Val Asp His Glu Asp His	
370 375 380	
CAT GAG GGC ATG AGA TGG TTG CAA AAT TTT AAA TAC CAT GAC AGC GAT	1203
His Glu Gly Met Arg Trp Leu Gln Asn Phe Lys Tyr His Asp Ser Asp	
385 390 395	
TTG AAA AAC GAC CCT AAG GAA TTT TAC GAA CTC GCT AAG AAC GAT TTG	1251
Leu Lys Asn Asp Pro Lys Glu Phe Tyr Glu Leu Ala Lys Asn Asp Leu	
400 405 410	
TAT CGT GAA GAT ATT GTC GTT TTT TCG CCT CAT GGG GAC ACT TAC ACT	1299
Tyr Arg Glu Asp Ile Val Val Phe Ser Pro His Gly Asp Thr Tyr Thr	
415 420 425	
TTA CCG GTG GGT GCG ATC GCT TTA GAT TTT GCT TAC ATG GTG CAT AGC	1347
Leu Pro Val Gly Ala Ile Ala Leu Asp Phe Ala Tyr Met Val His Ser	
430 435 440 445	
GAT TTG GGC GAT AAA GCC ACG GAC GCT TAT ATC AAT AGT AAA AAA GCC	1395
Asp Leu Gly Asp Lys Ala Thr Asp Ala Tyr Ile Asn Ser Lys Lys Ala	
450 455 460	
TTA CTC AAT CAG GAA TTA AGA AGT GGG GAT GTG GTT AAA ATC ATT AAA	1443
Leu Leu Asn Gln Glu Leu Arg Ser Gly Asp Val Val Lys Ile Ile Lys	
465 470 475	
GGC GAT AAA ATA ATA CCT CGT TTC ATT TGG ATG GAT CAG CTT AAA ACT	1491
Gly Asp Lys Ile Ile Pro Arg Phe Ile Trp Met Asp Gln Leu Lys Thr	
480 485 490	
TCT AAG GCT AAA AAC CAT TTG CGC ATC CAA AGA AGA AAC CGC TTG AAA	1539
Ser Lys Ala Lys Asn His Leu Arg Ile Gln Arg Arg Asn Arg Leu Lys	
495 500 505	
GAG GTT GAC ACT AAG AGC ATG ATC AAT ATC TTA GCG ACT TTT TTT GGG	1587
Glu Val Asp Thr Lys Ser Met Ile Asn Ile Leu Ala Thr Phe Phe Gly	
510 515 520 525	
CGC TCT GTT TTT GAA GAC ATG GAT TTA AAG GAT TAT AAA AAC TTT GAA	1635
Arg Ser Val Phe Glu Asp Met Asp Leu Lys Asp Tyr Lys Asn Phe Glu	
530 535 540	
GAA AGA TTA ACA GAT TGC GGG GTG GAG ACC ACC TTA ACA GAA GCG ATG	1683
Glu Arg Leu Thr Asp Cys Gly Val Glu Thr Thr Leu Thr Glu Ala Met	
545 550 555	

CAA GAT GTG GCT AAT TTA GTG GAT GCG CTC ACT AAA ATC ACT GAA ATC	387
Gln Asp Val Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile	
110 115 120 125	
AGG AAA GAA GAA TTA GGC GTG AGC TCT CAA GAT CCC AGA ATG GTG GTT	435
Arg Lys Glu Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val	
130 135 140	
TCA GCG CTC ACT TTC AGA AAG ATT TTA ATT AGC GCG ATA CAA GAT CCA	483
Ser Ala Leu Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro	
145 150 155	
AGA GCC TTA GTG GTA AAG ATT AGC GAC AGG TTG CAC AAC ATG CTC ACC	531
Arg Ala Leu Val Val Lys Ile Ser Asp Arg Leu His Asn Met Leu Thr	
160 165 170	
TTA GAC GCC TTG CCT CAT GAC AAG CAA GTG CGT ATT TCT AAA GAG ACT	579
Leu Asp Ala Leu Pro His Asp Lys Gln Val Arg Ile Ser Lys Glu Thr	
175 180 185	
CTA GCG GTG TAT GCC CCT ATA GCG AGC CGA TTG GGC ATG TCT TCA ATC	627
Leu Ala Val Tyr Ala Pro Ile Ala Ser Arg Leu Gly Met Ser Ser Ile	
190 195 200 205	
AAA AAT GAA TTA GAA GAC AAG AGC TTT TAT TAT ATT TAT CCA GAA GAG	675
Lys Asn Glu Leu Glu Asp Lys Ser Phe Tyr Tyr Ile Tyr Pro Glu Glu	
210 215 220	
TAT AAA AAT ATC AAG GAA TAT TTG CAC AAA AAC AAG CAG TCT TTA CTC	723
Tyr Lys Asn Ile Lys Glu Tyr Leu His Lys Asn Lys Gln Ser Leu Leu	
225 230 235	
TTA AAG CTC AAC GCT TTT GCG AGC AAG TTA GAA AAA AAA CTT TTT GAT	771
Leu Lys Leu Asn Ala Phe Ala Ser Lys Leu Glu Lys Lys Leu Phe Asp	
240 245 250	
AGT GGG TTT AGC CAT TCG GAT TTT AAA CTC GTT ACA AGG GTG AAA CGC	819
Ser Gly Phe Ser His Ser Asp Phe Lys Leu Val Thr Arg Val Lys Arg	
255 260 265	
CCT TAT TCT ATC TAT CTT AAG ATG CAA CGA AAG GGC GCG GTT AAT ATT	867
Pro Tyr Ser Ile Tyr Leu Lys Met Gln Arg Lys Gly Ala Val Asn Ile	
270 275 280 285	
GAT GAA ATT TTG GAC TTG TTA GCC ATT AGG ATT TTA TTG AAA AAC CCG	915
Asp Glu Ile Leu Asp Leu Leu Ala Ile Arg Ile Leu Leu Lys Asn Pro	
290 295 300	
ATT GAT TGC TAT AAA GTT TTA GGG ATT ATC CAT TTG AAT TTC AAA CCC	963
Ile Asp Cys Tyr Lys Val Leu Gly Ile Ile His Leu Asn Phe Lys Pro	
305 310 315	
ATT GTC TCT CGT TTT AAA GAT TAC ATC GCT TTG CCC AAA GAA AAT GGC	1011
Ile Val Ser Arg Phe Lys Asp Tyr Ile Ala Leu Pro Lys Glu Asn Gly	
320 325 330	

```

Val Ala Pro Cys Asn Arg Gly Glu Glu Ala Lys Lys Val Gly Tyr Cys
305          310          315          320
Ile Ala Asp Gly Leu Gly Arg Ser Tyr Leu Gly Asn Arg Glu Glu Gly
          325          330          335
Leu Tyr Phe Thr Gly Ala Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser
          340          345          350
Val His Glu Leu Ile Lys Glu Leu Thr Glu Gly
          355          360

```

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...2337
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

```

TAGACAGGAT AG ATG AAC GAA ATT GAT AAA TCC GTT GAT ATC GGA TTC TTA      51
      Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu
          1          5          10

CGG ATT CTT GAT GTT ATT AAA AAA GTT ACG ACC CCA AAG GGT GGC ATT      99
Arg Ile Leu Asp Val Ile Lys Lys Val Thr Thr Pro Lys Gly Gly Ile
      15          20          25

GAA ATC TTA AGG ACT TTA ATT GAT TTT ACG CCC AAA ATT GAA AAC GCC      147
Glu Ile Leu Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala
      30          35          40          45

CTG AAT TTA GCG GCC AAA AGC CAT AAG GGG CAA TAC AGA AAA AGC GGC      195
Leu Asn Leu Ala Ala Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly
          50          55          60

GAG CCT TAT ATT GTC CAT CCT ATT TGC GTG GCA AGC TTG GTA GCG TTT      243
Glu Pro Tyr Ile Val His Pro Ile Cys Val Ala Ser Leu Val Ala Phe
          65          70          75

TGT GGG GGC GAT GAG GCG ATG GTG TGT GCT GCG CTT TTG CAT GAT GTG      291
Cys Gly Gly Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val
          80          85          90

GTG GAA GAC ACG CCT TGT AAG ATT GAA ACG ATT GAG CAA GAA TTT GGG      339
Val Glu Asp Thr Pro Cys Lys Ile Glu Thr Ile Glu Gln Glu Phe Gly
          95          100          105

```

GAG CTT ACA GAG GGT TAATTTGTAG TGCTTGTGAG GTTAGGGGTT GTTGCA
Glu Leu Thr Glu Gly
360

1161

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

Met	Val	Ser	Thr	Leu	Lys	Pro	Leu	Lys	Ile	Gly	Lys	His	Thr	Ile	Lys
1				5					10					15	
Phe	Pro	Ile	Phe	Gln	Gly	Gly	Met	Gly	Val	Gly	Ile	Ser	Trp	Asp	Glu
			20					25					30		
Leu	Ala	Gly	Asn	Val	Ala	Lys	Glu	Gly	Ala	Leu	Gly	Val	Ile	Ser	Ala
		35					40					45			
Val	Gly	Thr	Gly	Tyr	Tyr	Lys	Asn	Met	Arg	Phe	Val	Glu	Arg	Ile	Val
	50					55					60				
Ala	Lys	Lys	Pro	Phe	Glu	Ala	Leu	Asn	Phe	Tyr	Ser	Lys	Lys	Ala	Leu
65					70					75					80
Asn	Glu	Ile	Phe	Ala	Asn	Ala	Arg	Lys	Ile	Cys	Gly	Asn	Asn	Pro	Leu
			85						90					95	
Gly	Ala	Asn	Ile	Leu	Tyr	Ala	Ile	Asn	Asp	Tyr	Gly	Arg	Val	Leu	Arg
			100					105					110		
Asp	Ser	Cys	Glu	Ala	Gly	Ala	Asn	Ile	Ile	Ile	Thr	Gly	Ala	Gly	Leu
		115					120					125			
Pro	Thr	Asn	Met	Pro	Glu	Phe	Ala	Lys	Asp	Phe	Ser	Asp	Val	Ala	Leu
	130					135					140				
Ile	Pro	Ile	Ile	Ser	Ser	Ala	Lys	Ala	Leu	Lys	Ile	Leu	Cys	Lys	Arg
145					150					155					160
Trp	Ser	Asp	Arg	Tyr	Lys	Arg	Ile	Pro	Asp	Ala	Phe	Ile	Val	Glu	Gly
			165						170					175	
Pro	Leu	Ser	Gly	Gly	His	Gln	Gly	Phe	Lys	Tyr	Glu	Asp	Cys	Phe	Lys
			180					185					190		
Glu	Glu	Phe	Arg	Leu	Glu	Asn	Leu	Val	Pro	Lys	Val	Val	Glu	Ala	Ser
		195					200					205			
Lys	Glu	Trp	Gly	Asn	Ile	Pro	Ile	Ile	Ala	Ala	Gly	Gly	Ile	Trp	Asp
	210					215					220				
Arg	Lys	Asp	Ile	Asp	Thr	Met	Leu	Ser	Leu	Gly	Ala	Ser	Gly	Val	Gln
225					230					235					240
Met	Ala	Thr	Arg	Phe	Leu	Gly	Thr	Lys	Glu	Cys	Asp	Ala	Lys	Val	Tyr
			245						250					255	
Ala	Asp	Leu	Leu	Pro	Thr	Leu	Lys	Lys	Glu	Asp	Ile	Leu	Leu	Ile	Lys
		260						265					270		
Ser	Pro	Val	Gly	Tyr	Pro	Ala	Arg	Ala	Ile	Asn	Thr	Gly	Val	Ile	Lys
		275					280					285			
Arg	Ile	Glu	Glu	Gly	Asn	Ala	Pro	Lys	Ile	Ala	Cys	Val	Ser	Asn	Cys
	290					295					300				

TTC GCT AAG GAT TTT AGC GAT GTG GCG CTC ATC CCT ATT ATT TCT TCA	486
Phe Ala Lys Asp Phe Ser Asp Val Ala Leu Ile Pro Ile Ile Ser Ser	
135 140 145 150	
GCG AAG GCT TTA AAA ATC CTT TGT AAA AGA TGG AGC GAT CGC TAT AAA	534
Ala Lys Ala Leu Lys Ile Leu Cys Lys Arg Trp Ser Asp Arg Tyr Lys	
155 160 165	
AGA ATC CCG GAC GCG TTC ATT GTG GAA GGG CCT TTG AGT GGG GGG CAT	582
Arg Ile Pro Asp Ala Phe Ile Val Glu Gly Pro Leu Ser Gly Gly His	
170 175 180	
CAG GGC TTT AAA TAC GAA GAT TGT TTC AAA GAA GAA TTC CGA TTA GAA	630
Gln Gly Phe Lys Tyr Glu Asp Cys Phe Lys Glu Glu Phe Arg Leu Glu	
185 190 195	
AAC TTA GTG CCT AAA GTC GTG GAA GCT TCT AAA GAA TGG GGG AAT ATC	678
Asn Leu Val Pro Lys Val Val Glu Ala Ser Lys Glu Trp Gly Asn Ile	
200 205 210	
CCT ATC ATC GCC GCT GGG GGG ATT TGG GAT AGG AAG GAT ATA GAC ACC	726
Pro Ile Ile Ala Ala Gly Gly Ile Trp Asp Arg Lys Asp Ile Asp Thr	
215 220 225 230	
ATG TTA AGT CTT GGA GCG AGT GGG GTG CAG ATG GCG ACT CGT TTT TTA	774
Met Leu Ser Leu Gly Ala Ser Gly Val Gln Met Ala Thr Arg Phe Leu	
235 240 245	
GGC ACG AAA GAA TGC GAC GCT AAA GTG TAT GCC GAT CTT TTG CCC ACG	822
Gly Thr Lys Glu Cys Asp Ala Lys Val Tyr Ala Asp Leu Leu Pro Thr	
250 255 260	
CTC AAA AAA GAA GAT ATT TTA CTC ATT AAA TCG CCT GTA GGT TAT CCG	870
Leu Lys Lys Glu Asp Ile Leu Leu Ile Lys Ser Pro Val Gly Tyr Pro	
265 270 275	
GCT AGG GCT ATT AAT ACG GGA GTG ATC AAG CGC ATT GAA GAG GGT AAC	918
Ala Arg Ala Ile Asn Thr Gly Val Ile Lys Arg Ile Glu Glu Gly Asn	
280 285 290	
GCG CCC AAA ATC GCA TGC GTG AGC AAT TGT GTA GCG CCT TGC AAC AGG	966
Ala Pro Lys Ile Ala Cys Val Ser Asn Cys Val Ala Pro Cys Asn Arg	
295 300 305 310	
GGT GAA GAG GCT AAA AAG GTG GGC TAT TGT ATC GCT GAT GGT TTG GGG	1014
Gly Glu Glu Ala Lys Lys Val Gly Tyr Cys Ile Ala Asp Gly Leu Gly	
315 320 325	
CGC AGT TAT TTA GGG AAC AGA GAA GAG GGG CTT TAT TTT ACC GGG GCT	1062
Arg Ser Tyr Leu Gly Asn Arg Glu Gly Leu Tyr Phe Thr Gly Ala	
330 335 340	
AAT GGC TAT AGA GTG GAT AAG ATT ATC AGC GTG CAT GAA TTG ATT AAA	1110
Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser Val His Glu Leu Ile Lys	
345 350 355	

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...1125
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

TGAAATTAAA TATTAATAA TATTAAGGAA AGAGCT ATG GTA TCA ACA CTC AAA	54
Met Val Ser Thr Leu Lys	
1 5	
CCG CTA AAA ATC GGT AAG CAC ACC ATA AAA TTC CCT ATC TTT CAA GGG	102
Pro Leu Lys Ile Gly Lys His Thr Ile Lys Phe Pro Ile Phe Gln Gly	
10 15 20	
GGA ATG GGT GTG GGG ATT AGC TGG GAT GAA CTA GCT GGA AAT GTT GCC	150
Gly Met Gly Val Gly Ile Ser Trp Asp Glu Leu Ala Gly Asn Val Ala	
25 30 35	
AAA GAA GGG GCT TTA GGA GTG ATT TCA GCC GTA GGG ACT GGT TAT TAT	198
Lys Glu Gly Ala Leu Gly Val Ile Ser Ala Val Gly Thr Gly Tyr Tyr	
40 45 50	
AAA AAC ATG CGT TTT GTA GAA AGG ATT GTG GCT AAA AAA CCC TTT GAA	246
Lys Asn Met Arg Phe Val Glu Arg Ile Val Ala Lys Lys Pro Phe Glu	
55 60 65 70	
GCC TTG AAT TTT TAC TCC AAA AAA GCG TTG AAT GAG ATT TTT GCA AAC	294
Ala Leu Asn Phe Tyr Ser Lys Lys Ala Leu Asn Glu Ile Phe Ala Asn	
75 80 85	
GCT AGG AAG ATT TGC GGG AAC AAC CCT TTA GGA GCG AAT ATT TTA TAC	342
Ala Arg Lys Ile Cys Gly Asn Asn Pro Leu Gly Ala Asn Ile Leu Tyr	
90 95 100	
GCT ATC AAT GAC TAT GGC CGT GTT TTA AGG GAC TCT TGT GAA GCG GGA	390
Ala Ile Asn Asp Tyr Gly Arg Val Leu Arg Asp Ser Cys Glu Ala Gly	
105 110 115	
GCG AAT ATC ATT ATT ACA GGG GCT GGT TTG CCC ACC AAC ATG CCT GAA	438
Ala Asn Ile Ile Ile Thr Gly Ala Gly Leu Pro Thr Asn Met Pro Glu	
120 125 130	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

```

Met Val Phe Asn Gln Glu Val Lys Lys Phe Lys Glu Val Ser Leu Lys
 1           5           10           15
Asn Phe Lys Ser Tyr Leu Glu Leu Glu Ala Ile Leu Thr Ile Pro Lys
          20           25           30
Lys His Tyr Gln Phe Ser Lys Gln Ser Phe Ile Thr Ile Ala Gln Phe
          35           40           45
Ser Pro Lys Leu Val Arg Val Val Ile Gly Tyr Ala Pro Lys Met Thr
          50           55           60
Tyr Glu Val Lys Ile Leu Lys Asp Lys Leu Tyr Val Ser Ile Val Glu
65           70           75           80
Lys Lys Pro Leu Ile Arg His Gln Met Ala Leu Lys Pro Pro Lys His
          85           90           95
His Ala Leu Lys His Thr Thr Pro Lys Pro Ala His Lys Pro Ile Lys
          100          105          110
Lys Glu Ala Lys Lys Val Lys Glu Lys Thr Pro Thr Lys His Ala His
          115          120          125
Ser Lys His Thr His Ser Pro Leu Asn Glu Arg Ser Thr Lys Lys Glu
          130          135          140
Ile Pro Lys Lys Glu Ile Pro Lys Lys Glu Ala Glu Asn Glu Ser Lys
145          150          155          160
Asn Gln Val Phe Ile Ala Glu Lys Asn Asp Thr Phe Ile Lys Thr Lys
          165          170          175
Arg Lys Lys His Lys Lys Ile Val Leu Asp Ala Gly His Gly Gly Lys
          180          185          190
Asp Cys Gly Ala Met Ser Ala Asn Leu Val Cys Glu Lys Asp Ile Val
          195          200          205
Leu Glu Val Val Lys Phe Leu His Lys Glu Leu Lys Lys Arg Asp Tyr
          210          215          220
Ser Val Leu Leu Thr Arg Asp Lys Asp Ile Tyr Ile Asp Leu Val Ala
225          230          235          240
Arg Thr Glu Leu Ala Asn Lys Lys Ser Ala Asp Leu Phe Ile Ser Val
          245          250          255
His Ala Asn Ser Ile Pro Lys His Ser Thr Ser Asn Ala His Gly Ile
          260          265          270
Glu Thr Tyr Phe Leu Ser Thr Ala Arg Ser Glu Arg Ala Arg Lys Val
          275          280          285
Ala Glu Gln Glu Asn Lys Asp Asp Val Asn Leu Met Asp Tyr Phe Ser
          290          295          300
Lys Ser Leu Phe Leu Asn Ser Leu Asn Thr Gln Arg Leu Ile Val Ser
305          310          315          320
Asn Lys Leu Ala Ile Asp Val Gln Tyr Gly Met Leu Gln Ser Val Arg
          325          330          335
Lys Asn Tyr Pro Asp Val Val Asp Gly Gly Val Arg Glu Gly Pro Phe
          340          345          350
Trp Val Leu Ala Gly Ala Leu Met Pro Ser Ile Leu Ile Glu Ile Gly
          355          360          365
Tyr Asn Ser His Ala Ile Glu Ser Lys Arg Ile Gln Ser Lys Pro Tyr
          370          375          380
Gln Lys Ile Leu Ala Lys Gly Ile Ala Asp Gly Ile Asp Ser Phe Phe
385          390          395          400
Ser Lys Asn Asp

```

GTG GCT CGC ACG GAA TTA GCC AAT AAA AAA AGC GCG GAT TTA TTC ATC	831
Val Ala Arg Thr Glu Leu Ala Asn Lys Lys Ser Ala Asp Leu Phe Ile	
240 245 250	
TCA GTG CAT GCC AAT TCC ATC CCC AAA CAT TCC ACT TCT AAC GCT CAT	879
Ser Val His Ala Asn Ser Ile Pro Lys His Ser Thr Ser Asn Ala His	
255 260 265 270	
GGT ATA GAG ACT TAT TTT TTA TCC ACC GCA AGG AGC GAA AGG GCT AGG	927
Gly Ile Glu Thr Tyr Phe Leu Ser Thr Ala Arg Ser Glu Arg Ala Arg	
275 280 285	
AAA GTG GCT GAG CAA GAA AAT AAA GAC GAT GTG AAT TTA ATG GAT TAT	975
Lys Val Ala Glu Gln Glu Asn Lys Asp Asp Val Asn Leu Met Asp Tyr	
290 295 300	
TTT TCT AAA AGT TTG TTT TTA AAT TCA TTG AAC ACG CAG CGA TTG ATC	1023
Phe Ser Lys Ser Leu Phe Leu Asn Ser Leu Asn Thr Gln Arg Leu Ile	
305 310 315	
GTC TCT AAC AAA TTA GCG ATT GAT GTG CAA TAC GGC ATG CTC CAA AGC	1071
Val Ser Asn Lys Leu Ala Ile Asp Val Gln Tyr Gly Met Leu Gln Ser	
320 325 330	
GTC CGC AAA AAT TAC CCT GAT GTG GTG GAT GGA GGC GTG AGA GAG GGG	1119
Val Arg Lys Asn Tyr Pro Asp Val Val Asp Gly Gly Val Arg Glu Gly	
335 340 345 350	
CCT TTT TGG GTG TTG GCC GGG GCT TTA ATG CCT TCA ATC TTA ATA GAA	1167
Pro Phe Trp Val Leu Ala Gly Ala Leu Met Pro Ser Ile Leu Ile Glu	
355 360 365	
ATT GGT TAT AAT TCC CAT GCG ATA GAA TCT AAA CGC ATC CAA AGC AAA	1215
Ile Gly Tyr Asn Ser His Ala Ile Glu Ser Lys Arg Ile Gln Ser Lys	
370 375 380	
CCG TAT CAA AAG ATC TTG GCT AAG GGC ATT GCT GAT GGC ATT GAT AGT	1263
Pro Tyr Gln Lys Ile Leu Ala Lys Gly Ile Ala Asp Gly Ile Asp Ser	
385 390 395	
TTC TTC AGC AAG AAT GAT TAGGCAATGA TTAGGTTGTA GATGAATTTT TATCAAAA	1319
Phe Phe Ser Lys Asn Asp	
400	
AATATACACT CATAAAGTC	1338

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Leu	Lys	Asn	Phe	Lys	Ser	Tyr	Leu	Glu	Leu	Glu	Ala	Ile	Leu	Thr	Ile	
15					20					25					30	
CCT	AAA	AAG	CAT	TAC	CAA	TTC	TCC	AAG	CAA	TCG	TTC	ATC	ACG	ATC	GCG	207
Pro	Lys	Lys	His	Tyr	Gln	Phe	Ser	Lys	Gln	Ser	Phe	Ile	Thr	Ile	Ala	
			35						40					45		
CAA	TTC	AGC	CCT	AAG	TTA	GTG	CGA	GTG	GTT	ATC	GGC	TAT	GCT	CCT	AAG	255
Gln	Phe	Ser	Pro	Lys	Leu	Val	Arg	Val	Val	Ile	Gly	Tyr	Ala	Pro	Lys	
			50					55					60			
ATG	ACT	TAT	GAA	GTT	AAA	ATC	CTT	AAA	GAC	AAG	CTT	TAT	GTT	TCT	ATC	303
Met	Thr	Tyr	Glu	Val	Lys	Ile	Leu	Lys	Asp	Lys	Leu	Tyr	Val	Ser	Ile	
		65					70					75				
GTG	GAG	AAA	AAG	CCC	TTA	ATT	AGG	CAT	CAA	ATG	GCG	TTA	AAA	CCA	CCC	351
Val	Glu	Lys	Lys	Pro	Leu	Ile	Arg	His	Gln	Met	Ala	Leu	Lys	Pro	Pro	
	80					85					90					
AAA	CAC	CAT	GCA	CTC	AAA	CAC	ACA	ACG	CCA	AAA	CCC	GCC	CAT	AAG	CCC	399
Lys	His	His	Ala	Leu	Lys	His	Thr	Thr	Pro	Lys	Pro	Ala	His	Lys	Pro	
95					100					105					110	
ATT	AAA	AAA	GAG	GCT	AAA	AAG	GTT	AAA	GAA	AAA	ACG	CCA	ACT	AAA	CAT	447
Ile	Lys	Lys	Glu	Ala	Lys	Lys	Val	Lys	Glu	Lys	Thr	Pro	Thr	Lys	His	
			115						120					125		
GCG	CAT	TCA	AAA	CAC	ACG	CAT	TCC	CCA	TTG	AAC	GAA	AGG	AGC	ACT	AAA	495
Ala	His	Ser	Lys	His	Thr	His	Ser	Pro	Leu	Asn	Glu	Arg	Ser	Thr	Lys	
			130					135					140			
AAA	GAA	ATT	CCT	AAA	AAA	GAA	ATT	CCT	AAA	AAA	GAA	GCG	GAA	AAT	GAG	543
Lys	Glu	Ile	Pro	Lys	Lys	Glu	Ile	Pro	Lys	Lys	Glu	Ala	Glu	Asn	Glu	
		145					150					155				
AGC	AAG	AAC	CAA	GTC	TTT	ATA	GCA	GAA	AAA	AAT	GAT	ACT	TTC	ATC	AAA	591
Ser	Lys	Asn	Gln	Val	Phe	Ile	Ala	Glu	Lys	Asn	Asp	Thr	Phe	Ile	Lys	
	160					165					170					
ACC	AAA	CGC	AAA	AAA	CAC	AAA	AAG	ATC	GTT	TTA	GAC	GCT	GGG	CAT	GGG	639
Thr	Lys	Arg	Lys	Lys	His	Lys	Lys	Ile	Val	Leu	Asp	Ala	Gly	His	Gly	
175					180					185					190	
GGG	AAA	GAT	TGC	GGG	GCG	ATG	AGC	GCG	AAT	TTG	GTG	TGT	GAA	AAA	GAC	687
Gly	Lys	Asp	Cys	Gly	Ala	Met	Ser	Ala	Asn	Leu	Val	Cys	Glu	Lys	Asp	
			195					200					205			
ATT	GTT	TTA	GAA	GTG	GTG	AAG	TTT	TTA	CAC	AAA	GAG	CTT	AAA	AAA	AGA	735
Ile	Val	Leu	Glu	Val	Val	Lys	Phe	Leu	His	Lys	Glu	Leu	Lys	Lys	Arg	
			210					215					220			
GAT	TAT	AGC	GTT	TTA	TTG	ACA	AGG	GAT	AAG	GAT	ATT	TAT	ATT	GAT	TTA	783
Asp	Tyr	Ser	Val	Leu	Leu	Thr	Arg	Asp	Lys	Asp	Ile	Tyr	Ile	Asp	Leu	
		225					230					235				

50		55		60	
Cys Gly Arg Val Ala Phe Leu Lys Asp Ile Val Ser Asn Ser Pro Asn					
65		70		75	80
Glu Thr Ile Gln Ser Phe Asp Gly Asp Leu Glu Val Ala Met His Leu					
	85		90		95
Glu Lys Ile Gly Ile Glu Cys Tyr Lys Ile Phe Ile Asp Tyr Gly Ser					
	100		105		110
Gln Lys Ile Asp Asp Asn Glu Leu Ser Cys Arg Leu Leu His Thr Gly					
	115		120		125
Thr Lys Ile Leu Gly Thr Lys Ala Met Ala Val Val Gly Gln Thr Phe					
	130		135		140
Ile Pro Ile Pro Gly Val Gly Ala Ile Ile Gly Asn Phe Val Gly Ala					
145		150		155	160
Leu Leu Ser Lys Thr Leu Cys Glu Asn Leu Arg Asp Val Leu Lys Glu					
	165		170		175
Ala Lys Leu Ala Arg Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg					
	180		185		190
Glu Ser Ile Arg Leu Leu Glu Ile Tyr Arg Asn Gln Phe Lys Glu Val					
	195		200		205
Phe Glu Arg Tyr Phe His Gly Asn Val Lys Phe Phe Asn Glu Asn Phe					
	210		215		220
Asn Asn Leu Glu Arg Ala Leu Tyr Ala Gly Asp Ala Asp Leu Ala Ile					
225		230		235	240
Gly Val Asn Asn Glu Ile Gln Glu Arg Leu Gly Gln Lys Pro Leu Phe					
	245		250		255
Asn Asn Thr Gln Glu Phe Leu Glu Leu Met Asn Asn Gly Gly Lys Ile					
	260		265		270
Glu Ile					

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...1281
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

CTTCATTACG CTTACGCTAC AACCCCTTAAG ATCACCAATG TTGTGCCTTT TGGCTCTAGC	60
AGCGTTAAA ATG GTG TTC AAT CAA GAG GTT AAA AAA TTC AAA GAA GTT TCG	111
Met Val Phe Asn Gln Glu Val Lys Lys Phe Lys Glu Val Ser	
1 5 10	
CTC AAA AAT TTC AAG AGT TAT TTG GAA TTA GAA GCC ATT TTA ACC ATT	159

140	145	150	
ATA ATT GGA AAT TTT GTG GGT GCA TTA CTG AGC AAA ACT CTC TGT GAA			533
Ile Ile Gly Asn Phe Val Gly Ala Leu Leu Ser Lys Thr Leu Cys Glu			
155	160	165	
AAT TTG CGA GAT GTT TTA AAA GAG GCT AAA TTG GCG CGC CAA AGG CGT			581
Asn Leu Arg Asp Val Leu Lys Glu Ala Lys Leu Ala Arg Gln Arg Arg			
170	175	180	
ATA GAG ATT GAA AAA GAA TGC CGT GAA AGT ATT AGG CTG TTA GAG ATC			629
Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser Ile Arg Leu Leu Glu Ile			
185	190	195	200
TAT CGC AAT CAA TTT AAG GAA GTG TTT GAG CGG TAT TTT CAT GGG AAT			677
Tyr Arg Asn Gln Phe Lys Glu Val Phe Glu Arg Tyr Phe His Gly Asn			
205	210	215	
GTA AAA TTC TTT AAT GAG AAT TTT AAT AAT CTT GAG AGG GCG CTT TAT			725
Val Lys Phe Phe Asn Glu Asn Phe Asn Asn Leu Glu Arg Ala Leu Tyr			
220	225	230	
GCA GGA GAT GCG GAT TTG GCC ATA GGA GTC AAT AAT GAG ATT CAA GAA			773
Ala Gly Asp Ala Asp Leu Ala Ile Gly Val Asn Asn Glu Ile Gln Glu			
235	240	245	
AGA CTA GGT CAA AAA CCC TTG TTT AAT AAT ACC CAA GAA TTT TTG GAA			821
Arg Leu Gly Gln Lys Pro Leu Phe Asn Asn Thr Gln Glu Phe Leu Glu			
250	255	260	
CTC ATG AAT AAT GGT GGA AAA ATA GAA ATT TAAAGGAGAA ATCATGGAAG AAC			874
Leu Met Asn Asn Gly Gly Lys Ile Glu Ile			
265	270		
AAAAGGATAT GGGTCAAAGT			894

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

Met	Leu	Glu	Asn	Met	Gln	Asp	Ile	Ser	Leu	Gln	Ser	Ser	His	Glu	Val
1				5				10						15	
Gly	Val	Asp	Ile	Thr	Glu	Ser	Lys	Met	Leu	Thr	Lys	Phe	Ala	Ser	Ser
			20					25					30		
Leu	Leu	Met	Asn	Leu	Tyr	Glu	Tyr	Ile	Gly	Asn	Gly	Lys	Asp	Pro	Lys
		35					40					45			
Glu	Ala	Ser	Asp	His	Ala	Met	Arg	Asp	Ala	Lys	Asp	Val	Val	Leu	Ser

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...851
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

TATTAACACC GTTAAAGAGG GGGTAATTC ATG TTA GAA AAC ATG CAA GAT ATT	53
Met Leu Glu Asn Met Gln Asp Ile	
1 5	
TCA TTG CAA AGC TCT CAT GAA GTA GGA GTG GAT ATT ACA GAG AGC AAA	101
Ser Leu Gln Ser Ser His Glu Val Gly Val Asp Ile Thr Glu Ser Lys	
10 15 20	
ATG CTT ACA AAA TTT GCA TCC TCG TTA TTA ATG AAT TTA TAT GAA TAT	149
Met Leu Thr Lys Phe Ala Ser Ser Leu Leu Met Asn Leu Tyr Glu Tyr	
25 30 35 40	
ATT GGA AAT GGC AAG GAT CCC AAA GAA GCG TCC GAT CAT GCC ATG AGG	197
Ile Gly Asn Gly Lys Asp Pro Lys Glu Ala Ser Asp His Ala Met Arg	
45 50 55	
GAT GCA AAG GAT GTG GTG CTT AGT TGT GGT AGA GTA GCC TTT CTT AAA	245
Asp Ala Lys Asp Val Val Leu Ser Cys Gly Arg Val Ala Phe Leu Lys	
60 65 70	
GAC ATA GTT TCA AAT AGT CCA AAC GAA ACA ATC CAA AGT TTT GAT GGA	293
Asp Ile Val Ser Asn Ser Pro Asn Glu Thr Ile Gln Ser Phe Asp Gly	
75 80 85	
GAC TTA GAA GTT GCG ATG CAT TTA GAA AAA ATT GGC ATA GAA TGT TAT	341
Asp Leu Glu Val Ala Met His Leu Glu Lys Ile Gly Ile Glu Cys Tyr	
90 95 100	
AAG ATA TTT ATT GAC TAT GGT TCT CAA AAG ATC GAT GAT AAT GAG CTT	389
Lys Ile Phe Ile Asp Tyr Gly Ser Gln Lys Ile Asp Asp Asn Glu Leu	
105 110 115 120	
TCT TGT CGT TTG TTA CAC ACT GGC ACG AAA ATT TTA GGC ACA AAA GCT	437
Ser Cys Arg Leu Leu His Thr Gly Thr Lys Ile Leu Gly Thr Lys Ala	
125 130 135	
ATG GCA GTT GTT GGT CAA ACA TTC ATC CCC ATT CCT GGA GTT GGA GCG	485
Met Ala Val Val Gly Gln Thr Phe Ile Pro Ile Pro Gly Val Gly Ala	

```

Xaa Tyr Gly Val Lys Lys Lys Val Asp Ala Asp Ile Leu Ser Glu Glu
      20                      25                      30
Thr Asn Glu Tyr Ile Lys Tyr Ile Asn Glu Gly Asn Asp Leu Leu Glu
      35                      40                      45
Glu Ala Glu Glu Val Ile Lys Ala Val Ala Ser Asp Cys Glu Phe Ala
      50                      55                      60
Leu Ala Arg Phe Glu Glu Lys Arg Cys Tyr Ile Arg Asn His Val Ile
      65                      70                      75                      80
Ser Glu Phe Leu His His Phe Asn Gln Leu Glu Gly Phe Glu Leu Thr
      85                      90                      95
Asn Lys Lys Asp Ser Met Glu Asn Ile Gln Leu Asp Val Ser Asn Thr
      100                     105                     110
Leu Lys Ile Ile Asp Lys Asn Leu Lys Met Ser Ser Phe Asp Thr Leu
      115                     120                     125
Gly Ala Val Gly Asn Val Val Gly Gly Phe Ser Met Gly Phe Gly Leu
      130                     135                     140
Ala Ala Gly Gly Ile Val Gly Ser Val Gly Leu Leu Ala Gly Pro Thr
      145                     150                     155                     160
Leu Ala Ile Phe Gly Ala Leu Arg Ala Ala Glu Met Glu Lys Lys Leu
      165                     170                     175
Glu Asp Ala Lys Ala Tyr Cys Ser Gln Val Glu Ala Ala Val Lys Lys
      180                     185                     190
Ala Asp Ala Met Ile Asp Asn Leu Gln Ala Val Arg Lys Met Ala Asp
      195                     200                     205
Leu Phe Thr Arg Gln Ile Thr Lys Phe Asp Ala Leu Phe Phe Ser Leu
      210                     215                     220
Ala Gln Glu Ala Ile Ala Thr Met Lys Lys His Asn Tyr Asp Phe Ser
      225                     230                     235                     240
His Tyr Asn Gln Lys Glu Gln Asp Gln Leu Ala Thr Ala Ser Ser Thr
      245                     250                     255
Leu Lys Thr Leu Gly Ala Phe Leu Lys Val Pro Ile Met Asp Lys His
      260                     265                     270
Gln Lys Leu Asn Glu Ala Thr Gln Ser Lys Leu Glu Phe Met Gln Arg
      275                     280                     285
Glu Met Ser Ser Leu Glu Ala Lys His Tyr Asp Ser Val Lys Ile Lys
      290                     295                     300
Phe Gly Leu Val Arg Arg Leu Phe Glu Phe Phe Arg Ser Leu Trp Gly
      305                     310                     315                     320
Lys Asn Gly Arg Ile Gln Arg Ala Lys Thr Thr Pro Asp Arg Phe Pro
      325                     330                     335
Cys Thr Ser Cys Gly Leu Cys Cys Lys Asn Ile Ala Gly Ile Ile Glu
      340                     345                     350
Leu Ile Gly Phe Asp Ala Gly Asn Gly Val Cys Lys Phe Leu Asp Leu
      355                     360                     365
Glu Thr Asn Leu Cys Lys Ile Tyr Glu Ser Arg Pro Leu Ile Cys Arg
      370                     375                     380
Ile Asp Glu Ala His Lys Lys Leu Tyr Pro His Ile Pro Leu Lys Glu
      385                     390                     395                     400
Phe Tyr Ala Lys Asn Ala Glu Val Cys Asn Ala Leu Gln Glu Ala Asn
      405                     410                     415
His Met Asp Lys Ser Phe Arg Val Ile Leu Lys Lys
      420                     425

```

(2) INFORMATION FOR SEQ ID NO:839:

CTA GAG TTT ATG CAA AGG GAG ATG AGT AGC CTA GAA GCT AAG CAT TAT	915
Leu Glu Phe Met Gln Arg Glu Met Ser Ser Leu Glu Ala Lys His Tyr	
285 290 295	
GAT TCA GTT AAA ATC AAA TTT GGA TTG GTA CGC AGA TTA TTT GAA TTT	963
Asp Ser Val Lys Ile Lys Phe Gly Leu Val Arg Arg Leu Phe Glu Phe	
300 305 310	
TTT AGA TCG CTT TGG GGA AAA AAT GGA AGA ATC CAA AGA GCG AAA ACA	1011
Phe Arg Ser Leu Trp Gly Lys Asn Gly Arg Ile Gln Arg Ala Lys Thr	
315 320 325 330	
ACT CCT GAT CGC TTC CCT TGC ACC TCT TGC GGG CTT TGC TGC AAG AAT	1059
Thr Pro Asp Arg Phe Pro Cys Thr Ser Cys Gly Leu Cys Cys Lys Asn	
335 340 345	
ATC GCC GGG ATT ATT GAG CTT ATT GGG TTT GAT GCT GGC AAT GGG GTG	1107
Ile Ala Gly Ile Ile Glu Leu Ile Gly Phe Asp Ala Gly Asn Gly Val	
350 355 360	
TGC AAA TTT TTG GAT TTA GAA ACC AAT CTG TGC AAG ATT TAT GAA TCG	1155
Cys Lys Phe Leu Asp Leu Glu Thr Asn Leu Cys Lys Ile Tyr Glu Ser	
365 370 375	
CGC CCG TTA ATT TGC AGG ATT GAT GAA GCG CAC AAA AAG CTT TAT CCC	1203
Arg Pro Leu Ile Cys Arg Ile Asp Glu Ala His Lys Lys Leu Tyr Pro	
380 385 390	
CAC ATC CCG CTT AAG GAG TTT TAT GCC AAA AAC GCA GAG GTT TGT AAC	1251
His Ile Pro Leu Lys Glu Phe Tyr Ala Lys Asn Ala Glu Val Cys Asn	
395 400 405 410	
GCT TTG CAA GAA GCA AAC CAT ATG GAT AAG AGC TTT AGG GTT ATT CTT	1299
Ala Leu Gln Glu Ala Asn His Met Asp Lys Ser Phe Arg Val Ile Leu	
415 420 425	
AAG AAA TAATTTAGAA TTTATTGTCC CA	1327
Lys Lys	

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

Met	Pro	Leu	Pro	Phe	Ile	Ile	Ala	Ala	Gly	Val	Ala	Leu	Val	Ala	Ala
1				5					10					15	

TCT GAT TGT GAG TTT GCT CTT GCG AGA TTT GAA GAG AAA AGG TGC TAT	243
Ser Asp Cys Glu Phe Ala Leu Ala Arg Phe Glu Glu Lys Arg Cys Tyr	
60 65 70	
ATT AGA AAT CAT GTA ATT TCA GAA TTT TTG CAC CAT TTT AAT CAA TTA	291
Ile Arg Asn His Val Ile Ser Glu Phe Leu His His Phe Asn Gln Leu	
75 80 85 90	
GAA GGA TTC GAG CTT ACC AAC AAA AAA GAT AGC ATG GAA AAT ATC CAA	339
Glu Gly Phe Glu Leu Thr Asn Lys Lys Asp Ser Met Glu Asn Ile Gln	
95 100 105	
CTC GAT GTA TCA AAT ACA CTA AAA ATT ATT GAT AAA AAT CTC AAG ATG	387
Leu Asp Val Ser Asn Thr Leu Lys Ile Ile Asp Lys Asn Leu Lys Met	
110 115 120	
AGC TCT TTT GAC ACC CTT GGT GCC GTT GGA AAT GTT GTG GGA GGT TTT	435
Ser Ser Phe Asp Thr Leu Gly Ala Val Gly Asn Val Val Gly Gly Phe	
125 130 135	
TCT ATG GGA TTT GGT TTG GCT GCT GGA GGT ATA GTT GGA AGT GTA GGG	483
Ser Met Gly Phe Gly Leu Ala Ala Gly Gly Ile Val Gly Ser Val Gly	
140 145 150	
CTT TTA GCC GGA CCC ACA CTC GCT ATT TTT GGA GCT TTG AGA GCT GCT	531
Leu Leu Ala Gly Pro Thr Leu Ala Ile Phe Gly Ala Leu Arg Ala Ala	
155 160 165 170	
GAA ATG GAA AAA AAA TTA GAA GAT GCT AAG GCT TAT TGC TCT CAA GTT	579
Glu Met Glu Lys Lys Leu Glu Asp Ala Lys Ala Tyr Cys Ser Gln Val	
175 180 185	
GAA GCA GCC GTC AAA AAA GCC GAT GCG ATG ATT GAT AAT CTT CAA GCC	627
Glu Ala Ala Val Lys Lys Ala Asp Ala Met Ile Asp Asn Leu Gln Ala	
190 195 200	
GTT AGG AAA ATG GCA GAT CTT TTC ACT AGG CAG ATC ACA AAA TTT GAC	675
Val Arg Lys Met Ala Asp Leu Phe Thr Arg Gln Ile Thr Lys Phe Asp	
205 210 215	
GCA CTG TTT TTC TCG CTT GCT CAA GAG GCA ATC GCC ACG ATG AAA AAG	723
Ala Leu Phe Phe Ser Leu Ala Gln Glu Ala Ile Ala Thr Met Lys Lys	
220 225 230	
CAC AAC TAC GAT TTT TCG CAT TAC AAT CAA AAA GAA CAA GAT CAG CTA	771
His Asn Tyr Asp Phe Ser His Tyr Asn Gln Lys Glu Gln Asp Gln Leu	
235 240 245 250	
GCT ACT GCT TCT TCA ACC CTT AAA ACT TTG GGT GCT TTT TTG AAA GTG	819
Ala Thr Ala Ser Ser Thr Leu Lys Thr Leu Gly Ala Phe Leu Lys Val	
255 260 265	
CCT ATC ATG GAC AAA CAC CAA AAG CTC AAT GAA GCT ACA CAA AGT AAG	867
Pro Ile Met Asp Lys His Gln Lys Leu Asn Glu Ala Thr Gln Ser Lys	
270 275 280	

```

Gly Gln Asn Leu Gly Ala Asn Lys Pro Lys Ile Ala Thr Glu Tyr Ala
      245                      250                      255
His Leu Ile Leu Lys Ile Ser Met Gly Leu Met Gly Val Leu Gly Ile
      260                      265                      270
Val Leu Val Leu Phe Ala Lys Glu Phe Ala Ser Leu Phe Ser Gln Asp
      275                      280                      285
Glu Glu Val Leu Glu Val Ala Arg Ser Tyr Leu Ile Ala Val Gly Leu
      290                      295                      300
Ser Gln Ala Pro Leu Ile Gly Tyr Phe Val Leu Asp Gly Val Phe Arg
      305                      310                      315                      320
Gly Ala Gly Ile Ser Lys Val Ser Leu Tyr Ile Asn Thr Leu Ser Leu
      325                      330                      335
Trp Gly Leu Arg Ile Met Pro Ile Tyr Leu Leu Leu Ile His His Phe
      340                      345                      350
Lys Val Glu Phe Ile Phe Val Val Ile Ala Ser Glu Thr Phe Leu Arg
      355                      360                      365
Ser Phe Ile Tyr Tyr Lys Val Phe Ser Lys Gly Ile Trp Lys Arg Cys
      370                      375                      380
Gly Lys Lys Ala
      385

```

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1305
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

```

TAAACATCTA AAGGATAAAA C ATG CCA TTG CCA TTT ATT ATA GCA GCT GGA      51
      Met Pro Leu Pro Phe Ile Ile Ala Ala Gly
      1                      5                      10

GTG GCC TTA GTG GCC GCA GNA TAC GGA GTT AAA AAA AAA GTT GAT GCA      99
Val Ala Leu Val Ala Ala Xaa Tyr Gly Val Lys Lys Lys Val Asp Ala
      15                      20                      25

GAC ATT CTC AGT GAA GAG ACC AAT GAA TAT ATT AAG TAT ATC AAT GAA      147
Asp Ile Leu Ser Glu Glu Thr Asn Glu Tyr Ile Lys Tyr Ile Asn Glu
      30                      35                      40

GGC AAT GAC TTG CTA GAG GAA GCA GAA GAA GTT ATT AAA GCT GTG GCT      195
Gly Asn Asp Leu Leu Glu Glu Ala Glu Glu Val Ile Lys Ala Val Ala
      -45                      50                      55

```

```

CAT CAT TTT AAG GTG GAA TTT ATT TTT GTA GTG ATC GCA TCA GAA ACT      1167
His His Phe Lys Val Glu Phe Ile Phe Val Val Ile Ala Ser Glu Thr
350                               355                               360                               365

TTT TTG CGC TCA TTC ATC TAT TAT AAA GTT TTT TCT AAA GGC ATT TGG      1215
Phe Leu Arg Ser Phe Ile Tyr Tyr Lys Val Phe Ser Lys Gly Ile Trp
                               370                               375                               380

AAA AGG TGC GGG AAA AAG GCT TGATTATTGC TTGAGCGTAG CGGT              1260
Lys Arg Cys Gly Lys Lys Ala
                               385

```

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

```

Met Leu Phe Tyr Gly Ile Asn Thr Ile Leu Tyr Thr Gly Thr Asn Ala
 1           5           10           15
Ile Leu Ser Arg Leu Val Gly Ala Arg Asp Phe Thr Gln Ile Asn His
 20           25           30
Ala Phe Ser Ser Ile Phe Ile Gly Ala Phe Met Ile Cys Leu Gly Val
 35           40           45
Leu Phe Val Ser Tyr Phe Leu Ile Glu Pro Phe Leu Asn Trp Met Gln
 50           55           60
Leu Gln Asp Pro Ser Arg Gln Leu Thr Gln Asp Tyr Leu Glu Val Leu
 65           70           75           80
Val Val Ala Leu Pro Ser Ile Phe Leu Lys Asn Ile Leu Val Ser Ala
 85           90           95
Leu Ala Ser Phe Ser Asp Thr Leu Thr Pro Phe Ile Val Lys Ile Ile
100          105          110
Met Val Ile Ala Cys Ile Phe Leu Asn Gln Ala Leu Ile Phe Gly Asp
115          120          125
Phe Gly Phe Lys Glu Met Gly Ile Val Gly Ser Ala Leu Ala Asn Val
130          135          140
Val Val Ser Tyr Leu Glu Leu Leu Ala Leu Gly Val Trp Ile Gln Ile
145          150          155          160
Lys Lys Ile Pro Leu Lys Phe Lys Ile Thr Phe His Phe Ser Phe Leu
165          170          175
Lys Thr Met Phe Arg Val Gly Trp Pro Ala Gly Phe Glu Arg Leu Leu
180          185          190
Ser Leu Phe Ser Leu Ile Leu Leu Ser Lys Phe Val Ala Ser Tyr Gly
195          200          205
Asp Lys Val Leu Ala Gly Met Gln Ile Gly Ile Arg Val Glu Thr Phe
210          215          220
Ser Phe Met Pro Gly Phe Gly Phe Met Ile Ala Ala Met Val Leu Thr
225          230          235          240

```


Phe Gly Asp Phe Gly Phe Lys Glu Met Gly Ile Val Gly Ser Ala Leu	
130 135 140	
GCG AAT GTG GTT GTC TCT TAT TTG GAA TTA CTC GCA CTT GGC GTT TGG	543
Ala Asn Val Val Ser Tyr Leu Glu Leu Leu Ala Leu Gly Val Trp	
145 150 155	
ATA CAA ATC AAA AAA ATC CCT TTA AAA TTC AAA ATA ACC TTT CAT TTT	591
Ile Gln Ile Lys Lys Ile Pro Leu Lys Phe Lys Ile Thr Phe His Phe	
160 165 170	
TCT TTT TTA AAA ACC ATG TTT AGA GTG GGT TGG CCA GCC GGG TTT GAG	639
Ser Phe Leu Lys Thr Met Phe Arg Val Gly Trp Pro Ala Gly Phe Glu	
175 180 185	
CGC TTA TTG AGT TTA TTT TCT TTA ATC CTC TTA TCC AAA TTT GTA GCG	687
Arg Leu Leu Ser Leu Phe Ser Leu Ile Leu Leu Ser Lys Phe Val Ala	
190 195 200 205	
AGC TAT GGG GAT AAA GTG TTA GCG GGC ATG CAA ATA GGC ATT AGG GTT	735
Ser Tyr Gly Asp Lys Val Leu Ala Gly Met Gln Ile Gly Ile Arg Val	
210 215 220	
GAA ACC TTT TCG TTC ATG CCC GGA TTT GGG TTT ATG ATC GCA GCG ATG	783
Glu Thr Phe Ser Phe Met Pro Gly Phe Gly Phe Met Ile Ala Ala Met	
225 230 235	
GTT TTA ACA GGG CAA AAT TTA GGG GCA AAC AAG CCA AAG ATC GCC ACA	831
Val Leu Thr Gly Gln Asn Leu Gly Ala Asn Lys Pro Lys Ile Ala Thr	
240 245 250	
GAA TAC GCG CAT TTG ATT TTA AAA ATC TCT ATG GGT TTA ATG GGG GTT	879
Glu Tyr Ala His Leu Ile Leu Lys Ile Ser Met Gly Leu Met Gly Val	
255 260 265	
TTA GGG ATT GTT TTA GTC TTA TTC GCT AAA GAA TTT GCG AGC CTT TTT	927
Leu Gly Ile Val Leu Val Leu Phe Ala Lys Glu Phe Ala Ser Leu Phe	
270 275 280 285	
TCT CAA GAT GAA GAA GTC TTG GAA GTG GCG CGA TCT TAT TTG ATC GCT	975
Ser Gln Asp Glu Glu Val Leu Glu Val Ala Arg Ser Tyr Leu Ile Ala	
290 295 300	
GTG GGC CTC TCT CAA GCC CCC TTA ATT GGG TAT TTT GTG CTA GAT GGA	1023
Val Gly Leu Ser Gln Ala Pro Leu Ile Gly Tyr Phe Val Leu Asp Gly	
305 310 315	
GTT TTT AGA GGG GCT GGC ATT TCT AAA GTC TCA CTG TAT ATT AAC ACC	1071
Val Phe Arg Gly Ala Gly Ile Ser Lys Val Ser Leu Tyr Ile Asn Thr	
320 325 330	
CTA AGC TTA TGG GGG TTA AGG ATC ATG CCC ATT TAC TTG CTT TTA ATT	1119
Leu Ser Leu Trp Gly Leu Arg Ile Met Pro Ile Tyr Leu Leu Leu Ile	
335 340 345	

210

215

220

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...1236
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

```

CTCTCGGTTT TTTTGTGGG TAAGATTTTCG CACCATCACA TTGTGGCTTT AGGGGTGGGC      60
TTGCAATTTT TG ATG CTT TTT TAT GGC ATC AAC ACG ATT TTA TAC ACC GGC      111
      Met Leu Phe Tyr Gly Ile Asn Thr Ile Leu Tyr Thr Gly
              1              5              10

ACT AAC GCC ATT CTT TCT AGG CTT GTG GGG GCT AGG GAT TTT ACT CAA      159
Thr Asn Ala Ile Leu Ser Arg Leu Val Gly Ala Arg Asp Phe Thr Gln
      15              20              25

ATC AAC CAC GCT TTT TCC AGT ATT TTC ATA GGG GCT TTT ATG ATC TGT      207
Ile Asn His Ala Phe Ser Ser Ile Phe Ile Gly Ala Phe Met Ile Cys
      30              35              40              45

TTG GGC GTG CTG TTT GTT TCT TAT TTT TTG ATT GAG CCT TTT TTA AAT      255
Leu Gly Val Leu Phe Val Ser Tyr Phe Leu Ile Glu Pro Phe Leu Asn
              50              55              60

TGG ATG CAA TTA CAA GAT CCT TCG CGC CAA TTG ACG CAA GAT TAT TTA      303
Trp Met Gln Leu Gln Asp Pro Ser Arg Gln Leu Thr Gln Asp Tyr Leu
              65              70              75

GAA GTC TTA GTT GTA GCG CTA CCG AGT ATT TTT TTA AAA AAT ATT TTA      351
Glu Val Leu Val Val Ala Leu Pro Ser Ile Phe Leu Lys Asn Ile Leu
              80              85              90

GTT TCA GCG CTC GCT AGT TTT TCA GAC ACC CTA ACC CCC TTT ATT GTC      399
Val Ser Ala Leu Ala Ser Phe Ser Asp Thr Leu Thr Pro Phe Ile Val
              95              100              105

AAA ATC ATC ATG GTC ATT GCA TGC ATT TTT TTG AAT CAA GCC TTG ATT      447
Lys Ile Ile Met Val Ile Ala Cys Ile Phe Leu Asn Gln Ala Leu Ile
      110              115              120              125

TTT GGG GAT TTT GGT TTT AAA GAA ATG GGG ATT GTA GGC TCT GCT TTA      495

```

165	170	175	
CGT TTT AAA GGG GAT TTT AAA GTG GTT TTT AGC CCT GAA ATT CCG CAT			576
Arg Phe Lys Gly Asp Phe Lys Val Val Phe Ser Pro Glu Ile Pro His			
180	185	190	
TGC ATA GAG CTT GGG AGT TTT AAT GCG GTT ACG GCG AGT TTT GGT TTG			624
Cys Ile Glu Leu Gly Ser Phe Asn Ala Val Thr Ala Ser Phe Gly Leu			
195	200	205	
CAA ATA GCG AGT GAA GTC GTG CAA GAC ATT ATC AAC GAT AAA AGG AAG T			673
Gln Ile Ala Ser Glu Val Val Gln Asp Ile Ile Asn Asp Lys Arg Lys			
210	215	220	
GAGATGAAAG ATTACGAAGA CGAATTGG			701

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

Arg	Leu	Ser	Glu	Pro	Ile	Asp	Arg	Phe	Thr	Arg	Ile	Arg	Trp	Leu	Phe
1				5					10					15	
Lys	Asn	Asp	Phe	Glu	Lys	Ile	Arg	Gln	Arg	Val	Leu	Ile	Cys	Gly	
			20					25					30		
Val	Gly	Gly	Val	Gly	Gly	Phe	Ala	Leu	Asp	Ala	Leu	Tyr	Arg	Val	Gly
			35				40					45			
Ile	Gly	Gln	Ile	Thr	Ile	Ile	Asp	Lys	Asp	Val	Phe	Asp	Val	Thr	Asn
			50			55					60				
Gln	Asn	Arg	Gln	Ile	Gly	Ser	Glu	Arg	Ile	Gly	Glu	Ser	Lys	Val	Leu
65				70					75					80	
Val	Leu	Gln	Asp	Leu	Tyr	Lys	Gly	Ile	Gln	Ala	Leu	Asn	Leu	His	Ile
			85						90					95	
Asp	Glu	Ala	Phe	Leu	Asn	Ser	Phe	Asn	Phe	Arg	Asp	Tyr	Asp	Tyr	Ile
			100					105					110		
Leu	Asp	Cys	Met	Asp	Asp	Leu	Pro	Ile	Lys	Thr	Ser	Leu	Ala	Ile	Lys
			115				120					125			
Cys	Gln	Asn	Phe	Ala	Tyr	Gly	Lys	Phe	Ile	Ser	Ser	Met	Gly	Ser	Ala
			130			135					140				
Lys	Arg	Leu	Asn	Pro	Lys	His	Ile	Gln	Val	Gly	Ser	Val	Trp	Glu	Ser
145				150						155				160	
Tyr	Gly	Asp	Lys	Phe	Gly	Arg	Lys	Phe	Arg	Asp	Phe	Leu	Lys	Lys	Arg
			165						170					175	
Arg	Phe	Lys	Gly	Asp	Phe	Lys	Val	Val	Phe	Ser	Pro	Glu	Ile	Pro	His
			180					185					190		
Cys	Ile	Glu	Leu	Gly	Ser	Phe	Asn	Ala	Val	Thr	Ala	Ser	Phe	Gly	Leu
			195				200					205			
Gln	Ile	Ala	Ser	Glu	Val	Val	Gln	Asp	Ile	Ile	Asn	Asp	Lys	Arg	Lys

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...672

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

AGG TTG TCT GAA CCC ATA GAT AGA TTC ACG CGC ATA AGG TGG TTG TTT	48
Arg Leu Ser Glu Pro Ile Asp Arg Phe Thr Arg Ile Arg Trp Leu Phe	
1 5 10 15	
AAA AAC GAT TTT GAA AAA ATC CGC CAA CAA AGG GTT TTA ATC TGT GGC	96
Lys Asn Asp Phe Glu Lys Ile Arg Gln Gln Arg Val Leu Ile Cys Gly	
20 25 30	
GTG GGG GGC GTT GGG GGC TTT GCG CTA GAC GCT TTG TAT CGT GTG GGG	144
Val Gly Gly Val Gly Gly Phe Ala Leu Asp Ala Leu Tyr Arg Val Gly	
35 40 45	
ATA GGG CAA ATC ACT ATC ATT GAT AAA GAC GTG TTT GAT GTT ACC AAT	192
Ile Gly Gln Ile Thr Ile Ile Asp Lys Asp Val Phe Asp Val Thr Asn	
50 55 60	
CAA AAC CGC CAG ATT GGC TCA GAA AGG ATA GGA GAA TCT AAA GTG TTG	240
Gln Asn Arg Gln Ile Gly Ser Glu Arg Ile Gly Glu Ser Lys Val Leu	
65 70 75 80	
GTG TTG CAA GAT CTC TAT AAG GGC ATT CAA GCT TTG AAC TTG CAT ATA	288
Val Leu Gln Asp Leu Tyr Lys Gly Ile Gln Ala Leu Asn Leu His Ile	
85 90 95	
GAT GAA GCG TTT TTA AAT TCA TTT AAT TTT AGA GAT TAT GAT TAC ATT	336
Asp Glu Ala Phe Leu Asn Ser Phe Asn Phe Arg Asp Tyr Asp Tyr Ile	
100 105 110	
TTA GAT TGC ATG GAC GAT TTG CCT ATT AAA ACA AGC TTA GCG ATA AAA	384
Leu Asp Cys Met Asp Asp Leu Pro Ile Lys Thr Ser Leu Ala Ile Lys	
115 120 125	
TGC CAG AAT TTC GCT TAC GGA AAA TTT ATC AGC TCT ATG GGG AGT GCG	432
Cys Gln Asn Phe Ala Tyr Gly Lys Phe Ile Ser Ser Met Gly Ser Ala	
130 135 140	
AAA CGC TTG AAC CCT AAA CAC ATC CAA GTG GGG AGC GTG TGG GAA AGC	480
Lys Arg Leu Asn Pro Lys His Ile Gln Val Gly Ser Val Trp Glu Ser	
145 150 155 160	
TAT GGC GAT AAA TTC GGG CGT AAA TTT AGG GAT TTT TTA AAA AAA CGC	528
Tyr Gly Asp Lys Phe Gly Arg Lys Phe Arg Asp Phe Leu Lys Lys Arg	

GCGATATTGC TAAAGATATC CAA

900

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

```

Met Gly Lys Phe Met Asn Thr Leu Lys Lys His Leu Ala Phe Ile Ile
 1           5           10           15
Pro Leu Val Ala Leu Leu Phe Ser Leu Glu Cys Val Leu Phe Ile Asn
          20           25           30
Gln Ala Ile Glu Gln Lys Glu Lys Lys Leu Ile Glu Asp Tyr Ser Val
          35           40           45
Val Leu Ala Ser Thr Gln Lys Leu Asn Leu Glu Leu Leu Arg Gln Asn
          50           55           60
Phe Ser Glu Ile Ile Ala Leu Lys Glu Ile Asp Pro Asn Tyr Ser Leu
65           70           75           80
Glu Pro Leu Gln Lys Thr Leu Gly Ile Asp Gly Leu Lys Glu Leu Arg
          85           90           95
Lys Asn Leu Pro Phe Phe Tyr Ser Leu Gln Leu Ser Thr Phe Pro Thr
          100          105          110
Gln Glu Arg Leu Glu Asn Ile Lys Glu Lys Leu Leu Lys Ile Pro Gly
          115          120          125
Val Gln Lys Val Glu Val Phe Ala Lys Thr Tyr Met Gln Val Tyr Asp
          130          135          140
Leu Leu Ser Phe Ile Lys Thr Ala Val Tyr Ile Phe Ala Leu Val Val
          145          150          155          160
Phe Val Leu Ser Val Leu Leu Met Phe Lys Gln Val Arg Ile Trp Ile
          165          170          175
Tyr Gln Tyr His Glu Arg Leu Glu Ile Met Asp Leu Leu Gly Ala Ser
          180          185          190
Val Ser Phe Lys Asn Gly Phe Leu Tyr Lys Ile Ala Leu Met Asp Ser
          195          200          205
Val Ile Ala Ser Phe Leu Ala Pro Met Leu Met Leu Tyr Thr Thr Ser
          210          215          220
Gln Lys Gly Phe Glu Lys Thr Met Asp Thr Leu Gly Ile Ile Gly Gly
          225          230          235          240
Ala Phe Val Leu Asn His Phe Leu Trp Gly Leu Leu Phe Ser Leu Val
          245          250          255
Val Ser Phe Val Ser Val Leu Leu Val Ala Trp Arg Thr Arg His Val
          260          265          270

```

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

AAT TTT AGC GAA ATC ATA GCG TTA AAA GAA ATT GAT CCT AAT TAT TCT	242
Asn Phe Ser Glu Ile Ile Ala Leu Lys Glu Ile Asp Pro Asn Tyr Ser	
65 70 75	
TTA GAA CCT CTT CAA AAA ACC TTA GGC ATA GAT GGG CTT AAG GAA TTA	290
Leu Glu Pro Leu Gln Lys Thr Leu Gly Ile Asp Gly Leu Lys Glu Leu	
80 85 90 95	
AGA AAA AAT TTG CCC TTT TTT TAT TCT TTA CAA CTT TCC ACA TTC CCC	338
Arg Lys Asn Leu Pro Phe Phe Tyr Ser Leu Gln Leu Ser Thr Phe Pro	
100 105 110	
ACT CAA GAG CGT TTA GAA AAC ATT AAA GAA AAA TTG CTC AAA ATC CCT	386
Thr Gln Glu Arg Leu Glu Asn Ile Lys Glu Lys Leu Leu Lys Ile Pro	
115 120 125	
GGC GTT CAA AAA GTT GAA GTC TTT GCC AAA ACT TAC ATG CAA GTG TAT	434
Gly Val Gln Lys Val Glu Val Phe Ala Lys Thr Tyr Met Gln Val Tyr	
130 135 140	
GAT CTC TTG AGT TTT ATT AAA ACA GCG GTC TAT ATC TTT GCG TTA GTG	482
Asp Leu Leu Ser Phe Ile Lys Thr Ala Val Tyr Ile Phe Ala Leu Val	
145 150 155	
GTC TTT GTT TTA TCG GTT TTA TTG ATG TTT AAA CAA GTC CGC ATC TGG	530
Val Phe Val Leu Ser Val Leu Leu Met Phe Lys Gln Val Arg Ile Trp	
160 165 170 175	
ATC TAT CAA TAC CAT GAG AGA TTA GAG ATC ATG GAT TTA TTA GGG GCT	578
Ile Tyr Gln Tyr His Glu Arg Leu Glu Ile Met Asp Leu Leu Gly Ala	
180 185 190	
TCG GTG TCT TTT AAA AAC GGG TTT TTG TAT AAA ATA GCT TTA ATG GAT	626
Ser Val Ser Phe Lys Asn Gly Phe Leu Tyr Lys Ile Ala Leu Met Asp	
195 200 205	
TCT GTA ATC GCT AGT TTT TTA GCC CCC ATG CTC ATG CTC TAT ACC ACT	674
Ser Val Ile Ala Ser Phe Leu Ala Pro Met Leu Met Leu Tyr Thr Thr	
210 215 220	
TCG CAA AAA GGT TTT GAA AAA ACG ATG GAT ACT TTG GGT ATT ATA GGA	722
Ser Gln Lys Gly Phe Glu Lys Thr Met Asp Thr Leu Gly Ile Ile Gly	
225 230 235	
GGC GCG TTT GTT TTA AAC CAT TTT TTA TGG GGA CTG CTT TTT AGC CTT	770
Gly Ala Phe Val Leu Asn His Phe Leu Trp Gly Leu Leu Phe Ser Leu	
240 245 250 255	
GTG GTC TCA TTT GTT TCT GTT TTA CTT GTA GCT TGG AGG ACT AGG CAT	818
Val Val Ser Phe Val Ser Val Leu Leu Val Ala Trp Arg Thr Arg His	
260 265 270	
GTA TAAATTAGGG GTGTTTTTGT TAGCCACCTT ACTATCAGCT AACACGCAAA AAGTGA	877
Val	

```

      50              55              60
Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala Ile Ala Pro Ile Gln
65              70              75              80
Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe Gly Met Asp Leu Asp
      85              90              95
Lys Ser Val Ala Ala Ser Leu Ile Thr Gly Leu Leu Gly Val Thr Ala
      100              105              110
Val Ala Gln Val Gly Arg Thr Leu Val Asn Gly Phe Leu Lys Phe Ile
      115              120              125
Pro Val Val Gly Ser Val Ala Gly Gly Thr Thr Ala Val Ile Ile Thr
      130              135              140
Glu Gly Ile Gly Phe Ala Tyr Leu Lys Val Leu Glu Lys Cys Phe Asn
145              150              155              160
Asp Glu Thr Gly Glu Val Asn Leu Pro Asp Glu Val Gly Met Ile Thr
      165              170              175
Ser Leu Phe Lys Glu Asn Tyr Leu Asn Leu Asp Thr Ile Lys Lys Leu
      180              185              190
Thr Gln

```

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 6...821
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

```

AGAAG ATG GGG AAG TTT ATG AAT ACT CTT AAA AAG CAT TTA GCC TTT ATC      50
Met Gly Lys Phe Met Asn Thr Leu Lys Lys His Leu Ala Phe Ile
      1              5              10              15

ATT CCC CTA GTA GCG TTA TTG TTT AGC TTG GAG TGC GTG TTA TTT ATC      98
Ile Pro Leu Val Ala Leu Leu Phe Ser Leu Glu Cys Val Leu Phe Ile
      20              25              30

AAT CAA GCG ATC GAA CAG AAA GAA AAA AAA TTG ATT GAA GAT TAT TCG      146
Asn Gln Ala Ile Glu Gln Lys Glu Lys Lys Leu Ile Glu Asp Tyr Ser
      35              40              45

GTC GTG TTG GCC AGC ACG CAA AAA TTA AAC TTG GAA TTG TTG CGT CAA      194
Val Val Leu Ala Ser Thr Gln Lys Leu Asn Leu Glu Leu Leu Arg Gln
      50              55              60

```

55														60														65																											
ATA	CCC	TTT	AGC	GAT	GCA	CTC	GCT	ATC	GCG	CCC	ATT	CAA	GCA	GGA	ATG	295																																							
Ile	Pro	Phe	Ser	Asp	Ala	Leu	Ala	Ile	Ala	Pro	Ile	Gln	Ala	Gly	Met																																								
70														75														80																											
ATC	TAC	AAA	ATG	AAT	GAC	GCT	TTT	GGA	ATG	GAT	TTG	GAT	AAA	TCT	GTA	343																																							
Ile	Tyr	Lys	Met	Asn	Asp	Ala	Phe	Gly	Met	Asp	Leu	Asp	Lys	Ser	Val																																								
85														90														95																											
GCC	GCA	TCA	TTA	ATC	ACC	GGA	TTG	TTA	GGC	GTA	ACC	GCT	GTC	GCG	CAA	391																																							
Ala	Ala	Ser	Leu	Ile	Thr	Gly	Leu	Leu	Gly	Val	Thr	Ala	Val	Ala	Gln																																								
100														105														110														115													
GTG	GGG	AGA	ACG	CTT	GTT	AAT	GGT	TTC	CTT	AAA	TTC	ATT	CCT	GTT	GTG	439																																							
Val	Gly	Arg	Thr	Leu	Val	Asn	Gly	Phe	Leu	Lys	Phe	Ile	Pro	Val	Val																																								
120														125														130																											
GGG	AGT	GTT	GCA	GGG	GGC	ACA	ACC	GCT	GTA	ATT	ATC	ACA	GAA	GGC	ATT	487																																							
Gly	Ser	Val	Ala	Gly	Gly	Thr	Thr	Ala	Val	Ile	Ile	Thr	Glu	Gly	Ile																																								
135														140														145																											
GGG	TTT	GCG	TAT	TTG	AAA	GTG	CTA	GAA	AAG	TGC	TTT	AAT	GAT	GAG	ACG	535																																							
Gly	Phe	Ala	Tyr	Leu	Lys	Val	Leu	Glu	Lys	Cys	Phe	Asn	Asp	Glu	Thr																																								
150														155														160																											
GGC	GAA	GTC	AAT	TTG	CCT	GAT	GAA	GTT	GGC	ATG	ATA	ACT	TCT	CTC	TTT	583																																							
Gly	Glu	Val	Asn	Leu	Pro	Asp	Glu	Val	Gly	Met	Ile	Thr	Ser	Leu	Phe																																								
165														170														175																											
AAG	GAG	AAT	TAT	CTC	AAC	TTG	GAT	ACA	ATC	AAG	AAA	TTA	ACA	CAA	TAAGA	633																																							
Lys	Glu	Asn	Tyr	Leu	Asn	Leu	Asp	Thr	Ile	Lys	Lys	Leu	Thr	Gln																																									
180														185														190																											
TTAGGGGTTA TGAAAAACGC ATGGCATTAG ACAAAGGAT TTGGATGCAT TTT																686																																							

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met	Glu	Val	Pro	Ile	Glu	Gly	Leu	Glu	Glu	Leu	Val	Asp	Glu	Thr	Lys
1				5				10					15		
Lys	Cys	Leu	Ile	Glu	Ala	Lys	Lys	Asn	Lys	Gln	Asn	His	Phe	Leu	Leu
		20					25					30			
Ile	Gln	Lys	Ala	Asn	Ile	Gln	Ala	Arg	Lys	Gln	Ala	Met	Ile	Asp	Glu
	35					40					45				
Ser	Lys	Thr	Ile	Ile	His	Val	Ala	Ser	Gly	Ala	Ala	Gly	Ala	Ala	Gly

				165					170					175			
Cys	Phe	Ser	Tyr	Val	Glu	Glu	Pro	Asn	Lys	Gln	Glu	Phe	Leu	Asp	Phe		
			180					185					190				
Lys	Gln	Lys	Tyr	Leu	Asp	Phe	Ser	Arg	Asn	Lys	Ala	Pro	Lys	Ala	Asn		
		195					200				205						
Leu	Ser	Asn	Ala	Leu	Glu	Glu	Gln	Leu	Lys	Glu	Asn	Phe	Lys	Lys	Leu		
	210				215					220							
Tyr	Asn	Asp	Leu	Phe	Asp	Gly	Ala	Ile	Ile	Arg	Cys	Asp	Phe	Phe	Val		
225			230						235						240		
Ile	Lys	Asn	Glu	Val	Tyr	Leu	Asn	Glu	Ile	Asn	Pro	Ile	Pro	Gly	Ser		
			245					250						255			
Leu	Ala	Asn	Tyr	Leu	Phe	Asp	Asp	Phe	Lys	Thr	Thr	Leu	Glu	Asn	Leu		
		260					265						270				
Ala	Gln	Ser	Leu	Pro	Lys	Thr	Pro	Lys	Ile	Gln	Ile	Lys	Asn	Ser	Tyr		
		275					280					285					
Leu	Leu	Gln	Ile	Gln	Lys	Asn	Lys										
	290					295											

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...628
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

CAAAGCCTAT GCGAGAGTCA ATTCCGTTGC ATTTTCATTT AGAGGC ATG GAA GTC	55
Met Glu Val	
1	
CCC ATT GAA GGT TTA GAA GAA TTG GTA GAT GAA ACG AAA AAA TGC TTG	103
Pro Ile Glu Gly Leu Glu Glu Leu Val Asp Glu Thr Lys Lys Cys Leu	
5 10 15	
ATA GAA GCT AAG AAA AAC AAA CAA AAC CAT TTC TTG CTG ATT CAA AAA	151
Ile Glu Ala Lys Lys Asn Lys Gln Asn His Phe Leu Leu Ile Gln Lys	
20 25 30 35	
GCT AAC ATC CAA GCA AGA AAA CAA GCC ATG ATA GAT GAA AGT AAA ACC	199
Ala Asn Ile Gln Ala Arg Lys Gln Ala Met Ile Asp Glu Ser Lys Thr	
40 45 50	
ATT ATC CAT GTT GCA TCA GGA GCG GCT GGA GCG GCC GGG CTT ATC CCC	247
Ile Ile His Val Ala Ser Gly Ala Ala Gly Ala Ala Gly Leu Ile Pro	

```

AAA CTC TAT AAC GAT TTG TTT GAT GGC GCG ATC ATT CGT TGC GAT TTT      783
Lys Leu Tyr Asn Asp Leu Phe Asp Gly Ala Ile Ile Arg Cys Asp Phe
      225                      230                      235

TTT GTC ATA AAA AAT GAA GTG TAT CTT AAT GAG ATC AAC CCC ATT CCT      831
Phe Val Ile Lys Asn Glu Val Tyr Leu Asn Glu Ile Asn Pro Ile Pro
      240                      245                      250

GGC AGT TTG GCC AAT TAT TTG TTT GAT GAT TTT AAA ACA ACG CTA GAA      879
Gly Ser Leu Ala Asn Tyr Leu Phe Asp Asp Phe Lys Thr Thr Leu Glu
      255                      260                      265                      270

AAT TTA GCG CAA TCA TTA CCC AAA ACC CCT AAG ATC CAA ATC AAA AAC      927
Asn Leu Ala Gln Ser Leu Pro Lys Thr Pro Lys Ile Gln Ile Lys Asn
      275                      280                      285

TCT TAT TTG TTG CAA ATC CAA AAG AAT AAG TAATGGCCAA ACGCAGTATC GCT      980
Ser Tyr Leu Leu Gln Ile Gln Lys Asn Lys
      290                      295

TATTTGGATA GCGTTTTTGA CATTTCTAC ACTTTTATAG A      1021

```

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

```

Met His Ser Lys Tyr Phe Ala Gln Ile Lys Glu Lys Lys Leu Pro Pro
 1           5           10           15
Leu Ile Leu Thr His Asn Gly Leu Leu Lys Asn Ser Phe Leu Gly Ala
      20           25           30
Lys Ile Ile Glu Leu Pro Leu Val Ile Asn Leu Val His Gly Gly Asp
      35           40           45
Gly Glu Asp Gly Lys Leu Ala Ser Leu Leu Glu Phe Tyr Arg Ile Ala
      50           55           60
Phe Ile Gly Pro Arg Ile Glu Ala Ser Val Leu Ser Tyr Asn Lys Tyr
      65           70           75           80
Leu Thr Lys Leu Tyr Ala Lys Asp Leu Gly Val Lys Thr Leu Asp His
      85           90           95
Val Leu Leu Asn Glu Lys Asn Arg Ala Asn Ala Leu Asp Leu Met Asn
      100          105          110
Phe Asn Phe Pro Phe Ile Ile Lys Pro Asn Asn Ala Gly Ser Ser Leu
      115          120          125
Gly Val Asn Val Val Lys Glu Lys Glu Leu Val Tyr Ala Leu Asp
      130          135          140
Gly Ala Phe Glu Tyr Ser Lys Glu Val Leu Ile Glu Pro Phe Ile Gln
      145          150          155          160
Gly Val Lys Glu Tyr Asn Leu Ala Gly Cys Lys Ile Lys Lys Asp Phe

```

GAATCCAAC ATG CAT TCA AAA TAC TTC GCT CAA ATC AAA GAA AAA AAA TTA	111
Met His Ser Lys Tyr Phe Ala Gln Ile Lys Glu Lys Lys Leu	
1 5 10	
CCT CCC CTA ATC CTC ACA CAC AAT GGC TTG CTT AAA AAC TCA TTT TTA	159
Pro Pro Leu Ile Leu Thr His Asn Gly Leu Leu Lys Asn Ser Phe Leu	
15 20 25 30	
GGT GCT AAG ATT ATA GAA TTG CCT TTA GTG ATC AAT CTC GTG CAT GGG	207
Gly Ala Lys Ile Ile Glu Leu Pro Leu Val Ile Asn Leu Val His Gly	
35 40 45	
GGC GAT GGC GAA GAT GGG AAA TTA GCG AGC TTG TTA GAA TTT TAT CGT	255
Gly Asp Gly Glu Asp Gly Lys Leu Ala Ser Leu Leu Glu Phe Tyr Arg	
50 55 60	
ATC GCT TTT ATA GGC CCT AGG ATT GAA GCG AGC GTG CTG AGT TAT AAC	303
Ile Ala Phe Ile Gly Pro Arg Ile Glu Ala Ser Val Leu Ser Tyr Asn	
65 70 75	
AAA TAT TTA ACC AAG CTT TAC GCC AAA GAC TTA GGG GTA AAG ACT TTA	351
Lys Tyr Leu Thr Lys Leu Tyr Ala Lys Asp Leu Gly Val Lys Thr Leu	
80 85 90	
GAT CAT GTT CTT TTG AAT GAA AAA AAC CGC GCT AAC GCC TTG GAT TTG	399
Asp His Val Leu Leu Asn Glu Lys Asn Arg Ala Asn Ala Leu Asp Leu	
95 100 105 110	
ATG AAC TTT AAT TTC CCT TTC ATA ATC AAG CCT AAT AAC GCC GGA AGC	447
Met Asn Phe Asn Phe Pro Phe Ile Ile Lys Pro Asn Asn Ala Gly Ser	
115 120 125	
TCT TTA GGG GTG AAT GTT GTG AAA GAA GAA AAA GAA TTG GTT TAC GCT	495
Ser Leu Gly Val Asn Val Val Lys Glu Glu Lys Glu Leu Val Tyr Ala	
130 135 140	
TTA GAC GGT GCG TTT GAA TAT TCT AAA GAG GTC TTG ATA GAG CCT TTC	543
Leu Asp Gly Ala Phe Glu Tyr Ser Lys Glu Val Leu Ile Glu Pro Phe	
145 150 155	
ATT CAG GGA GTG AAA GAA TAC AAT TTG GCC GGT TGC AAG ATC AAA AAG	591
Ile Gln Gly Val Lys Glu Tyr Asn Leu Ala Gly Cys Lys Ile Lys Lys	
160 165 170	
GAT TTT TGT TTT TCC TAT GTG GAA GAG CCT AAC AAA CAG GAA TTT TTA	639
Asp Phe Cys Phe Ser Tyr Val Glu Glu Pro Asn Lys Gln Glu Phe Leu	
175 180 185 190	
GAT TTC AAA CAA AAA TAT TTG GAT TTT TCA CGC AAT AAA GCC CCT AAA	687
Asp Phe Lys Gln Lys Tyr Leu Asp Phe Ser Arg Asn Lys Ala Pro Lys	
195 200 205	
GCG AAT CTT TCT AAC GCC CTA GAA GAG CAA TTA AAA GAA AAT TTT AAA	735
Ala Asn Leu Ser Asn Ala Leu Glu Glu Gln Leu Lys Glu Asn Phe Lys	
210 215 220	

Asp Lys Glu Val Lys Gly Gly Leu Gly Val Val Ala Asp Asp Ala Leu
 40 45 50

GCG GGT GTT TTA GCC GGA TTG AGC GCG TTA TTA GTC ATC CAT ATT TTA 249
 Ala Gly Val Leu Ala Gly Leu Ser Ala Leu Leu Val Ile His Ile Leu
 55 60 65

GGA TTT TTT AAC ATT AAA CTT TAATTTTAAG AAAAT 285
 Gly Phe Phe Asn Ile Lys Leu
 70 75

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

Met Trp Leu Ala Met Ala Ile Ser Gly Leu Ser Leu Ala Gly Val Ile
 1 5 10 15

Leu Ser Phe Ile Phe Phe Arg Ile Tyr Asp Ile Thr Lys Pro Ser Leu
 20 25 30

Ile Gly Lys Ile Asp Lys Glu Val Lys Gly Gly Leu Gly Val Val Ala
 35 40 45

Asp Asp Ala Leu Ala Gly Val Leu Ala Gly Leu Ser Ala Leu Leu Val
 50 55 60

Ile His Ile Leu Gly Phe Phe Asn Ile Lys Leu
 65 70 75

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...957
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

AAAGATAGGA TTAAATATTT TATTTTTTTTA GATGAAAACC ATCATTTTTTA TTGATTGAA 60

```

Asn Val Gly Phe Tyr Phe Asn Leu Lys Ser Glu Leu Lys Asn Gln Arg
 210                215                220
Asn Asn Thr Thr Ser Tyr Thr Ala Pro Ile Leu His Thr Leu Gly Leu
225                230                235                240
Gln Arg Tyr Phe Glu Leu Val Gln Asn Leu Gly Gly Phe Glu Ala Leu
                245                250                255
Tyr Arg Glu Thr Lys Lys Ala Ala Leu Ala Thr Gln Lys Ala Val Leu
                260                265                270
Ala Leu Gly Leu Lys Ile Phe Pro Lys Ser Pro Ser Leu Ser Met Thr
                275                280                285
Thr Ile Val Asn Glu His Ala Lys Glu Leu Arg Asn Leu Leu Lys Glu
                290                295                300
Lys Tyr Gln Val Gln Phe Ala Gly Gly Gln Glu Pro Tyr Lys Asp Ala
305                310                315                320
Leu Ile Arg Ile Asn His Met Gly Ile Ile Pro Val Tyr Lys Ser Ala
                325                330                335
Tyr Ala Leu Asn Ala Leu Glu Leu Ala Leu Asn Asp Leu Asp Leu Arg
                340                345                350
Glu Phe Asp Gly Val Ala Asn Ala Thr Phe Leu Lys Gln Tyr Tyr Gly
                355                360                365
Ile

```

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...270
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

```

AAGAGGCATG ACAGCTCTTA CATTGTGATA GACGAATTAG TGGGC ATG TGG TTG GCG      57
                                     Met Trp Leu Ala
                                     1

ATG GCG ATT AGC GGG TTA TCG TTA GCG GGT GTG ATC TTG AGT TTT ATC      105
Met Ala Ile Ser Gly Leu Ser Leu Ala Gly Val Ile Leu Ser Phe Ile
  5                10                15                20

TTT TTT AGG ATC TAT GAT ATT ACT AAA CCC TCA CTC ATT GGC AAG ATA      153
Phe Phe Arg Ile Tyr Asp Ile Thr Lys Pro Ser Leu Ile Gly Lys Ile
                25                30                35

GAT AAA GAA GTT AAA GGG GGC TTA GGG GTT GTG GCT GAT GAC GCT TTA      201

```

Glu Pro Tyr Lys Asp Ala Leu Ile Arg Ile Asn His Met Gly Ile Ile
 315 320 325 330

CCT GTT TAT AAA AGC GCT TAC GCT TTA AAC GCC CTA GAG TTA GCC CTA 1061
 Pro Val Tyr Lys Ser Ala Tyr Ala Leu Asn Ala Leu Glu Leu Ala Leu
 335 340 345

AAC GAC TTG GAT TTA AGG GAA TTT GAT GGC GTG GCG AAC GCA ACT TTT 1109
 Asn Asp Leu Asp Leu Arg Glu Phe Asp Gly Val Ala Asn Ala Thr Phe
 350 355 360

TTA AAG CAA TAT TAT GGA ATT TAAGGATCAC AATGCATTAT TCTTATGAAA CCTT 1164
 Leu Lys Gln Tyr Tyr Gly Ile
 365

TTTAAA 1170

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

Met Leu Leu Phe Thr Pro Gly Pro Val Ala Ile Asn Glu Glu Met Arg
 1 5 10 15
 Thr Ser Phe Ser Gln Pro Met Pro His Arg Thr Lys Asp Phe Glu
 20 25 30
 Lys Ile Phe Gln Ser Val Arg Glu Asn Leu Lys Lys Met Thr Gly Leu
 35 40 45
 Glu Glu Val Leu Leu Leu Ser Ser Ser Gly Thr Gly Ala Met Glu Ala
 50 55 60
 Ser Val Ile Ser Leu Cys Gln Lys Glu Leu Leu Phe Val Asn Ala Gly
 65 70 75 80
 Lys Phe Gly Glu Arg Phe Gly Lys Ile Ala Lys Ala His Ser Ile Lys
 85 90 95
 Ala His Glu Leu Val Tyr Glu Trp Asp Thr Pro Ala Gln Val Asp Glu
 100 105 110
 Ile Leu Ser Val Leu Lys Ala Asn Pro Asn Ile Asp Ala Phe Cys Ile
 115 120 125
 Gln Ala Cys Glu Ser Ser Gly Gly Leu Arg His Pro Val Glu Lys Ile
 130 135 140
 Ala Gln Ala Ile Lys Glu Thr Asn Pro Asn Val Phe Val Ile Val Asp
 145 150 155 160
 Ala Ile Thr Ala Leu Gly Val Glu Pro Leu Glu Ile Thr His Val Asp
 165 170 175
 Ala Leu Ile Gly Ser Gln Lys Ala Phe Met Leu Pro Pro Ala Met
 180 185 190
 Ser Leu Val Ala Leu Ser Gln Asn Ala Ile Glu Arg Ile Glu Glu Arg
 195 200 205

- 1236 -

```

                260                265                270
Asn Leu His Ala Tyr Ala Lys Gly Glu Met Gln Ala Ser Ala Phe Arg
                275                280                285
Asn Cys Val Asn Thr Leu Thr Glu Ile Lys Ser Met Arg Glu Ser Ile
                290                295                300
Glu Glu Phe Phe Asn Gln Glu Met Leu Gln Ser Glu Val Pro Leu Trp
305                310                315                320
Val Glu Leu Asn Gln Lys Ser Val
                325

```

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...1130
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

```

TCAAAAATTA AAGGTTAATT TTA ATG TTG CTT TTC ACT CCA GGC CCT GTA GCC      53
              Met Leu Leu Phe Thr Pro Gly Pro Val Ala
              1              5              10

ATT AAT GAA GAG ATG CGC ACA AGC TTT TCT CAG CCA ATG CCC CAC CAC      101
Ile Asn Glu Glu Met Arg Thr Ser Phe Ser Gln Pro Met Pro His His
              15              20              25

CGC ACT AAA GAT TTT GAA AAG ATT TTC CAA AGC GTG CGA GAA AAT TTG      149
Arg Thr Lys Asp Phe Glu Lys Ile Phe Gln Ser Val Arg Glu Asn Leu
              30              35              40

AAA AAA ATG ACC GGT TTA GAA GAG GTT TTG CTT CTA AGC AGC AGC GGG      197
Lys Lys Met Thr Gly Leu Glu Glu Val Leu Leu Leu Ser Ser Ser Gly
              45              50              55

ACA GGG GCT ATG GAA GCG AGC GTG ATT TCC TTG TGT CAA AAA GAG TTG      245
Thr Gly Ala Met Glu Ala Ser Val Ile Ser Leu Cys Gln Lys Glu Leu
              60              65              70

CTT TTT GTT AAT GCG GGC AAG TTT GGC GAA AGG TTT GGC AAG ATC GCT      293
Leu Phe Val Asn Ala Gly Lys Phe Gly Glu Arg Phe Gly Lys Ile Ala
              75              80              85              90

AAA GCC CAT TCT ATC AAA GCC CAT GAA TTA GTC TAT GAA TGG GAC ACA      341
Lys Ala His Ser Ile Lys Ala His Glu Leu Val Tyr Glu Trp Asp Thr

```


AGC ATG CGA GAG AGC ATA GAG GAA TTT TTT AAT CAA GAA ATG TTG CAA 963
 Ser Met Arg Glu Ser Ile Glu Glu Phe Phe Asn Gln Glu Met Leu Gln
 300 305 310

AGT GAA GTG CCG TTA TGG GTA GAA TTG AAT CAA AAA AGC GTT TGAAAGCGC 1014
 Ser Glu Val Pro Leu Trp Val Glu Leu Asn Gln Lys Ser Val
 315 320 325

TTGTTTTTTTT AGCCAGCTTG GGGG 1038

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

Met Asp Phe Lys Asn Lys Lys Trp Leu Phe Leu Ala Pro Leu Ala Gly
 1 5 10 15
 Tyr Thr Asp Leu Pro Phe Arg Ser Val Val Lys Lys Phe Gly Val Asp
 20 25 30
 Val Thr Thr Ser Glu Met Val Ser Ser His Ser Leu Val Tyr Ala Phe
 35 40 45
 Asp Lys Thr Ser Lys Met Leu Glu Lys Ser Pro Leu Glu Asp His Phe
 50 55 60
 Met Ala Gln Ile Ser Gly Ser Lys Glu Ser Val Val Lys Glu Ala Val
 65 70 75 80
 Glu Lys Ile Asn Ala Leu Glu His Val Asn Gly Ile Asp Phe Asn Cys
 85 90 95
 Gly Cys Pro Ala Pro Lys Val Ala Asn His Gly Asn Gly Ser Gly Leu
 100 105 110
 Leu Lys Asp Leu Asn His Leu Val Lys Leu Leu Lys Thr Ile Arg Glu
 115 120 125
 Asn Thr Ser Lys Lys Ile Thr Ser Val Lys Val Arg Leu Gly Phe Glu
 130 135 140
 Lys Lys Ile Pro Lys Glu Ile Ala His Ala Leu Asn Asp Ala Pro Val
 145 150 155 160
 Asp Tyr Val Val Val His Gly Arg Thr Arg Ser Asp Lys Tyr Gln Lys
 165 170 175
 Asp Lys Ile Asp Tyr Glu Ser Ile Ala Leu Met Lys Lys Ile Leu Lys
 180 185 190
 Lys Pro Val Ile Ala Asn Gly Glu Ile Asp Ser Val Lys Lys Ala Phe
 195 200 205
 Glu Val Leu Gln Ile Thr Gln Ala Asp Gly Leu Met Ile Gly Arg Ala
 210 215 220
 Ala Leu Arg Ala Pro Trp Ile Phe Trp Gln Ile Arg Asn Asn Thr Thr
 225 230 235 240
 Lys Leu Pro Ala Val Val Lys Lys Asp Leu Val Leu Glu His Phe Asp
 245 250 255
 Lys Met Val Glu Phe Tyr Gly Asp Met Gly Val Ile Met Phe Arg Lys

GTA GTC AAA GAA GCG GTG GAG AAA ATC AAC GCT TTA GAG CAT GTG AAT	291
Val Val Lys Glu Ala Val Glu Lys Ile Asn Ala Leu Glu His Val Asn	
75 80 85 90	
GGG ATT GAT TTT AAT TGC GGT TGT CCC GCT CCT AAA GTG GCT AAT CAT	339
Gly Ile Asp Phe Asn Cys Gly Cys Pro Ala Pro Lys Val Ala Asn His	
95 100 105	
GGT AAT GGT AGT GGG TTA TTG AAG GAT TTA AAC CAC TTA GTG AAG CTT	387
Gly Asn Gly Ser Gly Leu Leu Lys Asp Leu Asn His Leu Val Lys Leu	
110 115 120	
TTA AAA ACC ATC AGA GAA AAC ACT AGT AAA AAA ATC ACA AGC GTG AAA	435
Leu Lys Thr Ile Arg Glu Asn Thr Ser Lys Lys Ile Thr Ser Val Lys	
125 130 135	
GTG CGT TTA GGC TTT GAA AAG AAA ATC CCT AAA GAA ATC GCT CAT GCC	483
Val Arg Leu Gly Phe Glu Lys Lys Ile Pro Lys Glu Ile Ala His Ala	
140 145 150	
CTA AAT GAC GCA CCG GTG GAT TAT GTG GTG GTG CAT GGG AGG ACA CGA	531
Leu Asn Asp Ala Pro Val Asp Tyr Val Val Val His Gly Arg Thr Arg	
155 160 165 170	
AGC GAT AAA TAC CAA AAA GAC AAA ATA GAT TAC GAA AGC ATC GCT TTA	579
Ser Asp Lys Tyr Gln Lys Asp Lys Ile Asp Tyr Glu Ser Ile Ala Leu	
175 180 185	
ATG AAA AAG ATT TTA AAA AAG CCG GTG ATA GCC AAT GGC GAA ATT GAC	627
Met Lys Lys Ile Leu Lys Lys Pro Val Ile Ala Asn Gly Glu Ile Asp	
190 195 200	
AGC GTG AAA AAG GCT TTT GAA GTT TTA CAA ATC ACT CAA GCG GAT GGG	675
Ser Val Lys Lys Ala Phe Glu Val Leu Gln Ile Thr Gln Ala Asp Gly	
205 210 215	
CTA ATG ATA GGG CGA GCG GCC TTA AGA GCC CCA TGG ATA TTT TGG CAA	723
Leu Met Ile Gly Arg Ala Ala Leu Arg Ala Pro Trp Ile Phe Trp Gln	
220 225 230	
ATC AGA AAC AAC ACC ACA AAA TTA CCC GCA GTC GTG AAA AAA GAC CTG	771
Ile Arg Asn Asn Thr Thr Lys Leu Pro Ala Val Val Lys Lys Asp Leu	
235 240 245 250	
GTT TTA GAA CAT TTT GAT AAA ATG GTG GAG TTT TAT GGG GAT ATG GGG	819
Val Leu Glu His Phe Asp Lys Met Val Glu Phe Tyr Gly Asp Met Gly	
255 260 265	
GTA ATC ATG TTT AGG AAA AAT TTG CAT GCT TAC GCT AAG GGC GAA ATG	867
Val Ile Met Phe Arg Lys Asn Leu His Ala Tyr Ala Lys Gly Glu Met	
270 275 280	
CAA GCG AGC GCG TTT CGT AAC TGC GTC AAT ACC CTT ACA GAA ATA AAG	915
Gln Ala Ser Ala Phe Arg Asn Cys Val Asn Thr Leu Thr Glu Ile Lys	
285 290 295	

65		70		75		80									
Lys	Ile	Leu	Arg	Lys	His	Pro	Lys	Gln	Ile	Asn	Tyr	Leu	Ala	Pro	Ser
			85					90						95	
Val	Ala	Tyr	Cys	Leu	Thr	Ile	Leu	Ala	Gly	Thr	Gly	His	Thr	Val	Phe
		100					105						110		
Ser	Leu	Ile	Pro	Val	Ile	Val	Glu	Val	Ser	Gln	Ser	Gln	Asn	Ile	Lys
		115					120					125			
Pro	Lys	Ala	Pro	Leu	Ser	Leu	Ala	Val	Val	Ser	Ser	Gln	Val	Ala	Ile
	130					135					140				
Thr	Ala	Ser	Pro	Val	Ser	Ala	Ala	Xaa	Gly	Val	Tyr	Glu	Arg	His	Phe
145				150						155					160
Arg	Ala	Phe	Arg	Ser	Lys	Leu	Leu	Asp	Pro	Phe	Asn	Gly	Leu	Asp	Pro
			165					170					175		
Tyr	Asp	Phe	Phe	Ser	Met	His	Ala	His	Gly	Ile	Tyr	Tyr	Gly	Phe	Tyr
		180						185					190		

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1005
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

AAAAC	TTTGA	TATGAGAATA	A	ATG	GAC	TTT	AAA	AAT	AAA	AAA	TGG	CTT	TTT		51	
				Met	Asp	Phe	Lys	Asn	Lys	Lys	Trp	Leu	Phe			
				1				5					10			
CTA	GCC	CCT	TTA	GCA	GGC	TAT	ACG	GAT	TTG	CCT	TTC	AGG	AGC	GTG	GTG	99
Leu	Ala	Pro	Leu	Ala	Gly	Tyr	Thr	Asp	Leu	Pro	Phe	Arg	Ser	Val	Val	
			15					20					25			
AAA	AAA	TTT	GGC	GTG	GAT	GTT	ACC	ACG	AGC	GAA	ATG	GTG	AGC	TCG	CAT	147
Lys	Lys	Phe	Gly	Val	Asp	Val	Thr	Thr	Ser	Glu	Met	Val	Ser	Ser	His	
			30					35					40			
TCG	TTG	GTG	TAT	GCG	TTT	GAT	AAA	ACT	TCT	AAA	ATG	TTG	GAA	AAA	TCC	195
Ser	Leu	Val	Tyr	Ala	Phe	Asp	Lys	Thr	Ser	Lys	Met	Leu	Glu	Lys	Ser	
		45					50					55				
CCT	TTA	GAA	GAT	CAT	TTC	ATG	GCG	CAA	ATT	TCA	GGC	TCT	AAA	GAA	AGC	243
Pro	Leu	Glu	Asp	His	Phe	Met	Ala	Gln	Ile	Ser	Gly	Ser	Lys	Glu	Ser	
		60				65					70					

GGC TTG GAT TAC TTA GTC AAA ATC GCT GAA AAA ATT TTA AGG AAA CAC 294
 Gly Leu Asp Tyr Leu Val Lys Ile Ala Glu Lys Ile Leu Arg Lys His
 75 80 85

CCC AAG CAA ATC AAT TAC CTT GCG CCA AGC GTG GCG TAT TGT TTA ACG 342
 Pro Lys Gln Ile Asn Tyr Leu Ala Pro Ser Val Ala Tyr Cys Leu Thr
 90 95 100

ATA CTA GCC GGC ACC GGG CAT ACG GTT TTT TCC TTG ATC CCG GTG ATT 390
 Ile Leu Ala Gly Thr Gly His Thr Val Phe Ser Leu Ile Pro Val Ile
 105 110 115

GTG GAA GTG AGC CAG AGC CAA AAC ATC AAG CCT AAA GCG CCT TTA AGC 438
 Val Glu Val Ser Gln Ser Gln Asn Ile Lys Pro Lys Ala Pro Leu Ser
 120 125 130

TTA GCG GTA GTC TCT AGT CAA GTC GCT ATT ACT GCA AGC CCG GTG AGC 486
 Leu Ala Val Val Ser Ser Gln Val Ala Ile Thr Ala Ser Pro Val Ser
 135 140 145 150

GCA GCG GTN GGT GTT TAT GAG CGG CAT TTT AGA GCC TTT AGG AGC AAA 534
 Ala Ala Xaa Gly Val Tyr Glu Arg His Phe Arg Ala Phe Arg Ser Lys
 155 160 165

TTA CTT GAC CCT TTT AAT GGT TTG GAT CCC TAC GAC TTT TTT AGC ATG 582
 Leu Leu Asp Pro Phe Asn Gly Leu Asp Pro Tyr Asp Phe Phe Ser Met
 170 175 180

CAT GCT CAC GGC ATT TAT TAT GGG TTT TAC TGATTTGAAA TTAGACAGCG ATC 635
 His Ala His Gly Ile Tyr Tyr Gly Phe Tyr
 185 190

CGCATTATTT AGAGCGCTTG AAAGCGGGCA AAATCTCGCC CCC 678

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

Met Val Asp Ala Phe Phe Gln Ile Ala Val Leu Leu Phe Ser Leu Phe
 1 5 10 15
 Leu Gly Ala Arg Leu Gly Gly Leu Gly Val Gly Tyr Ala Gly Gly Leu
 20 25 30
 Gly Val Leu Ile Leu Cys Leu Phe Leu Gly Leu Asn Pro Gly Lys Ile
 35 40 45
 Pro Phe Asp Val Ile Leu Ile Ile Met Ala Val Ile Ser Ala Ile Ser
 50 55 60
 Ala Met Gln Lys Ala Gly Gly Leu Asp Tyr Leu Val Lys Ile Ala Glu

```

Ser Glu Phe Ser Leu Ser Gln Leu Lys Thr Pro Leu Pro Lys Val Asp
                245                250                255
Ile Ile Tyr Thr His Ala Gly Met Thr Pro Asp Leu Phe Gln Ala Ser
                260                265                270
Leu Asn Ser His Ala Lys Gly Val Val Ile Ala Gly Val Gly Asn Gly
                275                280                285
Asn Val Ser Ala Gly Phe Leu Lys Ala Met Gln Glu Ala Ser Gln Met
                290                295                300
Gly Val Val Ile Val Arg Ser Ser Arg Val Asn Ser Gly Glu Ile Thr
305                310                315                320
Ser Gly Glu Ile Asp Asp Lys Ala Phe Ile Thr Ser Asp Asn Leu Asn
                325                330                335
Pro Gln Lys Ala Arg Val Leu Leu Gln Leu Ala Leu Thr Lys Thr Asn
                340                345                350
Asn Lys Glu Lys Ile Gln Glu Met Phe Glu Glu Tyr
355                360

```

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...612
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

```

AGTAAAACAT CGTTAAATA AATTTAAAAA GGGTTA ATG GTG GAT GCC TTT TTC      54
                Met Val Asp Ala Phe Phe
                1                5

CAA ATT GCA GTG TTA CTT TTT TCG CTT TTT TTA GGG GCA AGG CTA GGG      102
Gln Ile Ala Val Leu Leu Phe Ser Leu Phe Leu Gly Ala Arg Leu Gly
                10                15                20

GGC TTG GGA GTG GGC TAT GCG GGG GGC TTG GGC GTG CTT ATT TTA TGC      150
Gly Leu Gly Val Gly Tyr Ala Gly Gly Leu Gly Val Leu Ile Leu Cys
                25                30                35

TTA TTT TTG GGG CTA AAT CCG GGC AAA ATC CCT TTT GAT GTG ATT TTA      198
Leu Phe Leu Gly Leu Asn Pro Gly Lys Ile Pro Phe Asp Val Ile Leu
                40                45                50

ATC ATC ATG GCA GTC ATT AGC GCT ATT AGC GCG ATG CAA AAA GCG GGG      246
Ile Ile Met Ala Val Ile Ser Ala Ile Ser Ala Met Gln Lys Ala Gly
55                60                65                70

```

Asp Lys Ala Phe Ile Thr Ser Asp Asn Leu Asn Pro Gln Lys Ala Arg
 330 335 340

GTG CTT TTA CAA CTC GCT TTA ACT AAA ACA AAT AAT AAA GAA AAA ATC 1111
 Val Leu Leu Gln Leu Ala Leu Thr Lys Thr Asn Asn Lys Glu Lys Ile
 345 350 355

CAA GAA ATG TTT GAA GAG TAT TGAAAGATTC TCTTAAATCA CCCAATTATC AAAG 1166
 Gln Glu Met Phe Glu Glu Tyr
 360

ATAATTGGGT GATTGTGGTTT ATTTTGTTTT 1196

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

Met Phe Tyr Tyr Thr Ile Lys Ser Phe Asn Phe Lys Arg Trp Ser Ile
 1 5 10 15

Met Arg Ile Phe Leu Lys Leu Leu Ile Leu Leu Phe Cys Leu Lys Gly
 20 25 30

Gln Val Met Ala Gln Asn Leu Pro Thr Ile Ala Leu Leu Ala Thr Gly
 35 40 45

Gly Thr Ile Ala Gly Ser Gly Ala Ser Ala Ser Leu Gly Ser Tyr Lys
 50 55 60

Ser Gly Glu Leu Gly Ile Lys Glu Leu Leu Lys Ala Ile Pro Ser Leu
 65 70 75 80

Asn Arg Leu Ala Arg Ile Gln Gly Glu Gln Ile Ser Asn Ile Gly Ser
 85 90 95

Gln Asp Met Asn Glu Glu Val Trp Phe Lys Leu Ala Lys Arg Ala Gln
 100 105 110

Glu Leu Leu Asp Asp Ser Arg Ile Gln Gly Val Val Ile Thr His Gly
 115 120 125

Thr Asp Thr Leu Glu Glu Ser Ala Tyr Phe Leu Asn Leu Val Leu Arg
 130 135 140

Ser Thr Lys Pro Val Val Leu Val Gly Ala Met Arg Asn Ala Ala Ser
 145 150 155 160

Leu Ser Ala Asp Gly Ala Leu Asn Leu Tyr Asn Ala Val Ser Val Ala
 165 170 175

Leu Asn Glu Lys Ser Ala Asn Lys Gly Val Leu Val Val Met Asp Asp
 180 185 190

Asn Ile Phe Ser Ala Arg Glu Val Ile Lys Thr His Thr His Thr
 195 200 205

Ser Thr Phe Lys Ala Leu Asn Ser Gly Ala Ile Gly Ser Val Tyr Tyr
 210 215 220

Gly Lys Thr Arg Tyr Tyr Met Gln Pro Leu Arg Lys His Thr Thr Glu
 225 230 235 240

105	110	115	
AGC CGT ATT CAA GGC GTG GTC ATC ACG CAT GGC ACG GAC ACT TTA GAA			439
Ser Arg Ile Gln Gly Val Val Ile Thr His Gly Thr Asp Thr Leu Glu			
120	125	130	
GAG AGC GCG TAT TTT TTA AAC TTA GTT TTA CGC TCC ACA AAA CCG GTC			487
Glu Ser Ala Tyr Phe Leu Asn Leu Val Leu Arg Ser Thr Lys Pro Val			
135	140	145	
GTG CTG GTG GGA GCG ATG CGT AAT GCT GCT TCT TTG AGC GCG GAT GGG			535
Val Leu Val Gly Ala Met Arg Asn Ala Ala Ser Leu Ser Ala Asp Gly			
150	155	160	165
GCT TTG AAT TTA TAT AAT GCT GTG AGC GTA GCG CTC AAT GAA AAA AGT			583
Ala Leu Asn Leu Tyr Asn Ala Val Ser Val Ala Leu Asn Glu Lys Ser			
170	175	180	
GCG AAT AAA GGC GTG TTA GTG GTG ATG GAC GAT AAT ATT TTT AGC GCT			631
Ala Asn Lys Gly Val Leu Val Val Met Asp Asp Asn Ile Phe Ser Ala			
185	190	195	
AGA GAA GTG ATT AAA ACG CAC ACC ACC CAC ACT TCC ACC TTT AAA GCC			679
Arg Glu Val Ile Lys Thr His Thr Thr His Thr Ser Thr Phe Lys Ala			
200	205	210	
TTA AAT AGC GGC GCG ATA GGG AGC GTG TAT TAT GGC AAA ACG CGC TAT			727
Leu Asn Ser Gly Ala Ile Gly Ser Val Tyr Tyr Gly Lys Thr Arg Tyr			
215	220	225	
TAC ATG CAG CCT TTG AGA AAA CAC ACC ACA GAG AGC GAA TTT TCC CTT			775
Tyr Met Gln Pro Leu Arg Lys His Thr Thr Glu Ser Glu Phe Ser Leu			
230	235	240	245
TCA CAA CTC AAA ACC CCC CTG CCT AAA GTG GAT ATT ATT TAC ACG CAT			823
Ser Gln Leu Lys Thr Pro Leu Pro Lys Val Asp Ile Ile Tyr Thr His			
250	255	260	
GCT GGC ATG ACC CCT GAT TTA TTC CAA GCG AGC CTA AAC TCG CAT GCA			871
Ala Gly Met Thr Pro Asp Leu Phe Gln Ala Ser Leu Asn Ser His Ala			
265	270	275	
AAA GGC GTT GTG ATA GCC GGG GTG GGT AAT GGG AAT GTG AGC GCT GGG			919
Lys Gly Val Val Ile Ala Gly Val Gly Asn Gly Asn Val Ser Ala Gly			
280	285	290	
TTT TTA AAA GCG ATG CAA GAA GCG AGC CAA ATG GGG GTG GTT ATT GTT			967
Phe Leu Lys Ala Met Gln Glu Ala Ser Gln Met Gly Val Val Ile Val			
295	300	305	
CGT TCT AGC AGG GTA AAT AGC GGT GAG ATT ACT TCA GGC GAG ATT GAT			1015
Arg Ser Ser Arg Val Asn Ser Gly Glu Ile Thr Ser Gly Glu Ile Asp			
310	315	320	325
GAC AAG GCC TTC ATC ACA AGC GAC AAT TTA AAC CCC CAA AAA GCT AGG			1063

130	135	140
Leu Pro Ser Asp Pro Ala Glu Ile Arg Ala Glu Phe Leu Ser Val Leu		
145	150	155
Ser Val		160

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 41...1132
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

AAGGCATCCA CCATTAACCC TTTTAAATT TATTTTAACG	ATG TTT TAC TAT ACT	55
	Met Phe Tyr Tyr Thr	
	1 5	
ATA AAA TCT TTT AAT TTC AAA AGG TGG TCC ATA ATG AGA ATA TTT TTG		103
Ile Lys Ser Phe Asn Phe Lys Arg Trp Ser Ile Met Arg Ile Phe Leu		
10 15 20		
AAA TTG TTG ATT CTT TTA TTT TGT TTG AAG GGG CAG GTT ATG GCT CAA		151
Lys Leu Leu Ile Leu Leu Phe Cys Leu Lys Gly Gln Val Met Ala Gln		
25 30 35		
AAT TTA CCC ACC ATT GCT TTA CTG GCG ACA GGG GGG ACG ATT GCA GGG		199
Asn Leu Pro Thr Ile Ala Leu Leu Ala Thr Gly Gly Thr Ile Ala Gly		
40 45 50		
AGT GGT GCG AGC GCG AGT TTG GGT AGT TAT AAG AGT GGT GAG TTG GGC		247
Ser Gly Ala Ser Ala Ser Leu Gly Ser Tyr Lys Ser Gly Glu Leu Gly		
55 60 65		
ATC AAA GAG CTT TTG AAG GCT ATC CCT AGT CTT AAC AGA CTC GCT CGC		295
Ile Lys Glu Leu Leu Lys Ala Ile Pro Ser Leu Asn Arg Leu Ala Arg		
70 75 80 85		
ATT CAA GGG GAG CAG ATT TCT AAC ATC GGC TCA CAA GAC ATG AAT GAA		343
Ile Gln Gly Glu Gln Ile Ser Asn Ile Gly Ser Gln Asp Met Asn Glu		
90 95 100		
GAG GTA TGG TTC AAG CTC GCC AAA CGT GCC CAA GAA TTG CTA GAT GAT		391
Glu Val Trp Phe Lys Leu Ala Lys Arg Ala Gln Glu Leu Leu Asp Asp		


```

TTT TAT CCT TTT AAA TTA AAT TTA TCT CAC TTA GGA GAG CAA TGC TCG      294
Phe Tyr Pro Phe Lys Leu Asn Leu Ser His Leu Gly Glu Gln Cys Ser
              75                      80                      85

TCT TTT TTC TTA ACA GCC CTA CAC CAA ACT TTT CTC GTA TCG CCG CTG      342
Ser Phe Phe Leu Thr Ala Leu His Gln Thr Phe Leu Val Ser Pro Leu
              90                      95                      100

CAA ACG CTC ACA TTA AGT CCT TTT GCC TTG ATT TCT TCA TCG CTC AAA      390
Gln Thr Leu Thr Leu Ser Pro Phe Ala Leu Ile Ser Ser Ser Leu Lys
              105                      110                      115

CCT TTG GTT TTT TCT TCT AAT TCT TTA CGC ACT TCT TCA CGC ATT TTT      438
Pro Leu Val Phe Ser Ser Asn Ser Leu Arg Thr Ser Ser Arg Ile Phe
              120                      125                      130

TTG AAA TCC TTC GCT CAT TTT GGA AAG ATT CTT CCT AGC GAT CCG GCT      486
Leu Lys Ser Phe Ala His Phe Gly Lys Ile Leu Pro Ser Asp Pro Ala
              135                      140                      145                      150

GAA ATT CGC GCG GAA TTT CTT AGC GTC CTC AGC GTT TAAAGTTTTA AGGCGT      538
Glu Ile Arg Ala Glu Phe Leu Ser Val Leu Ser Val
              155                      160

TTAGACACTT CCATGCGATA AT                                          560

```

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

```

Met Gln Leu Leu Met Glu Arg Leu Ser Leu Val Phe Arg His Leu Phe
 1          5          10          15
His Ala Leu Phe Gln Leu Phe Cys Val Ile His Asn Ile Leu Arg Xaa
          20          25          30
Thr Thr Pro Ala Ile Leu Ala Lys Ser Ser Ser Leu Val Leu Leu Lys
          35          40          45
Ser Leu Ala Phe Lys Ala Thr Asn Ser Asn Ala Leu Thr Glu Ser Ile
          50          55          60
Phe Asn Ala Phe Phe Ile Phe Tyr Pro Phe Lys Leu Asn Leu Ser His
65          70          75          80
Leu Gly Glu Gln Cys Ser Ser Phe Phe Leu Thr Ala Leu His Gln Thr
          85          90          95
Phe Leu Val Ser Pro Leu Gln Thr Leu Thr Leu Ser Pro Phe Ala Leu
          100          105          110
Ile Ser Ser Ser Leu Lys Pro Leu Val Phe Ser Ser Asn Ser Leu Arg
          115          120          125
Thr Ser Ser Arg Ile Phe Leu Lys Ser Phe Ala His Phe Gly Lys Ile

```

BNSDOCID: <WO 9843478A1 | >

CCT TAT AGC ACC AAA ACT TCA ACC GTC GCT TTT CAG GTA TGG TTG AAT	675
Pro Tyr Ser Thr Lys Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn	
205 210 215	
TTT GGG GTG AGA GCC AAT ATT TAC AAG CAT AAT GGC GTA GAG TTT GGC	723
Phe Gly Val Arg Ala Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly	
220 225 230 235	
GTG AGA GTG CCG CTA CTC ATC AAC AAG TTT TTG AGT GCG GGT CCT AAC	771
Val Arg Val Pro Leu Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn	
240 245 250	
GCT ACT AAT CTT TAT TAC CAT TTG AAA CGG GAT TAT TCG CTT TAT TTA	819
Ala Thr Asn Leu Tyr Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu	
255 260 265	
GGG TAT AAC TAC ACT TTT TAAACCCTTT AAAAGGGTGT CTTTAAGCCC TTTT TAGT	875
Gly Tyr Asn Tyr Thr Phe	
270	
CCTTATAAAA AGG	888

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

Met	Glu	Phe	Met	Lys	Lys	Phe	Val	Ala	Leu	Gly	Leu	Leu	Ser	Ala	Val
1				5					10					15	
Leu	Ser	Ser	Ser	Leu	Leu	Ala	Glu	Gly	Asp	Gly	Val	Tyr	Ile	Gly	Thr
			20					25					30		
Asn	Tyr	Gln	Leu	Gly	Gln	Ala	Arg	Leu	Asn	Ser	Asn	Ile	Tyr	Asn	Thr
		35					40					45			
Gly	Asp	Cys	Thr	Gly	Ser	Val	Val	Gly	Cys	Pro	Pro	Gly	Leu	Thr	Ala
	50					55				60					
Asn	Lys	His	Asn	Pro	Gly	Gly	Thr	Asn	Ile	Asn	Trp	His	Ala	Lys	Tyr
	65				70				75					80	
Ala	Asn	Gly	Ala	Leu	Asn	Gly	Leu	Gly	Leu	Asn	Val	Gly	Tyr	Lys	Lys
			85					90					95		
Phe	Phe	Gln	Phe	Lys	Ser	Phe	Asp	Met	Thr	Ser	Lys	Trp	Phe	Gly	Phe
		100					105					110			
Arg	Val	Tyr	Gly	Leu	Phe	Asp	Tyr	Gly	His	Ala	Thr	Leu	Gly	Lys	Gln
		115				120					125				
Val	Tyr	Ala	Pro	Asn	Lys	Ile	Gln	Leu	Asp	Met	Val	Ser	Trp	Gly	Val
	130				135						140				
Gly	Ser	Asp	Leu	Leu	Ala	Asp	Ile	Ile	Asp	Asn	Asp	Asn	Ala	Ser	Phe
	145				150				155					160	
Gly	Ile	Phe	Gly	Gly	Val	Ala	Ile	Gly	Gly	Asn	Thr	Trp	Lys	Ser	Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

AGATAGGAAT GTAAAGGA ATG GAA TTT ATG AAA AAG TTT GTA GCT TTA GGG	51
Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly	
1 5 10	
CTT CTA TCC GCA GTT TTA AGC TCT TCG TTG TTA GCC GAA GGT GAT GGT	99
Leu Leu Ser Ala Val Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly	
15 20 25	
GTT TAT ATA GGG ACT AAT TAT CAG CTT GGA CAA GCC CGT TTG AAT AGT	147
Val Tyr Ile Gly Thr Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser	
30 35 40	
AAT ATT TAT AAT ACA GGG GAT TGC ACA GGG AGT GTT GTA GGT TGC CCC	195
Asn Ile Tyr Asn Thr Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro	
45 50 55	
CCA GGT CTT ACC GCT AAT AAG CAT AAT CCA GGA GGC ACC AAT ATC AAT	243
Pro Gly Leu Thr Ala Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn	
60 65 70 75	
TGG CAT GCT AAA TAC GCT AAT GGG GCT TTG AAT GGT CTT GGG TTG AAT	291
Trp His Ala Lys Tyr Ala Asn Gly Ala Leu Asn Gly Leu Gly Leu Asn	
80 85 90	
GTG GGT TAT AAG AAG TTC TTC CAG TTC AAG TCT TTT GAT ATG ACA AGC	339
Val Gly Tyr Lys Lys Phe Phe Gln Phe Lys Ser Phe Asp Met Thr Ser	
95 100 105	
AAG TGG TTT GGT TTT AGA GTG TAT GGG CTT TTT GAT TAT GGG CAT GCC	387
Lys Trp Phe Gly Phe Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala	
110 115 120	
ACT TTA GGC AAG CAA GTT TAT GCA CCT AAT AAA ATC CAG TTG GAT ATG	435
Thr Leu Gly Lys Gln Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met	
125 130 135	
GTC TCT TGG GGT GTG GGG AGC GAT TTG TTA GCT GAT ATT ATT GAT AAC	483
Val Ser Trp Gly Val Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Asn	
140 145 150 155	
GAT AAC GCT TCT TTT GGT ATT TTT GGT GGG GTC GCT ATC GGC GGT AAC	531
Asp Asn Ala Ser Phe Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn	
160 165 170	
ACT TGG AAA AGC TCA GCG GCA AAC TAT TGG AAA GAG CAA ATC ATT GAA	579
Thr Trp Lys Ser Ser Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu	
175 180 185	
GCT AAG GGT CCT GAT GTT TGT ACC CCT ACT TAT TGT AAC CCT AAC GCT	627
Ala Lys Gly Pro Asp Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala	
190 195 200	

450		455		460
Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Asn Asn Lys Glu Pro Glu				
465		470		475
Lys His Asp Phe Ser Val Trp Asn Ile Thr Lys Lys Arg Gln Asn Glu				480
	485		490	495
Trp Ser Pro Ala Leu Asn Ile Gly Tyr Lys Pro Met Glu Asn Trp Ile				
	500		505	510
Trp Tyr Ala Asn Tyr Arg Arg Ser Phe Ile Pro Pro Gln His Thr Met				
	515		520	525
Leu Gly Ile Thr Arg Thr Asn Tyr Asn Gln Ile Phe Asn Glu Ile Glu				
	530		535	540
Val Gly Gln Arg Tyr Ser Tyr Lys Asn Leu Leu Ser Phe Asn Thr Asn				
545		550		555
Tyr Phe Val Ile Phe Ala Lys Arg Tyr Tyr Ala Gly Gly Tyr Ser Pro				560
	565		570	575
Gln Pro Ile Asn Ala Arg Ser Gln Gly Val Glu Leu Glu Leu Tyr Tyr				
	580		585	590
Ala Pro Ile Arg Gly Leu Gln Phe His Val Ala Tyr Thr Tyr Ile Asp				
	595		600	605
Ala Arg Ile Thr Ser Asn Ala Asp Asp Ile Ala Tyr Tyr Phe Thr Gly				
	610		615	620
Ile Val Asn Lys Pro Phe Asp Ile Lys Gly Lys Arg Leu Pro Tyr Val				
625		630		635
Ser Pro Asn Gln Phe Ile Phe Asp Met Met Tyr Thr Tyr Lys His Thr				
	645		650	655
Thr Phe Gly Ile Ser Ser Tyr Phe Tyr Ser Arg Ala Tyr Ser Ser Met				
	660		665	670
Leu Asn Gln Ala Lys Ser Gln Thr Val Cys Leu Pro Leu Asn Pro Glu				
	675		680	685
Tyr Thr Gly Gly Leu Glu Tyr Gly Cys Asn Ser Val Gly Leu Leu Pro				
	690		695	700
Leu Tyr Phe Val Leu Asn Val Gln Val Ser Ser Val Leu Trp Gln Ser				
705		710		715
Gly Arg His Lys Ile Thr Gly Ser Leu Gln Ile Asn Asn Leu Phe Asn				
	725		730	735
Met Lys Tyr Tyr Phe Arg Gly Ile Gly Thr Ser Pro Thr Gly Arg Glu				
	740		745	750
Pro Ala Pro Gly Arg Ser Ile Thr Ala Tyr Leu Asn Tyr Glu Phe				
	755		760	765

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...837
- (D) OTHER INFORMATION:

Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
 20 25 30
 Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
 35 40 45
 Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
 50 55 60
 Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His
 65 70 75 80
 Ile Arg Asn Ala Thr Gly Ile Gly Ala Val Pro Ser Phe Ser Val Arg
 85 90 95
 Gly Phe Gly Gly Gly Ser Ser Gly His Ser Asn Thr Ala Met Val Leu
 100 105 110
 Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Asp Ile Ser Ile
 115 120 125
 Pro Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
 130 135 140
 Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Val Phe Gly Gly Val
 145 150 155 160
 Ile Asn Val Ile Thr Lys Gly Ile Pro Thr Lys Trp Glu Ser Gln Val
 165 170 175
 Ser Glu Arg Ala Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
 180 185 190
 Asn Gln Asn Ser Lys Asn Leu Asp Lys Ser Leu Ala Asn Asn Met Leu
 195 200 205
 Phe Asp Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
 210 215 220
 Ile Gln Ala Gln Ala Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
 225 230 235 240
 Ser Pro Thr Asn Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
 245 250 255
 Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Asn Tyr Phe
 260 265 270
 Met Ala Asp Pro Gly Ser Leu Gly Ile Glu Ala Tyr Asn Gln Asn Arg
 275 280 285
 Phe Gln Asn Asn Arg Pro Asn Asn Asn Lys Ser Gly Arg Ala Lys Xaa
 290 295 300
 Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Lys Ile Gly
 305 310 315 320
 Gly Asp Phe Thr Phe Ser Tyr Tyr Gly His Asp Met Ser Arg Asp Phe
 325 330 335
 Gln Phe Asp Ser Asn Phe Leu Asn Val Asn Thr Asn Pro Lys Leu Gly
 340 345 350
 Pro Val Tyr Thr Asp Gln Asn Tyr Pro Gly Phe Phe Ile Phe Asp His
 355 360 365
 Leu Arg Arg Tyr Ile Met Asn Ala Phe Glu Pro Asn Leu Asn Leu Val
 370 375 380
 Val Asn Thr Asn Lys Val Lys Gln Thr Phe Asn Val Gly Met Arg Phe
 385 390 395 400
 Met Thr Met Asp Met Tyr Phe Arg Leu Asp Gln Ser Thr Cys Glu Lys
 405 410 415
 Thr Asp Ile Phe Asn Gly Val Cys Arg Met Pro Pro Phe Val Leu Ser
 420 425 430
 Lys Lys Pro Ser Asn Asn Gln Asn Leu Phe Asn Asn Tyr Thr Ala Val
 435 440 445
 Trp Leu Ser Asp Lys Ile Glu Leu Phe Asp Ser Lys Leu Val Ile Thr

TTT ACA GGC ATT GTC AAT AAA CCC TTT GAC ATT AAA GGG AAG CGT TTG	1923
Phe Thr Gly Ile Val Asn Lys Pro Phe Asp Ile Lys Gly Lys Arg Leu	
625 630 635	
CCT TAT GTG AGT CCT AAC CAA TTC ATA TTT GAC ATG ATG TAT ACT TAC	1971
Pro Tyr Val Ser Pro Asn Gln Phe Ile Phe Asp Met Met Tyr Thr Tyr	
640 645 650	
AAG CAC ACG ACT TTT GGT ATT AGC AGC TAT TTT TAT AGC CGT GCT TAT	2019
Lys His Thr Thr Phe Gly Ile Ser Ser Tyr Phe Tyr Ser Arg Ala Tyr	
655 660 665	
AGT TCT ATG CTC AAT CAG GCC AAA AGC CAA ACC GTG TGC CTG CCC TTA	2067
Ser Ser Met Leu Asn Gln Ala Lys Ser Gln Thr Val Cys Leu Pro Leu	
670 675 680 685	
AAC CCA GAA TAC ACA GGG GGG CTA GAG TAT GGT TGT AAT TCA GTA GGG	2115
Asn Pro Glu Tyr Thr Gly Gly Leu Glu Tyr Gly Cys Asn Ser Val Gly	
690 695 700	
TTA TTG CCC TTG TAT TTT GTG TTG AAC GTT CAA GTA AGC TCG GTT TTA	2163
Leu Leu Pro Leu Tyr Phe Val Leu Asn Val Gln Val Ser Ser Val Leu	
705 710 715	
TGG CAA AGC GGT AGG CAT AAA ATC ACA GGG AGT TTG CAA ATC AAT AAT	2211
Trp Gln Ser Gly Arg His Lys Ile Thr Gly Ser Leu Gln Ile Asn Asn	
720 725 730	
CTT TTT AAC ATG AAG TAT TAT TTT AGG GGA ATT GGC ACA AGC CCT ACA	2259
Leu Phe Asn Met Lys Tyr Tyr Phe Arg Gly Ile Gly Thr Ser Pro Thr	
735 740 745	
GGA AGA GAG CCC GCA CCA GGG CGA TCC ATT ACA GCG TAT TTG AAT TAT	2307
Gly Arg Glu Pro Ala Pro Gly Arg Ser Ile Thr Ala Tyr Leu Asn Tyr	
750 755 760 765	
GAG TTT TAAACTAGCT TCAAGCTTTT ATCGCTTGAA TGCTTGTTA	2352
Glu Phe	

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

Met	Lys	Arg	Ile	Leu	Val	Ser	Leu	Ala	Val	Leu	Ser	His	Ser	Ala	His
1				5				10						15	

ATG CGT TTT ATG ACA ATG GAT ATG TAT TTC AGA TTG GAT CAA AGC ACA	1251
Met Arg Phe Met Thr Met Asp Met Tyr Phe Arg Leu Asp Gln Ser Thr	
400 405 410	
TGC GAA AAA ACC GAT ATT TTT AAT GGG GTG TGC CGC ATG CCT CCT TTT	1299
Cys Glu Lys Thr Asp Ile Phe Asn Gly Val Cys Arg Met Pro Pro Phe	
415 420 425	
GTT CTT TCT AAA AAA CCC AGC AAC AAT CAA AAC CTG TTT AAC AAC TAT	1347
Val Leu Ser Lys Lys Pro Ser Asn Asn Gln Asn Leu Phe Asn Asn Tyr	
430 435 440 445	
ACA GCG GTA TGG TTG AGC GAT AAA ATA GAG CTT TTT GAT TCT AAA TTG	1395
Thr Ala Val Trp Leu Ser Asp Lys Ile Glu Leu Phe Asp Ser Lys Leu	
450 455 460	
GTG ATA ACT CCA GGG CTT AGA TAC ACT TTT TTG AAC TAT AAC AAC AAA	1443
Val Ile Thr Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Asn Asn Lys	
465 470 475	
GAG CCA GAA AAG CAT GAT TTT TCT GTG TGG AAT ATT ACA AAA AAG CGT	1491
Glu Pro Glu Lys His Asp Phe Ser Val Trp Asn Ile Thr Lys Lys Arg	
480 485 490	
CAA AAC GAA TGG AGT CCC GCC CTT AAC ATT GGC TAT AAA CCT ATG GAA	1539
Gln Asn Glu Trp Ser Pro Ala Leu Asn Ile Gly Tyr Lys Pro Met Glu	
495 500 505	
AAT TGG ATA TGG TAT GCG AAC TAC CGC CGC AGT TTT ATC CCC CCA CAA	1587
Asn Trp Ile Trp Tyr Ala Asn Tyr Arg Arg Ser Phe Ile Pro Pro Gln	
510 515 520 525	
CAT ACA ATG CTA GGC ATT ACT AGG ACT AAT TAC AAC CAA ATT TTT AAT	1635
His Thr Met Leu Gly Ile Thr Arg Thr Asn Tyr Asn Gln Ile Phe Asn	
530 535 540	
GAA ATT GAA GTG GGG CAA CGC TAT AGT TAT AAA AAT CTA TTG AGC TTT	1683
Glu Ile Glu Val Gly Gln Arg Tyr Ser Tyr Lys Asn Leu Leu Ser Phe	
545 550 555	
AAC ACG AAT TAT TTT GTG ATT TTT GCC AAG CGT TAC TAT GCG GGA GGC	1731
Asn Thr Asn Tyr Phe Val Ile Phe Ala Lys Arg Tyr Tyr Ala Gly Gly	
560 565 570	
TAT AGC CCA CAG CCT ATT AAC GCT AGG AGT CAA GGG GTA GAA TTG GAA	1779
Tyr Ser Pro Gln Pro Ile Asn Ala Arg Ser Gln Gly Val Glu Leu Glu	
575 580 585	
TTG TAT TAC GCG CCG ATT AGG GGT TTG CAA TTC CAT GTG GCT TAC ACC	1827
Leu Tyr Tyr Ala Pro Ile Arg Gly Leu Gln Phe His Val Ala Tyr Thr	
590 595 600 605	
TAT ATT GAT GCA CGC ATC ACT TCT AAC GCT GAT GAT ATT GCT TAT TAT	1875
Tyr Ile Asp Ala Arg Ile Thr Ser Asn Ala Asp Asp Ile Ala Tyr Tyr	
610 615 620	

AGT CAG GTG AGC GAG AGG GCC ACT TTT TGG GGC AAA TCT GAA AAT GGG Ser Gln Val Ser Glu Arg Ala Thr Phe Trp Gly Lys Ser Glu Asn Gly 175 180 185	579
GGC TTT TTC AAT CAA AAT TCT AAA AAC CTT GAC AAA AGC TTA GCC AAT Gly Phe Phe Asn Gln Asn Ser Lys Asn Leu Asp Lys Ser Leu Ala Asn 190 195 200 205	627
AAC ATG CTT TTT GAC ACT TAC TTA AGA ACA GGG GGC ATG ATG AAT AAG Asn Met Leu Phe Asp Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys 210 215 220	675
CAT TTT GGA ATC CAA GCT CAA GCC AAC TGG CTT AAA GGG CAA GGG TTT His Phe Gly Ile Gln Ala Gln Ala Asn Trp Leu Lys Gly Gln Gly Phe 225 230 235	723
AGA TAC AAC AGC CCT ACG AAC ATT CAA AAC TAC ATG CTA GAT TCC TTG Arg Tyr Asn Ser Pro Thr Asn Ile Gln Asn Tyr Met Leu Asp Ser Leu 240 245 250	771
TAT CAA ATT AAT GAT AGT AAT AAG ATC ACT GCT TTT TTC CAA TAC TAT Tyr Gln Ile Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr 255 260 265	819
AAT TAT TTT ATG GCA GAC CCC GGA TCT TTA GGC ATA GAA GCG TAT AAT Asn Tyr Phe Met Ala Asp Pro Gly Ser Leu Gly Ile Glu Ala Tyr Asn 270 275 280 285	867
CAA AAT CGT TTT CAA AAC AAC CGC CCT AAT AAC AAT AAA AGC GGG AGA Gln Asn Arg Phe Gln Asn Asn Arg Pro Asn Asn Asn Lys Ser Gly Arg 290 295 300	915
GCG AAG CGR TGG GGA GCT GTG TAT CAA AAC TTT TTT GGG GAT ACG GAC Ala Lys Xaa Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp 305 310 315	963
AAA ATA GGT GGG GAT TTC ACT TTT AGT TAC TAT GGG CAT GAC ATG TCA Lys Ile Gly Gly Asp Phe Thr Phe Ser Tyr Tyr Gly His Asp Met Ser 320 325 330	1011
AGG GAT TTT CAA TTT GAT TCT AAT TTT TTG AAT GTC AAT ACC AAT CCT Arg Asp Phe Gln Phe Asp Ser Asn Phe Leu Asn Val Asn Thr Asn Pro 335 340 345	1059
AAA TTA GGC CCT GTT TAT ACC GAT CAA AAT TAT CCA GGA TTT TTT ATT Lys Leu Gly Pro Val Tyr Thr Asp Gln Asn Tyr Pro Gly Phe Phe Ile 350 355 360 365	1107
TTT GAT CAT TTA AGG CGT TAC ATA ATG AAC GCT TTT GAG CCT AAT TTG Phe Asp His Leu Arg Arg Tyr Ile Met Asn Ala Phe Glu Pro Asn Leu 370 375 380	1155
AAC TTA GTT GTC AAT ACC AAT AAA GTT AAG CAA ACT TTT AAT GTG GGC Asn Leu Val Val Asn Thr Asn Lys Val Lys Gln Thr Phe Asn Val Gly 385 390 395	1203

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 13...2313

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

AAAAGGTGGT AA ATG AAA AGA ATT TTA GTC TCT TTG GCT GTT TTG AGT CAT	51
Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His	
1 5 10	
AGC GCG CAT GCT GTC AAA ACT CAT AAT TTG GAA AGG GTG GAA GCT TCA	99
Ser Ala His Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser	
15 20 25	
GGG GTG GCT AAC GAT AAG GAA GCG CCT TTA AGC TGG AGG AGC AAG GAA	147
Gly Val Ala Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu	
30 35 40 45	
GTG AGA AAC TAT ATG GGA TCT CGC ACG GTG ATT TCT AAC AAG CAA CTC	195
Val Arg Asn Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu	
50 55 60	
ACT AAA AGC GCC AAT CAG AGC ATT GAA GAA GCT TTG CAA AAT GTG CCA	243
Thr Lys Ser Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro	
65 70 75	
GGC GTG CAT ATT AGA AAC GCT ACG GGT ATT GGA GCT GTG CCT AGC TTT	291
Gly Val His Ile Arg Asn Ala Thr Gly Ile Gly Ala Val Pro Ser Phe	
80 85 90	
TCT GTT AGG GGC TTT GGT GGG GGA AGT TCA GGG CAT TCC AAT ACG GCT	339
Ser Val Arg Gly Phe Gly Gly Gly Ser Ser Gly His Ser Asn Thr Ala	
95 100 105	
ATG GTT TTA GTC AAT GGG ATC CCT ATT TAT GTT GCG CCC TAT GTT GAT	387
Met Val Leu Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Asp	
110 115 120 125	
ATT AGC ATT CCT ATT TTC CCT GTA ACC TTT CAA TCT GTA GAT AGA ATC	435
Ile Ser Ile Pro Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile	
130 135 140	
AGC GTA ACC AAG GGT GGG GAG AGC GTG CGT TAT GGC CCT AAT GTT TTT	483
Ser Val Thr Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Val Phe	
145 150 155	
GGC GGT GTG ATT AAT GTG ATC ACT AAG GGC ATT CCT ACC AAG TGG GAG	531
Gly Gly Val Ile Asn Val Ile Thr Lys Gly Ile Pro Thr Lys Trp Glu	
160 165 170	

ATG ATG CTC CCG CCT GTA ATG ATT TCT CTG CCT TTT AAA ATT TTA GTG 506
 Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys Ile Leu Val
 110 115 120 125

TTT ATT CTG GTA GAT GGG TTT AAT TTA TTG ACC GAA AAT TTA GTG GCG 554
 Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn Leu Val Ala
 130 135 140

AGT TTT AAA ATG GTT TGATATTAAC AAGCATTCAA GCGATAAAAG CTTGAAGCTA G 610
 Ser Phe Lys Met Val
 145

TTTAAACTC ATAATTCAAA 630

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp Thr Gly Ile Lys Pro Tyr
 1 5 10 15
 Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala Phe Glu Lys Ser Ala Leu
 20 25 30
 Pro Phe Lys Glu Phe Met Leu Lys Asn Thr Arg Glu Lys Asp Leu Ala
 35 40 45
 Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn Pro Lys Thr Pro Asp Glu
 50 55 60
 Val Ser Leu Ser Val Leu Ile Pro Ala Phe Met Ile Ser Glu Leu Lys
 65 70 75 80
 Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr Leu Pro Phe Leu Val Ile
 85 90 95
 Asp Met Val Ile Ser Ser Ile Leu Met Ala Met Gly Met Met Met Leu
 100 105 110
 Pro Pro Val Met Ile Ser Leu Pro Phe Lys Ile Leu Val Phe Ile Leu
 115 120 125
 Val Asp Gly Phe Asn Leu Leu Thr Glu Asn Leu Val Ala Ser Phe Lys
 130 135 140
 Met Val
 145

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

65		70		75		80									
Val	Asp	Arg	Glu	Pro	Gln	Asn	Lys	Glu	Pro	Gln	Ala	Pro	Arg	Glu	Pro
			85					90						95	
Ile	Arg	Asp	Leu	Tyr	Asp	Tyr	Gly	Tyr	Ser	Phe	Gly	His	Ala	Trp	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 132...569
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

GATTTTAGTG	ATGACGAGTT	TCACCCGTTT	GATCGTGGTG	TTTTCTTTTT	TAAGGACCGC	60										
TTTGGGCACG	CAACAAACCC	CCCCCACTC	AAATTTTAGT	CTCGCTCTCT	TTGATATTGA	120										
CTTTTTTCAT	C	ATG	GAA	CCT	AGC	CTA	AAA	AAG	GCC	TAT	GAT	ACA	GGG	ATT	170	
	Met	Glu	Pro	Ser	Leu	Lys	Lys	Ala	Tyr	Asp	Thr	Gly	Ile			
	1				5						10					
AAG	CCT	TAT	ATG	GAT	AAA	AAG	ATT	TCT	TAC	ACC	GAA	GCG	TTT	GAA	AAA	218
Lys	Pro	Tyr	Met	Asp	Lys	Lys	Ile	Ser	Tyr	Thr	Glu	Ala	Phe	Glu	Lys	
	15				20					25						
AGC	GCT	CTG	CCC	TTC	AAG	GAA	TTC	ATG	CTT	AAA	AAC	ACA	CGA	GAA	AAG	266
Ser	Ala	Leu	Pro	Phe	Lys	Glu	Phe	Met	Leu	Lys	Asn	Thr	Arg	Glu	Lys	
	30				35				40					45		
GAT	CTA	GCC	CTT	TTT	TTT	AGG	ATT	AGA	AAC	CTC	CCT	AAC	CCT	AAA	ACC	314
Asp	Leu	Ala	Leu	Phe	Phe	Arg	Ile	Arg	Asn	Leu	Pro	Asn	Pro	Lys	Thr	
			50					55						60		
CCT	GAT	GAG	GTG	AGT	TTG	AGC	GTT	TTG	ATC	CCG	GCA	TTT	ATG	ATA	AGC	362
Pro	Asp	Glu	Val	Ser	Leu	Ser	Val	Leu	Ile	Pro	Ala	Phe	Met	Ile	Ser	
			65					70					75			
GAG	TTG	AAA	ACA	GCG	TTT	CAA	ATC	GGC	TTT	TTA	CTC	TAC	TTG	CCT	TTT	410
Glu	Leu	Lys	Thr	Ala	Phe	Gln	Ile	Gly	Phe	Leu	Leu	Tyr	Leu	Pro	Phe	
		80					85					90				
TTG	GTG	ATT	GAT	ATG	GTG	ATC	AGC	TCT	ATT	TTA	ATG	GCG	ATG	GGC	ATG	458
Leu	Val	Ile	Asp	Met	Val	Ile	Ser	Ser	Ile	Leu	Met	Ala	Met	Gly	Met	
		95				100					105					

```

GTTGTGGTAT AAATATTCTT ATCAAGGTGT GCCAAACATG CCTTGAATCT CAATTTTGA      60
ATCTCAATTT T ATG AAA GGA TTT GTT ATG AGT GGA TTA AGA ACA TTT AGT      110
      Met Lys Gly Phe Val Met Ser Gly Leu Arg Thr Phe Ser
          1                      5                      10

TGT GTA GTG GTT TTA TGC GGT GCA ATG GCT AAT GTG GCT ATA GCT AGT      158
Cys Val Val Val Leu Cys Gly Ala Met Ala Asn Val Val Ala Ile Ala Ser
      15                      20                      25

CCT AAA ATA GAG GCA AGG GGT GAA TTA GGC AAA TTT ATA GGG GGT GGT      206
Pro Lys Ile Glu Ala Arg Gly Glu Leu Gly Lys Phe Ile Gly Gly Gly
      30                      35                      40                      45

GTT GGG GGT TTT GTT GGT GAT AAA ATG GGC GGA TTT GTT GGT GGT GCA      254
Val Gly Gly Phe Val Gly Asp Lys Met Gly Gly Phe Val Gly Gly Ala
          50                      55                      60

ATA GGA GGA TAT ATT GGG TCT GAA ATA GGC GAT AGG GTA GAA GAT TAT      302
Ile Gly Gly Tyr Ile Gly Ser Glu Ile Gly Asp Arg Val Glu Asp Tyr
          65                      70                      75

ATC CGT GGT GTT GAT AGA GAG CCA CAA AAC AAA GAA CCA CAA GCC CCA      350
Ile Arg Gly Val Asp Arg Glu Pro Gln Asn Lys Glu Pro Gln Ala Pro
          80                      85                      90

AGA GAA CCT ATC CGT GAT CTT TAT GAT TAC GGC TAT AGT TTT GGG CAT      398
Arg Glu Pro Ile Arg Asp Leu Tyr Asp Tyr Gly Tyr Ser Phe Gly His
          95                      100                      105

GCT TGG TGATCTTAAA TGAGTCAAGA      424
Ala Trp
110

```

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

```

Met Lys Gly Phe Val Met Ser Gly Leu Arg Thr Phe Ser Cys Val Val
 1          5          10          15
Val Leu Cys Gly Ala Met Ala Asn Val Ala Ile Ala Ser Pro Lys Ile
      20          25          30
Glu Ala Arg Gly Glu Leu Gly Lys Phe Ile Gly Gly Gly Val Gly Gly
      35          40          45
Phe Val Gly Asp Lys Met Gly Gly Phe Val Gly Gly Ala Ile Gly Gly
      50          55          60
Tyr Ile Gly Ser Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly

```

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

```

Met Ser Gln Gly Asp Gly Val Glu Gly Asn Asn Met Asp Thr Thr Lys
 1             5             10             15
Glu Asn Leu Asn Gly Ser Lys Glu Arg Leu Ser Asp Trp Glu Tyr Arg
          20             25             30
Trp Ala Met Ala Leu Val Tyr Gly Gly Cys Ile Ser Ile Thr Thr Arg
          35             40             45
Ile Phe Tyr Asp Ile Asn Gly Ser Ala Ser Asp Pro Leu Phe Asp Pro
          50             55             60
Lys Tyr Ser Tyr Tyr Val Trp Leu Val Ala Leu Ile Ala Ala Leu Leu
65             70             75             80
Ser Asn Leu Leu Phe Asn Pro Lys Gly Arg Ser Val Gly Tyr Leu Met
          85             90             95
Ile Glu Thr Trp Gln Gly Phe Pro Lys Phe Phe Lys Ala Ile Phe Lys
          100            105            110
Ala Arg Phe Phe Gly Ala Phe Tyr Asp Ala Val Leu Gly Ser Arg Leu
          115            120            125
Arg Asp Phe Tyr Val Met Leu Leu Thr Met Pro Phe Ile Ala Ala Ile
          130            135            140
His Glu Val Ser Ala Tyr Cys Gly His Pro Ser Asn Leu Leu Val Glu
145            150            155            160
Gly Leu Val Ile Leu Gly Phe Gln Gly Phe Leu Lys Leu Cys Ala Lys
          165            170            175
Trp Gly Trp

```

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 72...404
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

TTTGGGCATG CTTGGTGATC TTAA ATG AGT CAA GGT GAT GGG GTG GAA GGA	51
Met Ser Gln Gly Asp Gly Val Glu Gly	
1 5	
AAT AAT ATG GAT ACT ACG AAA GAG AAC TTG AAT GGC TCA AAA GAG CGT	99
Asn Asn Met Asp Thr Thr Lys Glu Asn Leu Asn Gly Ser Lys Glu Arg	
10 15 20 25	
TTG AGC GAT TGG GAA TAT CGA TGG GCA ATG GCT CTA GTC TAT GGA GGA	147
Leu Ser Asp Trp Glu Tyr Arg Trp Ala Met Ala Leu Val Tyr Gly Gly	
30 35 40	
TGT ATC TCC ATA ACC ACT AGG ATT TTT TAT GAC ATA AAT GGT TCA GCT	195
Cys Ile Ser Ile Thr Thr Arg Ile Phe Tyr Asp Ile Asn Gly Ser Ala	
45 50 55	
AGC GAT CCG CTT TTT GAC CCT AAA TAC AGC TAT TAT GTG TGG TTA GTG	243
Ser Asp Pro Leu Phe Asp Pro Lys Tyr Ser Tyr Tyr Val Trp Leu Val	
60 65 70	
GCT CTA ATA GCG GCT TTG TTG TCT AAT CTC TTG TTT AAT CCT AAA GGC	291
Ala Leu Ile Ala Ala Leu Leu Ser Asn Leu Leu Phe Asn Pro Lys Gly	
75 80 85	
AGG TCG GTA GGT TAT TTA ATG ATT GAA ACT TGG CAA GGG TTC CCC AAG	339
Arg Ser Val Gly Tyr Leu Met Ile Glu Thr Trp Gln Gly Phe Pro Lys	
90 95 100 105	
TTT TTT AAA GCC ATT TTT AAG GCT AGG TTT TTT GGT GCG TTT TAT GAC	387
Phe Phe Lys Ala Ile Phe Lys Ala Arg Phe Phe Gly Ala Phe Tyr Asp	
110 115 120	
GCT GTG TTA GGA TCA AGG CTA AGG GAT TTT TAT GTG ATG CTT TTA ACG	435
Ala Val Leu Gly Ser Arg Leu Arg Asp Phe Tyr Val Met Leu Leu Thr	
125 130 135	
ATG CCC TTT ATT GCC GCT ATC CAT GAG GTT TCG GCG TAT TGT GGG CAT	483
Met Pro Phe Ile Ala Ala Ile His Glu Val Ser Ala Tyr Cys Gly His	
140 145 150	
CCT AGC AAT CTC CTT GTA GAG GGT TTG GTC ATT TTG GGG TTT CAA GGT	531
Pro Ser Asn Leu Leu Val Glu Gly Leu Val Ile Leu Gly Phe Gln Gly	
155 160 165	
TTT CTT AAG CTT TGC GCT AAA TGG GGG TGG TGATTTAACC CAAATGTCAT TAA	584
Phe Leu Lys Leu Cys Ala Lys Trp Gly Trp	
170 175	
ATGGAGGGGG TATAAAAAA TTAAAAA	611

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

```

Met Leu Ala Tyr Cys Phe Ile Thr Pro Asp Asp Leu Lys Asn Leu Lys
 1           5           10           15
Glu Arg Leu Phe Ile Asp Ile Ile Asn Ala Ile Asn Gln Lys Lys Arg
          20           25           30
Val Ala Leu Asp His Ala Gln Ile Asp Asp Ile Gln Tyr Asn Val Leu
        35           40           45
Asp Asn Ala Phe Tyr Phe Ile Phe Asp Val Gly Asn Pro Ser Gln Leu
       50           55           60
Ala Ile Lys Val Pro Arg Lys Ser Leu Glu Asn Asp Glu Leu Pro Asn
      65           70           75           80
Thr Lys Lys Asn Ile Phe Asn Gly Leu Ile Arg Thr Ile Tyr Gly Cys
          85           90           95
Ile Asp Asp Glu Asn Ser Phe Leu Leu Glu Asn Asp Lys Thr Ile Lys
        100          105          110
Asp Leu Asn Ile Gln Asp Leu Leu Gly Pro Leu Lys Thr Gln Ala Phe
       115          120          125
Pro Leu Ser Tyr Ile Ile Thr Asp Ala Ile Asn Gln Lys Glu Gly Val
      130          135          140
Ala Leu Asp Tyr Ala Leu Ile Asn Asp Ile Lys Tyr Asn Leu Leu Asp
     145          150          155          160
Asn Thr Phe His Phe Ile Phe Asp Val Gly Asn Pro Leu Leu Lys Glu
          165          170          175
Ser Ser Gln Phe Ile Ile Glu Val Pro Arg Glu Ala Leu Asp Leu Glu
        180          185          190
Asn Val Asp Arg Leu Val Glu Tyr Thr Leu Ser Pro Asn Asn His Ser
       195          200          205
Gln Ser Ser Leu Val Tyr His Ile Ser Glu Gly Ser Tyr Ile Ile His
      210          215          220
Leu Ile Asp Asp
225

```

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...561
- (D) OTHER INFORMATION:

ATC AAC CAA AAA AAG AGA GTC GCG CTC GAT CAT GCT CAA ATA GAT GAC	147
Ile Asn Gln Lys Lys Arg Val Ala Leu Asp His Ala Gln Ile Asp Asp	
30 35 40	
ATC CAG TAT AAT GTG CTT GAT AAT GCG TTT TAT TTT ATC TTT GAT GTT	195
Ile Gln Tyr Asn Val Leu Asp Asn Ala Phe Tyr Phe Ile Phe Asp Val	
45 50 55	
GGT AAC CCT TCT CAA TTA GCT ATT AAA GTG CCT AGA AAA TCT TTA GAA	243
Gly Asn Pro Ser Gln Leu Ala Ile Lys Val Pro Arg Lys Ser Leu Glu	
60 65 70	
AAT GAT GAG TTG CCC AAC ACT AAA AAA AAC ATA TTC AAT GGA TTA ATA	291
Asn Asp Glu Leu Pro Asn Thr Lys Lys Asn Ile Phe Asn Gly Leu Ile	
75 80 85 90	
AGA ACT ATC TAT GGG TGT ATT GAT GAT GAA AAT TCA TTT TTA TTA GAA	339
Arg Thr Ile Tyr Gly Cys Ile Asp Asp Glu Asn Ser Phe Leu Leu Glu	
95 100 105	
AAC GAT AAA ACC ATC AAG GAT TTA AAT ATT CAG GAT TTA TTG GGG CCA	387
Asn Asp Lys Thr Ile Lys Asp Leu Asn Ile Gln Asp Leu Leu Gly Pro	
110 115 120	
TTA AAA ACT CAA GCA TTT CCA TTA TCA TAC ATT ATT ACT GAC GCT ATC	435
Leu Lys Thr Gln Ala Phe Pro Leu Ser Tyr Ile Ile Thr Asp Ala Ile	
125 130 135	
AAT CAA AAA GAA GGG GTG GCT CTC GAT TAC GCT CTA ATA AAC GAT ATT	483
Asn Gln Lys Glu Gly Val Ala Leu Asp Tyr Ala Leu Ile Asn Asp Ile	
140 145 150	
AAG TAT AAT TTG CTT GAT AAC ACA TTC CAT TTT ATC TTT GAT GTT GGT	531
Lys Tyr Asn Leu Leu Asp Asn Thr Phe His Phe Ile Phe Asp Val Gly	
155 160 165 170	
AAT CCT TTG TTG AAA GAG TCA AGT CAA TTT ATT ATT GAA GTG CCT AGA	579
Asn Pro Leu Leu Lys Glu Ser Ser Gln Phe Ile Ile Glu Val Pro Arg	
175 180 185	
GAG GCG TTG GAT CTA GAG AAT GTT GAT CGG CTT GTT GAA TAT ACG CTG	627
Glu Ala Leu Asp Leu Glu Asn Val Asp Arg Leu Val Glu Tyr Thr Leu	
190 195 200	
TCT CCT AAT AAT CAT AGT CAA AGT TCT TTA GTG TAT CAT ATT TCT GAA	675
Ser Pro Asn Asn His Ser Gln Ser Ser Leu Val Tyr His Ile Ser Glu	
205 210 215	
GGC TCT TAT ATC ATT CAC TTA ATA GAT GAC TAAACTTAAA TGAAA	720
Gly Ser Tyr Ile Ile His Leu Ile Asp Asp	
220 225	

(2) INFORMATION FOR SEQ ID NO:804:

```

Thr Ile Glu Asp Tyr Leu Ile Leu Asp Asn Leu Lys Ser Cys Phe Val
  210                      215                      220
Ile Gln Asn Lys Pro Asn Val Thr Leu Phe Asp Asn Asp Glu Asn Asp
225                      230                      235                      240
Arg Pro Phe Asn Leu Lys Arg Tyr Leu Leu Gly Leu Lys Glu Lys Leu
                      245                      250                      255
Gly Phe Glu Pro Thr Gly Ile Phe Tyr Cys Glu Asn Ala Asn Thr His
                      260                      265                      270
Lys Ile Glu Leu Ile Gly Asn Asp Ser Asp Phe Arg Glu Val Leu Leu
                      275                      280                      285
Glu Phe Ser Glu Asn Ile Pro Lys Ala Pro Asn Glu Leu Pro Gln Phe
                      290                      295                      300
Leu Thr Asn Phe Lys Asn Ser Lys Ile Pro Asn Gly Asn Ile Ser Phe
305                      310                      315                      320
Ser Pro Pro Lys Asn Ser Pro Ser Ile Ser Ser Tyr Ala Leu Ser Asp
                      325                      330                      335
Lys Ile Lys Arg Glu Val Arg Asp Thr Phe Asp Arg Tyr Leu Trp His
                      340                      345                      350
Gly Tyr Ser Lys Ile Pro Gln Glu Lys Arg Ile Ala Lys Ile Lys Glu
                      355                      360                      365
Gln Val Lys Glu Glu Ile Lys Leu Asn Pro Ser Phe Arg Asn Tyr Arg
                      370                      375                      380
Val Asp Ser Glu Gln Asn Arg Lys Ile Asn Glu Ile Ala Glu Gly Leu
385                      390                      395                      400
Lys Ser Gly Lys Ile Ile Gly Lys Lys Val Ile Ala Asn Ala Phe Asp
                      405                      410                      415
Leu Asn Ala Ser Leu Leu Phe Tyr Tyr Ser
                      420                      425

```

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...705
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

```

TTGCTAATGC GTTCGATCTA A ATG CTA GCT TAT TGT TTT ATT ACT CCT GAT      51
                      Met Leu Ala Tyr Cys Phe Ile Thr Pro Asp
                      1                      5                      10

GAT TTA AAG AAT TTA AAG GAA CGA TTA TTT ATA GAT ATT ATC AAT GCT      99
Asp Leu Lys Asn Leu Lys Glu Arg Leu Phe Ile Asp Ile Ile Asn Ala
                      15                      20                      25

```

CCT TCT TTT CGT AAT TAT AGA GTA GAC TCT GAA CAA AAC CGC AAG ATC	1203
Pro Ser Phe Arg Asn Tyr Arg Val Asp Ser Glu Gln Asn Arg Lys Ile	
380 385 390	
AAT GAA ATT GCT GAG GGT TTA AAA AGT GGT AAG ATA ATT GGT AAA AAG	1251
Asn Glu Ile Ala Glu Gly Leu Lys Ser Gly Lys Ile Ile Gly Lys Lys	
395 400 405	
GTT ATT GCT AAT GCG TTC GAT CTA AAT GCT AGC TTA TTG TTT TAT TAC	1299
Val Ile Ala Asn Ala Phe Asp Leu Asn Ala Ser Leu Leu Phe Tyr Tyr	
410 415 420 425	
TCC TGATGATTTA AAGAATTTAA AGGAACGATT ATTTATAGAT ATT	1345
Ser	

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

Met	Ala	Val	Arg	Phe	Gly	Ile	Ile	Phe	Ile	Ser	Asp	Ser	Ile	Asp	Asp
1				5					10					15	
Tyr	Lys	Ala	Lys	Gln	Leu	Arg	Ser	Ile	Leu	Glu	Arg	Lys	Lys	Glu	Cys
			20					25					30		
Asn	Phe	Ile	Trp	Phe	Asn	Glu	Ser	Ser	Ala	Ile	Ile	His	Asn	Thr	Pro
		35					40					45			
Lys	Val	Phe	Glu	Gly	Glu	Ser	Phe	Phe	Asp	His	Leu	Phe	Val	Ser	Ala
	50					55					60				
Lys	Ile	Thr	Ala	Phe	Val	Val	Ser	Thr	Asn	Glu	Ser	Asp	Thr	Ile	Phe
65					70					75				80	
Asn	Leu	Lys	Asn	Tyr	Leu	Leu	Val	Leu	Ala	Lys	Asn	Leu	Asn	Asn	Arg
			85						90					95	
Asp	Ile	Trp	Tyr	Cys	Glu	Asn	Thr	Ile	Cys	Asp	Lys	Lys	Gly	Thr	Tyr
			100					105					110		
Asn	Ile	Glu	Ile	Glu	Leu	Val	Ser	Asn	Ala	Asn	Asp	Phe	Arg	Gly	Val
		115					120					125			
Phe	Gly	Glu	Val	Leu	Gly	Ile	Val	Lys	Asp	Thr	Phe	Gly	Asp	Leu	Leu
	130					135					140				
Gln	Leu	Leu	Thr	Asn	Leu	Lys	Asn	Lys	Glu	Ile	Glu	Phe	Asn	Phe	His
145					150					155				160	
Lys	Lys	Ile	Asn	Tyr	Gly	Leu	Pro	Phe	Gly	Ile	Ile	Phe	Ile	Ala	Ser
			165						170					175	
Asn	Ser	Asp	Asn	Pro	Ile	Asp	Ile	Asp	Asn	Lys	Thr	Lys	Lys	Leu	Lys
			180					185					190		
Ser	Cys	Phe	Arg	Asp	Asp	Glu	Ser	Asn	Cys	Phe	Ile	Asp	Cys	Pro	Ile
		195					200					205			

Glu Ile Glu Phe Asn Phe His Lys Lys Ile Asn Tyr Gly Leu Pro Phe	
155	160 165
GGG ATT ATC TTT ATC GCT AGC AAC TCT GAC AAC CCT ATT GAT ATT GAC	579
Gly Ile Ile Phe Ile Ala Ser Asn Ser Asp Asn Pro Ile Asp Ile Asp	
170	175 180 185
AAT AAA ACC AAA AAG TTA AAA TCA TGC TTT CGT GAT GAT GAG AGT AAC	627
Asn Lys Thr Lys Lys Leu Lys Ser Cys Phe Arg Asp Asp Glu Ser Asn	
	190 195 200
TGT TTT ATT GAC TGC CCA ATT ACA ATT GAG GAT TAT TTA ATT TTA GAT	675
Cys Phe Ile Asp Cys Pro Ile Thr Ile Glu Asp Tyr Leu Ile Leu Asp	
	205 210 215
AAT CTA AAA AGC TGT TTT GTA ATC CAA AAT AAG CCA AAT GTA ACA TTA	723
Asn Leu Lys Ser Cys Phe Val Ile Gln Asn Lys Pro Asn Val Thr Leu	
	220 225 230
TTT GAT AAC GAC GAG AAC GAT AGA CCA TTC AAT TTA AAG CGA TAC TTG	771
Phe Asp Asn Asp Glu Asn Asp Arg Pro Phe Asn Leu Lys Arg Tyr Leu	
	235 240 245
TTA GGA TTG AAA GAA AAG TTA GGG TTT GAG CCA ACG GGT ATT TTC TAT	819
Leu Gly Leu Lys Glu Lys Leu Gly Phe Glu Pro Thr Gly Ile Phe Tyr	
	250 255 260 265
TGC GAA AAC GCA AAC ACA CAC AAA ATT GAA TTG ATT GGT AAT GAT TCT	867
Cys Glu Asn Ala Asn Thr His Lys Ile Glu Leu Ile Gly Asn Asp Ser	
	270 275 280
GAT TTC AGA GAG GTA TTA CTT GAA TTT TCA GAG AAT ATA CCA AAA GCC	915
Asp Phe Arg Glu Val Leu Leu Glu Phe Ser Glu Asn Ile Pro Lys Ala	
	285 290 295
CCT AAT GAA CTA CCA CAA TTT CTT ACA AAC TTT AAA AAT TCA AAA ATC	963
Pro Asn Glu Leu Pro Gln Phe Leu Thr Asn Phe Lys Asn Ser Lys Ile	
	300 305 310
CCC AAT GGA AAC ATT TCA TTT TCG CCA CCA AAA AAT TCT CCA TCA ATT	1011
Pro Asn Gly Asn Ile Ser Phe Ser Pro Pro Lys Asn Ser Pro Ser Ile	
	315 320 325
TCT TCA TAT GCT TTA TCT GAT AAG ATT AAA AGA GAA GTA AGA GAT ACC	1059
Ser Ser Tyr Ala Leu Ser Asp Lys Ile Lys Arg Glu Val Arg Asp Thr	
	330 335 340 345
TTT GAT CGC TAT TTG TGG CAT GGT TAT TCT AAA ATT CCA CAG GAG AAA	1107
Phe Asp Arg Tyr Leu Trp His Gly Tyr Ser Lys Ile Pro Gln Glu Lys	
	350 355 360
AGG ATA GCC AAA ATA AAA GAG CAA GTG AAG GAA GAA ATT AAA CTA AAT	1155
Arg Ile Ala Lys Ile Lys Glu Gln Val Lys Glu Glu Ile Lys Leu Asn	
	365 370 375

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 25...1302
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

CTAAATGAAT TTAAAAGGAA AAAT ATG GCA GTA AGA TTT GGG ATT ATC TTT	51
Met Ala Val Arg Phe Gly Ile Ile Phe	
1 5	
ATA TCT GAC TCT ATT GAT GAT TAT AAA GCC AAA CAA TTA AGA TCA ATT	99
Ile Ser Asp Ser Ile Asp Asp Tyr Lys Ala Lys Gln Leu Arg Ser Ile	
10 15 20 25	
TTA GAA CGC AAG AAA GAG TGT AAT TTT ATA TGG TTT AAT GAA TCA AGT	147
Leu Glu Arg Lys Lys Glu Cys Asn Phe Ile Trp Phe Asn Glu Ser Ser	
30 35 40	
GCT ATA ATT CAC AAT ACT CCT AAA GTT TTT GAA GGA GAG AGT TTT TTT	195
Ala Ile Ile His Asn Thr Pro Lys Val Phe Glu Gly Glu Ser Phe Phe	
45 50 55	
GAT CAT CTT TTC GTT AGT GCA AAA ATT ACT GCT TTT GTG GTA TCC ACA	243
Asp His Leu Phe Val Ser Ala Lys Ile Thr Ala Phe Val Val Ser Thr	
60 65 70	
AAC GAA TCA GAT ACA ATA TTC AAT TTA AAA AAC TAC TTG CTA GTA TTA	291
Asn Glu Ser Asp Thr Ile Phe Asn Leu Lys Asn Tyr Leu Leu Val Leu	
75 80 85	
GCC AAA AAT CTC AAT AAT AGA GAT ATT TGG TAT TGT GAA AAC ACT ATT	339
Ala Lys Asn Leu Asn Asn Arg Asp Ile Trp Tyr Cys Glu Asn Thr Ile	
90 95 100 105	
TGC GAT AAA AAA GGC ACT TAT AAT ATA GAA ATA GAA TTA GTG AGC AAT	387
Cys Asp Lys Lys Gly Thr Tyr Asn Ile Glu Ile Glu Leu Val Ser Asn	
110 115 120	
GCT AAT GAT TTT AGA GGA GTG TTT GGA GAA GTG TTA GGT ATA GTC AAA	435
Ala Asn Asp Phe Arg Gly Val Phe Gly Glu Val Leu Gly Ile Val Lys	
125 130 135	
GAC ACT TTC GGT GAT TTA CTG CAA CTT CTT ACA AAT TTA AAG AAC AAG	483
Asp Thr Phe Gly Asp Leu Leu Gln Leu Leu Thr Asn Leu Lys Asn Lys	
140 145 150	
GAA ATT GAA TTT AAT TTT CAT AAA AAA ATT AAT TAC GGA TTG CCT TTT	531

65					70					75				80	
Arg	Ile	Ile	Leu	Gly	His	Thr	Leu	Gly	Tyr	Ser	Ala	Pro	Ile	Thr	Leu
				85					90					95	
Tyr	Tyr	Glu	Trp	Leu	Phe	Asp	Asp	Trp	Ile	Asp	Pro	Glu	Lys	Ile	Met
			100					105					110		
Gly	Asp	Arg	Phe	Val	Cys	Arg	Thr	Asn	Tyr	Leu	Glu	Ser	Phe	Phe	Thr
	115						120					125			
Thr	Lys	Lys	His	Leu	Leu	Pro	Asp	Thr	Leu	Phe	Lys	Val	Asp	Glu	Ser
	130					135					140				
Gly	Cys	Glu	Ser	Tyr	His	Glu	Asn	Asn	Asp	Lys	Asp	Phe	Ile	Leu	Gln
145					150					155					160
Ser	Phe	Tyr	Ile	Gln	Asn	Asp	Phe	Leu	Ser	Gln	Arg	Tyr	Glu	Lys	Asp
			165					170						175	
Lys	Ile	Lys	Ala	Lys	Ser	Asn	Leu	Ile	Pro	Lys	Arg	Gln	Asn	Arg	Leu
			180					185					190		
Leu	Thr	Tyr	Gln	Phe	Asp	Leu	Ser	Leu	Glu	Cys	Asn	Ile	Ile	Phe	Glu
	195						200					205			
Thr	Leu	Glu	Lys	Leu	Ala	Leu	Ile	Ala	Gly	Ala	Ile	Lys	Asn	Phe	Phe
	210					215					220				
Ile	Leu	Ile	Tyr	Ala	His	Ser	Asn	Phe	Asp	Ile	Gln	Ile	Asp	Tyr	Ile
225					230					235					240
Gln	Phe	Lys	Leu	Ser	Asn	Lys	Asp	Ile	Thr	Ala	Ile	Arg	Asn	Thr	Tyr
			245					250					255		
Lys	Lys	Asp	Lys	Lys	Ser	Met	Glu	Ile	Asp	Leu	Tyr	Gly	Ile	Ala	Ile
			260					265					270		
Asn	Phe	Gln	Arg	Ile	Asp	Asn	Phe	Ser	Val	Ile	Leu	Glu	Lys	Trp	Ile
	275						280						285		
Val	Phe	Tyr	Ile	Lys	Asp	Asn	Arg	Asp	Phe	Gln	Leu	Ala	Ser	Ile	Leu
	290					295				300					
Asp	Ile	Ile	Asn	Lys	Lys	Asp	Pro	Ile	Ile	His	Leu	Tyr	Leu	Asp	Met
305				310						315					320
Phe	Val	Leu	Ile	Ser	Met	Ile	Glu	Ser	Phe	Leu	Lys	Lys	Pro	Gln	Gln
			325						330					335	
Thr	Lys	Leu	His	Glu	Lys	Leu	Ser	Glu	Phe	Phe	Lys	Ile	Ser	Leu	Ser
			340					345					350		
Arg	Thr	Lys	Cys	Asp	Gln	Thr	Lys	Asn	Tyr	Phe	Asn	Asp	Lys	Cys	Gln
	355						360					365			
Glu	Asp	Leu	Ile	Gln	Gln	Ile	Val	Asp	Cys	Arg	Asn	Ser	Leu	Ala	His
	370					375					380				
Gly	Arg	Ser	Leu	Lys	Leu	Asp	Thr	Asn	Lys	Ala	Thr	Asp	Ile	Ser	His
385					390					395					400
Ala	Phe	Ile	Asp	Phe	Lys	Gln	Ile	Val	Ile	Glu	Phe	Phe	Phe	Gly	Glu
			405						410					415	
Ile	Gly	Leu	Ser	Asp	Phe	Ile	Thr	Asn	Asn	Phe	Gly	Phe	Leu	Asn	Lys
			420					425					430		
Val	Lys	Leu	Arg	Asn	Pro	Pro	Lys	Thr	Glu	Lys	Ile	Thr	Glu	Pro	Asn
		435					440					445			
Arg															

(2) INFORMATION FOR SEQ ID NO:801:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1345 base pairs
 (B) TYPE: nucleic acid

```

TTA AAG AAA CCA CAA CAA ACA AAA CTC CAT GAA AAA CTC TCT GAA TTT      1061
Leu Lys Lys Pro Gln Gln Thr Lys Leu His Glu Lys Leu Ser Glu Phe
                      335                      340                      345

TTT AAA ATT TCA TTA TCT AGG ACA AAA TGC GAT CAA ACG AAA AAT TAT      1109
Phe Lys Ile Ser Leu Ser Arg Thr Lys Cys Asp Gln Thr Lys Asn Tyr
                      350                      355                      360

TTT AAT GAT AAA TGT CAA GAA GAT CTA ATC CAA CAG ATT GTT GAC TGC      1157
Phe Asn Asp Lys Cys Gln Glu Asp Leu Ile Gln Gln Ile Val Asp Cys
                      365                      370                      375

CGT AAC TCT CTA GCG CAC GGA AGA AGT TTA AAG CTT GAT ACA AAC AAA      1205
Arg Asn Ser Leu Ala His Gly Arg Ser Leu Lys Leu Asp Thr Asn Lys
                      380                      385                      390

GCT ACA GAC ATT AGC CAT GCT TTT ATA GAT TTC AAG CAA ATT GTC ATT      1253
Ala Thr Asp Ile Ser His Ala Phe Ile Asp Phe Lys Gln Ile Val Ile
                      395                      400                      405                      410

GAA TTT TTC TTT GGC GAG ATA GGA TTG AGC GAT TTT ATT ACA AAC AAT      1301
Glu Phe Phe Phe Gly Glu Ile Gly Leu Ser Asp Phe Ile Thr Asn Asn
                      415                      420                      425

TTT GGT TTT CTT AAC AAA GTT AAA TTA AGA AAC CCC CCA AAA ACA GAA      1349
Phe Gly Phe Leu Asn Lys Val Lys Leu Arg Asn Pro Pro Lys Thr Glu
                      430                      435                      440

AAA ATC ACC GAG CCA AAC CGC TAAACCCCT TAGAAAATTT AAAATTTTAA GTTT      1404
Lys Ile Thr Glu Pro Asn Arg
                      445

TAGGGGTGTT TTTCTTAAGA ATTTAGGTTT TTTATA                                1440

```

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

```

Val Ile Thr Ser Leu Gly Gly Val Glu Tyr Phe Glu Arg Gln Cys Leu
 1             5             10             15
Ala Phe Leu Lys Asn Pro Gln Thr Asn Pro Gln Asn Glu Gln Tyr Ile
 20             25             30
Pro Gly Val Phe Ser Tyr Gln Glu Asn Lys Ile Ser Phe Ser Phe Leu
 35             40             45
Val Leu Gly Glu Ile Glu Glu Ile His Ser Leu Gln Tyr Gln Thr Leu
 50             55             60
Tyr Ile Val Asp Asn Lys Lys Arg Tyr Thr Leu Tyr Lys Leu Tyr Asp

```

GAT CCA GAA AAA ATT ATG GGC GAT CGT TTT GTT TGT AGG ACA AAT TAT Asp Pro Glu Lys Ile Met Gly Asp Arg Phe Val Cys Arg Thr Asn Tyr 110 115 120	389
TTA GAA AGT TTT TTT ACG ACC AAG AAG CAT TTG CTA CCT GAT ACA TTA Leu Glu Ser Phe Phe Thr Thr Lys Lys His Leu Leu Pro Asp Thr Leu 125 130 135	437
TTT AAA GTA GAT GAA AGT GGG TGT GAA AGT TAT CAT GAG AAT AAC GAT Phe Lys Val Asp Glu Ser Gly Cys Glu Ser Tyr His Glu Asn Asn Asp 140 145 150	485
AAG GAC TTT ATC CTA CAA TCA TTT TAT ATT CAA AAT GAT TTT TTA TCC Lys Asp Phe Ile Leu Gln Ser Phe Tyr Ile Gln Asn Asp Phe Leu Ser 155 160 165 170	533
CAA AGA TAT GAA AAA GAC AAG ATA AAA GCA AAA TCT AAT TTG ATT CCT Gln Arg Tyr Glu Lys Asp Lys Ile Lys Ala Lys Ser Asn Leu Ile Pro 175 180 185	581
AAA AGA CAG AAT CGT TTA TTA ACT TAT CAA TTT GAT TTG TCT TTG GAA Lys Arg Gln Asn Arg Leu Leu Thr Tyr Gln Phe Asp Leu Ser Leu Glu 190 195 200	629
TGC AAT ATA ATT TTT GAA ACC CTT GAA AAA TTA GCA CTT ATT GCT GGA Cys Asn Ile Ile Phe Glu Thr Leu Glu Lys Leu Ala Leu Ile Ala Gly 205 210 215	677
GCG ATT AAA AAC TTT TTT ATT TTG ATT TAT GCT CAT TCT AAT TTT GAC Ala Ile Lys Asn Phe Phe Ile Leu Ile Tyr Ala His Ser Asn Phe Asp 220 225 230	725
ATC CAA ATT GAC TAT ATC CAA TTC AAG CTT TCT AAT AAA GAC ATT ACA Ile Gln Ile Asp Tyr Ile Gln Phe Lys Leu Ser Asn Lys Asp Ile Thr 235 240 245 250	773
GCA ATA AGA AAC ACT TAC AAA AAA GAT AAA AAG TCT ATG GAG ATA GAT Ala Ile Arg Asn Thr Tyr Lys Lys Asp Lys Lys Ser Met Glu Ile Asp 255 260 265	821
CTT TAT GGG ATT GCT ATA AAT TTC CAA CGG ATA GAC AAT TTT TCT GTA Leu Tyr Gly Ile Ala Ile Asn Phe Gln Arg Ile Asp Asn Phe Ser Val 270 275 280	869
ATA CTT GAA AAA TGG ATT GTT TTT TAT ATC AAA GAC AAT AGA GAT TTC Ile Leu Glu Lys Trp Ile Val Phe Tyr Ile Lys Asp Asn Arg Asp Phe 285 290 295	917
CAA CTT GCA AGT ATT TTA GAC ATT ATT AAT AAA AAA GAT CCA ATT ATT Gln Leu Ala Ser Ile Leu Asp Ile Ile Asn Lys Lys Asp Pro Ile Ile 300 305 310	965
CAC TTG TAT TTG GAC ATG TTT GTA TTG ATT AGC ATG ATT GAA AGT TTT His Leu Tyr Leu Asp Met Phe Val Leu Ile Ser Met Ile Glu Ser Phe 315 320 325 330	1013

				885					890					895					
Pro	Asn	Asp	Tyr	Ala	Gly	Gly	Lys	Tyr	Val	Phe	Glu	Leu	Leu	Cys	Arg				
				900					905					910					
Val	Ile	Thr	Leu	Ser	Val	Lys	Ser	Val	Asp	Leu	Ile	Glu	Lys	Ile	Ser				
			915				920					925							
Glu	Lys	Arg	Phe	Glu															
				930															

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...1370
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

AAGATCAGCG AAAAGAGGTT TGA GTG ATT ACA TCG CTT GGG GGT GTG GAA TAT	53
Val Ile Thr Ser Leu Gly Gly Val Glu Tyr	
1 5 10	
TTT GAA AGG CAA TGT CTT GCT TTC TTA AAA AAT CCA CAA ACT AAT CCA	101
Phe Glu Arg Gln Cys Leu Ala Phe Leu Lys Asn Pro Gln Thr Asn Pro	
15 20 25	
CAA AAT GAG CAA TAC ATT CCA GGA GTG TTT TCG TAT CAA GAA AAC AAA	149
Gln Asn Glu Gln Tyr Ile Pro Gly Val Phe Ser Tyr Gln Glu Asn Lys	
30 35 40	
ATT TCT TTT TCT TTT TTG GTT TTA GGA GAA ATT GAA GAG ATC CAC TCT	197
Ile Ser Phe Ser Phe Leu Val Leu Gly Glu Ile Glu Glu Ile His Ser	
45 50 55	
TTG CAA TAC CAA ACG CTC TAT ATT GTG GAT AAC AAA AAA AGA TAC ACT	245
Leu Gln Tyr Gln Thr Leu Tyr Ile Val Asp Asn Lys Lys Arg Tyr Thr	
60 65 70	
CTT TAC AAG CTT TAT GAT CGC ATT ATT TTG GGT CAT ACT TTA GGG TAT	293
Leu Tyr Lys Leu Tyr Asp Arg Ile Ile Leu Gly His Thr Leu Gly Tyr	
75 80 85 90	
TCT GCA CCA ATC ACG CTC TAT TAT GAA TGG CTG TTT GAT GAT TGG ATC	341
Ser Ala Pro Ile Thr Leu Tyr Tyr Glu Trp Leu Phe Asp Asp Trp Ile	
95 100 105	

Gly	Asn	Gln	Arg	Thr	Ser	Gly	Glu	Val	Ser	Lys	Lys	Glu	Gly	Gly	Lys
450						455					460				
Ile	Phe	Asp	Ser	Gly	Ser	Arg	Ala	Thr	Val	Ala	Ile	Ile	Phe	Phe	Val
465						470				475					480
Lys	Asp	Lys	Ser	Thr	Pro	Asp	Asn	Thr	Ile	Phe	Tyr	Tyr	Glu	Val	Glu
				485					490						495
Asp	Tyr	Leu	Lys	Arg	Glu	Ala	Lys	Leu	Asn	Trp	Leu	Ala	Asn	Phe	Glu
			500					505					510		
Asn	Leu	Asp	Phe	Val	Pro	Phe	Glu	Lys	Ile	Thr	Pro	Asn	Asp	Lys	Gly
		515					520					525			
Asp	Trp	Ile	Asn	Gln	Arg	Asn	Asp	Ala	Phe	Glu	Lys	Leu	Ile	Pro	Leu
	530					535						540			
Lys	Arg	Asp	Lys	Thr	Leu	Gln	Asn	Asp	Ser	Val	Phe	Asp	Ile	Asn	Ser
545					550					555					560
Leu	Gly	Val	Val	Ser	Gly	Arg	Asp	Pro	Trp	Val	Tyr	Asn	Phe	Ser	Pro
				565					570						575
Asn	Ile	Leu	Thr	Gln	Ser	Val	Gln	Lys	Cys	Ile	Asp	Thr	Tyr	Asn	Ala
			580					585					590		
Asp	Leu	Lys	Arg	Phe	Asn	Ala	Arg	Phe	Arg	Glu	Ala	Phe	Lys	Gln	Arg
		595					600					605			
Ala	Gln	Ser	Val	Lys	Ala	Gly	Asp	Leu	Tyr	Lys	Gln	Leu	Asn	Asp	Lys
		610				615					620				
Glu	Ile	Thr	Thr	Asp	Lys	Thr	Lys	Ile	Ala	Trp	Thr	Asp	Gly	Leu	Lys
625					630					635					640
Asn	Lys	Leu	Ile	Lys	Asn	Lys	Ser	Ala	Arg	Glu	Ser	Ser	Glu	Glu	Arg
				645					650						655
Val	Arg	Leu	Ala	Leu	Tyr	Arg	Pro	Phe	Asn	Lys	Gln	Trp	Leu	Tyr	Trp
		660						665					670		
Asp	Lys	Asp	Trp	Ile	Asn	Arg	Gln	Arg	Glu	Phe	Ser	Lys	Ile	Phe	Pro
		675					680					685			
Asp	Lys	Asp	Ala	Gln	Asn	Val	Val	Ile	Asn	Thr	Gly	Val	Gly	Asn	Gly
		690				695					700				
Lys	Asp	Phe	Ser	Ala	Leu	Val	Ser	Asp	Phe	Ile	Ser	Asp	Tyr	Ser	Leu
705					710					715					720
Ile	Ser	Pro	Asn	Gln	Ala	Tyr	Pro	Leu	Tyr	Tyr	Tyr	Asp	Asp	Leu	Gly
			725						730					735	
Asn	Arg	His	Tyr	Ala	Ile	Ser	Gly	Tyr	Cys	Leu	Asn	Leu	Phe	Arg	Arg
			740				745						750		
His	Tyr	Gly	Asp	Asn	Leu	Ile	Ala	Glu	Glu	Glu	Ile	Phe	Tyr	Tyr	Ile
		755					760					765			
Tyr	Ala	Ile	Phe	His	His	Lys	Gly	Tyr	Leu	Glu	Lys	Tyr	Lys	Asn	Ser
		770				775					780				
Leu	Ala	Lys	Glu	Ala	Pro	Arg	Ile	Ala	Leu	Ser	Glu	Asp	Phe	Lys	Glu
785					790					795					800
Leu	Ser	Val	Leu	Gly	Lys	Glu	Leu	Ala	Glu	Leu	His	Leu	Asn	Tyr	Glu
			805						810					815	
Ser	Gly	Glu	Met	His	Asp	Asn	Ile	Lys	Tyr	Thr	Thr	Leu	Met	Asn	Ala
			820					825					830		
Glu	Ile	Glu	Gly	Tyr	Tyr	Asp	Val	Asp	Lys	Met	Thr	Lys	Lys	Gly	Asp
		835					840					845			
Cys	Ile	Ile	Tyr	Asn	Gln	Asn	Ile	Ala	Ile	Thr	Lys	Ile	Pro	Lys	Lys
		850				855					860				
Ala	Phe	Asp	Tyr	Val	Ile	Asn	Gly	Lys	Ser	Ala	Ile	Asp	Trp	Val	Ile
865					870					875					880
Glu	Arg	Tyr	Gln	Lys	Thr	Met	Asp	Lys	Glu	Ser	Leu	Ile	Glu	Asn	Asn

```

1           5           10           15
Ser Leu Glu Ala Met Met Ala Thr Asn His Asn Asp Glu Lys Thr Leu
20           25           30
Phe Asp Ala Ile Leu Leu Gln Asp Leu Ala Asp Ala Met Tyr Asn Val
35           40           45
Met Pro Thr Lys Leu Gly Asp Arg Asn Tyr Trp Glu Asn Phe Thr Lys
50           55           60
Lys Thr Gly Asn Ile Ala Arg Thr Leu Asn Asn Arg Leu Lys Ile Ile
65           70           75           80
Phe Asp Lys Asn Pro Glu Phe Phe His Gly Phe Leu Asp Ser Leu Arg
85           90           95
Glu Asn Ile His Gln Asn Ile Lys Glu Asp Glu Ala Leu Asp Met Ile
100          105          110
Thr Ser His Ile Ile Thr Lys Pro Ile Phe Asp Ala Leu Phe Gly Asp
115          120          125
Asn Ile Lys Asn Pro Ile Ala Lys Ala Leu Asp Lys Met Val Glu Lys
130          135          140
Leu Ser Thr Leu Gly Leu Glu Gly Glu Thr Lys Asp Leu Lys Asn Leu
145          150          155          160
Tyr Glu Ser Val Lys Thr Glu Ala Leu His Ala Lys Ser Gln Lys Ser
165          170          175
Gln Gln Glu Leu Ile Lys Asn Leu Tyr Asn Thr Phe Phe Lys Glu Ala
180          185          190
Phe Lys Lys Gln Ser Glu Lys Leu Gly Ile Val Tyr Thr Pro Ile Glu
195          200          205
Val Val Asp Phe Ile Leu Arg Ala Thr Asn Gly Ile Leu Lys Lys His
210          215          220
Phe Asn Thr Asp Phe Asn Asp Gln Ser Ile Thr Ile Phe Asp Pro Phe
225          230          235          240
Thr Gly Thr Gly Ser Phe Ile Ala Arg Leu Leu Ser Lys Glu Asn Ala
245          250          255
Leu Ile Ser Asp Glu Ala Leu Lys Glu Lys Phe Gln Lys Asn Leu Phe
260          265          270
Ala Phe Asp Ile Val Leu Leu Ser Tyr Tyr Ile Ala Leu Ile Asn Ile
275          280          285
Thr Gln Ala Ala Gln Asn Arg Asp Gly Ser Leu Asn Asn Phe Lys Asn
290          295          300
Ile Ala Leu Thr Asp Ser Leu Asp Tyr Leu Glu Glu Lys Thr Asn Lys
305          310          315          320
Gly Val Leu Pro Leu Tyr Glu Asp Leu Lys Glu Asn Lys Gly Ile Lys
325          330          335
Asp Thr Leu Ala Asn Gln Asn Ile Arg Val Ile Ile Gly Asn Pro Pro
340          345          350
Tyr Ser Ala Gly Ala Lys Ser Gln Asn Asp Asn Asn Gln Asn Leu Ser
355          360          365
His Pro Lys Leu Glu Lys Leu Val Tyr Glu Lys Tyr Gly Lys Asn Ser
370          375          380
Thr Ser Arg Ser Val Gly Lys Thr Thr Arg Asp Thr Leu Ile Gln Ser
385          390          395          400
Ile Arg Met Ala Ser Asp Val Val Lys Asp Arg Gly Val Ile Gly Phe
405          410          415
Val Val Asn Gly Phe Ile Asp Ser Lys Ser Ala Asp Gly Phe Arg
420          425          430
Lys Cys Val Ala Lys Glu Phe Ser His Leu Tyr Val Leu Asn Leu Arg
435          440          445

```

TAC AAA AAT TCC CTC GCC AAA GAA GCG CCG CGC ATC GCT TTG AGC GAA	2403
Tyr Lys Asn Ser Leu Ala Lys Glu Ala Pro Arg Ile Ala Leu Ser Glu	
785 790 795	
GAT TTT AAA GAA CTC TCT GTG CTT GGC AAA GAA TTG GCC GAA TTG CAC	2451
Asp Phe Lys Glu Leu Ser Val Leu Gly Lys Glu Leu Ala Glu Leu His	
800 805 810	
CTG AAC TAT GAG AGT GGG GAA ATG CAT GAT AAT ATT AAA TAC ACC ACA	2499
Leu Asn Tyr Glu Ser Gly Glu Met His Asp Asn Ile Lys Tyr Thr Thr	
815 820 825	
CTG ATG AAC GCC GAA ATA GAG GGT TAT TAT GAT GTG GAT AAA ATG ACC	2547
Leu Met Asn Ala Glu Ile Glu Gly Tyr Tyr Asp Val Asp Lys Met Thr	
830 835 840	
AAA AAA GGG GAT TGC ATC ATC TAT AAC CAA AAC ATC GCT ATC ACT AAG	2595
Lys Lys Gly Asp Cys Ile Ile Tyr Asn Gln Asn Ile Ala Ile Thr Lys	
845 850 855 860	
ATC CCT AAA AAA GCC TTT GAC TAT GTC ATT AAT GGC AAG AGC GCG ATT	2643
Ile Pro Lys Lys Ala Phe Asp Tyr Val Ile Asn Gly Lys Ser Ala Ile	
865 870 875	
GAC TGG GTG ATC GAA CGC TAT CAA AAA ACT ATG GAT AAA GAA AGC CTG	2691
Asp Trp Val Ile Glu Arg Tyr Gln Lys Thr Met Asp Lys Glu Ser Leu	
880 885 890	
ATT GAA AAC AAC CCG AAC GAT TAC GCC GGC GGA AAA TAC GTT TTT GAA	2739
Ile Glu Asn Asn Pro Asn Asp Tyr Ala Gly Gly Lys Tyr Val Phe Glu	
895 900 905	
CTC CTT TGT AGG GTC ATC ACA CTT TCG GTA AAA AGC GTG GAT TTG ATA	2787
Leu Leu Cys Arg Val Ile Thr Leu Ser Val Lys Ser Val Asp Leu Ile	
910 915 920	
GAA AAG ATC AGC GAA AAG AGG TTT GAG TGATTACATC GCTTGGGGGT GTGGAAT	2841
Glu Lys Ile Ser Glu Lys Arg Phe Glu	
925 930	
ATTTTGAAAG GCAATGTCTT GCTTTCTTAA AAAATCCAC	2880

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

Met Thr-Gln Ala Trp Leu Met Lys Pro Leu Leu Lys Lys Lys Ser Lys

GAC ATC AAT TCT CTT GGC GTG GTG AGC GGT CGT GAT CCT TGG GTG TAT	1731
Asp Ile Asn Ser Leu Gly Val Val Ser Gly Arg Asp Pro Trp Val Tyr	
560 565 570	
AAC TTT TCT CCA AAC ATT TTA ACC CAA TCG GTG CAA AAA TGC ATT GAC	1779
Asn Phe Ser Pro Asn Ile Leu Thr Gln Ser Val Gln Lys Cys Ile Asp	
575 580 585	
ACT TAT AAC GCT GAT TTG AAG CGC TTC AAT GCG CGT TTT AGG GAA GCT	1827
Thr Tyr Asn Ala Asp Leu Lys Arg Phe Asn Ala Arg Phe Arg Glu Ala	
590 595 600	
TTC AAA CAA CGC GCT CAA AGC GTC AAA GCA GGC GAT CTT TAC AAA CAA	1875
Phe Lys Gln Arg Ala Gln Ser Val Lys Ala Gly Asp Leu Tyr Lys Gln	
605 610 615 620	
CTT AAT GAT AAA GAA ATC ACC ACC GAT AAA ACG AAA ATC GCT TGG ACT	1923
Leu Asn Asp Lys Glu Ile Thr Thr Asp Lys Thr Lys Ile Ala Trp Thr	
625 630 635	
GAT GGT TTG AAA AAC AAA CTC ATT AAA AAT AAA TCT GCA AGA GAA AGC	1971
Asp Gly Leu Lys Asn Lys Leu Ile Lys Asn Lys Ser Ala Arg Glu Ser	
640 645 650	
AGT GAG GAG CGT GTA AGG TTG GCC TTG TAT CGC CCT TTT AAC AAA CAA	2019
Ser Glu Glu Arg Val Arg Leu Ala Leu Tyr Arg Pro Phe Asn Lys Gln	
655 660 665	
TGG CTT TAT TGG GAT AAG GAT TGG ATA AAC AGG CAA AGA GAA TTT TCA	2067
Trp Leu Tyr Trp Asp Lys Asp Trp Ile Asn Arg Gln Arg Glu Phe Ser	
670 675 680	
AAA ATT TTC CCG GAT AAA GAC GCT CAG AAT GTG GTG ATT AAT ACC GGT	2115
Lys Ile Phe Pro Asp Lys Asp Ala Gln Asn Val Val Ile Asn Thr Gly	
685 690 695 700	
GTG GGA AAT GGT AAA GAT TTT AGC GCT TTG GTA AGC GAT TTT ATT TCT	2163
Val Gly Asn Gly Lys Asp Phe Ser Ala Leu Val Ser Asp Phe Ile Ser	
705 710 715	
GAT TAT AGT TTG ATC TCA CCC AAT CAA GCT TAC CCC TTG TAT TAT TAC	2211
Asp Tyr Ser Leu Ile Ser Pro Asn Gln Ala Tyr Pro Leu Tyr Tyr Tyr	
720 725 730	
GAT GAT TTG GGG AAT CGC CAT TAC GCC ATC AGC GGC TAT TGC TTA AAC	2259
Asp Asp Leu Gly Asn Arg His Tyr Ala Ile Ser Gly Tyr Cys Leu Asn	
735 740 745	
CTC TTC AGG AGG CAT TAT GGG GAT AAT CTG ATC GCT GAA GAA GAG ATT	2307
Leu Phe Arg Arg His Tyr Gly Asp Asn Leu Ile Ala Glu Glu Glu Ile	
750 755 760	
TTT TAT TAC ATT TAT GCG ATT TTC CAC CAT AAA GGC TAT TTA GAA AAA	2355
Phe Tyr Tyr Ile Tyr Ala Ile Phe His His Lys Gly Tyr Leu Glu Lys	
765 770 775 780	

AAA GGC ATC AAA GAC ACT CTA GCC AAC CAA AAT ATT AGA GTC ATC ATC	1059
Lys Gly Ile Lys Asp Thr Leu Ala Asn Gln Asn Ile Arg Val Ile Ile	
335 340 345	
GGC AAC CCG CCT TAT TCA GCC GGC GCA AAG AGC CAA AAC GAT AAC AAC	1107
Gly Asn Pro Pro Tyr Ser Ala Gly Ala Lys Ser Gln Asn Asp Asn Asn	
350 355 360	
CAA AAC CTC TCA CAC CCA AAG CTT GAA AAA TTA GTT TAT GAA AAA TAC	1155
Gln Asn Leu Ser His Pro Lys Leu Glu Lys Leu Val Tyr Glu Lys Tyr	
365 370 375 380	
GGA AAA AAT TCC ACA TCT AGA AGT GTG GGA AAA ACC ACA CGA GAC ACG	1203
Gly Lys Asn Ser Thr Ser Arg Ser Val Gly Lys Thr Thr Arg Asp Thr	
385 390 395	
CTC ATT CAA AGC ATC CGC ATG GCG AGC GAT GTT GTT AAA GAT AGG GGG	1251
Leu Ile Gln Ser Ile Arg Met Ala Ser Asp Val Val Lys Asp Arg Gly	
400 405 410	
GTG ATA GGC TTT GTG GTG AAC GGG GGT TTT ATT GAC TCT AAA AGC GCG	1299
Val Ile Gly Phe Val Val Asn Gly Gly Phe Ile Asp Ser Lys Ser Ala	
415 420 425	
GAT GGG TTC AGA AAA TGC GTG GCC AAA GAA TTT TCG CAT CTT TAT GTA	1347
Asp Gly Phe Arg Lys Cys Val Ala Lys Glu Phe Ser His Leu Tyr Val	
430 435 440	
TTG AAT TTG AGA GGC AAT CAG CGC ACT TCT GGG GAA GTG TCA AAA AAA	1395
Leu Asn Leu Arg Gly Asn Gln Arg Thr Ser Gly Glu Val Ser Lys Lys	
445 450 455 460	
GAG GGA GGG AAA ATC TTT GAT AGC GGA TCG AGG GCG ACG GTA GCG ATT	1443
Glu Gly Gly Lys Ile Phe Asp Ser Gly Ser Arg Ala Thr Val Ala Ile	
465 470 475	
ATC TTT TTT GTG AAA GAT AAG AGC ACT CCT GAT AAT ACG ATT TTT TAT	1491
Ile Phe Phe Val Lys Asp Lys Ser Thr Pro Asp Asn Thr Ile Phe Tyr	
480 485 490	
TAT GAA GTG GAA GAT TAC TTG AAA AGA GAA GCC AAA CTC AAC TGG CTC	1539
Tyr Glu Val Glu Asp Tyr Leu Lys Arg Glu Ala Lys Leu Asn Trp Leu	
495 500 505	
GCC AAT TTT GAA AAT TTG GAT TTT GTG CCT TTT GAG AAA ATC ACC CCG	1587
Ala Asn Phe Glu Asn Leu Asp Phe Val Pro Phe Glu Lys Ile Thr Pro	
510 515 520	
AAT GAT AAA GGC GAT TGG ATC AAC CAA AGG AAT GAC GCT TTT GAA AAA	1635
Asn Asp Lys Gly Asp Trp Ile Asn Gln Arg Asn Asp Ala Phe Glu Lys	
525 530 535 540	
CTC ATC CCT TTA AAA AGA GAC AAA ACA CTC CAA AAC GAC AGC GTT TTT	1683
Leu Ile Pro Leu Lys Arg Asp Lys Thr Leu Gln Asn Asp Ser Val Phe	
545 550 555	

Leu	Asp	Met	Ile	Thr	Ser	His	Ile	Ile	Thr	Lys	Pro	Ile	Phe	Asp	Ala		
110						115					120						
CTT	TTT	GGG	GAC	AAC	ATC	AAA	AAC	CCT	ATC	GCT	AAA	GCC	TTG	GAT	AAA	435	
Leu	Phe	Gly	Asp	Asn	Ile	Lys	Asn	Pro	Ile	Ala	Lys	Ala	Leu	Asp	Lys		
125					130					135					140		
ATG	GTA	GAA	AAA	CTC	TCC	ACT	TTA	GGA	TTA	GAA	GGA	GAA	ACT	AAA	GAT	483	
Met	Val	Glu	Lys	Leu	Ser	Thr	Leu	Gly	Leu	Glu	Gly	Glu	Thr	Lys	Asp		
				145					150					155			
CTG	AAA	AAC	CTC	TAT	GAA	AGC	GTG	AAA	ACC	GAA	GCC	TTG	CAC	GCC	AAA	531	
Leu	Lys	Asn	Leu	Tyr	Glu	Ser	Val	Lys	Thr	Glu	Ala	Leu	His	Ala	Lys		
			160					165					170				
AGC	CAA	AAA	AGC	CAA	CAA	GAA	CTC	ATT	AAA	AAC	CTC	TAC	AAC	ACT	TTC	579	
Ser	Gln	Lys	Ser	Gln	Gln	Glu	Leu	Ile	Lys	Asn	Leu	Tyr	Asn	Thr	Phe		
		175					180					185					
TTT	AAA	GAA	GCC	TTT	AAA	AAG	CAA	AGC	GAA	AAA	CTA	GGG	ATC	GTT	TAT	627	
Phe	Lys	Glu	Ala	Phe	Lys	Lys	Gln	Ser	Glu	Lys	Leu	Gly	Ile	Val	Tyr		
	190					195					200						
ACG	CCC	ATA	GAG	GTG	GTG	GAT	TTC	ATT	TTA	AGA	GCC	ACT	AAC	GGC	ATT	675	
Thr	Pro	Ile	Glu	Val	Val	Asp	Phe	Ile	Leu	Arg	Ala	Thr	Asn	Gly	Ile		
205					210					215					220		
TTG	AAA	AAG	CAT	TTC	AAC	ACG	GAT	TTT	AAC	GAT	CAA	AGC	ATC	ACG	ATT	723	
Leu	Lys	Lys	His	Phe	Asn	Thr	Asp	Phe	Asn	Asp	Gln	Ser	Ile	Thr	Ile		
			225					230					235				
TTT	GAC	CCA	TTC	ACC	GGC	ACC	GGG	AGT	TTT	ATC	GCT	CGT	TTG	CTT	TCT	771	
Phe	Asp	Pro	Phe	Thr	Gly	Thr	Gly	Ser	Phe	Ile	Ala	Arg	Leu	Leu	Ser		
			240					245					250				
AAA	GAA	AAC	GCG	CTC	ATT	AGC	GAT	GAA	GCC	TTA	AAA	GAG	AAG	TTT	CAA	819	
Lys	Glu	Asn	Ala	Leu	Ile	Ser	Asp	Glu	Ala	Leu	Lys	Glu	Lys	Phe	Gln		
		255					260					265					
AAA	AAT	TTG	TTC	GCT	TTT	GAC	ATC	GTG	CTT	TTG	TCT	TAT	TAT	ATC	GCT	867	
Lys	Asn	Leu	Phe	Ala	Phe	Asp	Ile	Val	Leu	Leu	Ser	Tyr	Tyr	Ile	Ala		
	270					275					280						
TTA	ATC	AAT	ATC	ACC	CAA	GCC	GCG	CAA	AAT	AGG	GAT	GGC	TCG	TTA	AAC	915	
Leu	Ile	Asn	Ile	Thr	Gln	Ala	Ala	Gln	Asn	Arg	Asp	Gly	Ser	Leu	Asn		
285					290				295						300		
AAT	TTC	AAA	AAC	ATC	GCG	CTC	ACG	GAC	AGC	CTG	GAT	TAT	TTA	GAA	GAA	963	
Asn	Phe	Lys	Asn	Ile	Ala	Leu	Thr	Asp	Ser	Leu	Asp	Tyr	Leu	Glu	Glu		
			305					310					315				
AAA	ACC	AAT	AAA	GGG	GTG	CTC	CCT	TTA	TAT	GAG	GAT	TTG	AAA	GAA	AAC	1011	
Lys	Thr	Asn	Lys	Gly	Val	Leu	Pro	Leu	Tyr	Glu	Asp	Leu	Lys	Glu	Asn		
			320					325					330				

```

Ile Trp Lys Val Ile Lys Ala Leu Arg Ser His Asp Pro Ser Leu Val
      515                      520                      525
Asp Glu Ala Thr Phe Lys Glu Lys Ile Lys Ile Phe Gly Ser Asp Asp
      530                      535                      540
Gly Asn Gln Ser Gln Arg
545                      550

```

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2880 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...2814
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

```

AAGCCTTAAG AAGCC ATG ACC CAA GCC TGG TTG ATG AAG CCA CTT TTA AAG      51
      Met Thr Gln Ala Trp Leu Met Lys Pro Leu Leu Lys
        1                      5                      10

AAA AAA TCA AAA TCT TTG GAA GCG ATG ATG GCA ACC AAT CAC AAC GAT      99
Lys Lys Ser Lys Ser Leu Glu Ala Met Met Ala Thr Asn His Asn Asp
      15                      20                      25

GAA AAA ACC CTT TTT GAC GCT ATC TTA CTG CAA GAT CTA GCG GAC GCT      147
Glu Lys Thr Leu Phe Asp Ala Ile Leu Leu Gln Asp Leu Ala Asp Ala
      30                      35                      40

ATG TAT AAT GTC ATG CCC ACT AAA TTA GGG GAC AGG AAT TAT TGG GAA      195
Met Tyr Asn Val Met Pro Thr Lys Leu Gly Asp Arg Asn Tyr Trp Glu
      45                      50                      55                      60

AAT TTC ACT AAA AAA ACG GGC AAC ATC GCA AGG ACC TTG AAC AAC CGC      243
Asn Phe Thr Lys Lys Thr Gly Asn Ile Ala Arg Thr Leu Asn Asn Arg
        65                      70                      75

CTA AAA ATT ATT TTT GAC AAA AAC CCT GAA TTT TTC CAC GGC TTT TTG      291
Leu Lys Ile Ile Phe Asp Lys Asn Pro Glu Phe Phe His Gly Phe Leu
        80                      85                      90

GAT TCC TTA AGG GAA AAT ATC CAT CAA AAC ATT AAA GAA GAT GAA GCC      339
Asp Ser Leu Arg Glu Asn Ile His Gln Asn Ile Lys Glu Asp Glu Ala
        95                      100                      105

TTA GAC ATG ATC ACT TCT CAC ATC ATC ACT AAG CCC ATT TTT GAT GCA      387

```


65					70					75					80
Met	Glu	Ala	Leu	Asp	Ser	Lys	Ile	Thr	Leu	Phe	Leu	Ala	Pro	Ser	Ile
				85						90				95	
Ala	Leu	Leu	Ser	Gln	Thr	Phe	Arg	Glu	Tyr	Ala	Gln	Glu	Lys	Ser	Glu
			100					105					110		
Pro	Phe	Tyr	Ala	Ser	Ile	Val	Cys	Ser	Asp	Asp	Lys	Val	Gly	Lys	Ser
		115					120					125			
Lys	Asp	Glu	Asp	Asn	Asp	Asp	Ile	Lys	Phe	Ser	Glu	Leu	Pro	Leu	Lys
	130					135					140				
Pro	Ser	Thr	Arg	Leu	Glu	Asp	Ile	Leu	Ser	Val	Arg	Lys	Lys	Ala	Gln
145					150					155					160
Lys	Glu	Asn	Lys	Arg	Phe	Ile	Ile	Phe	Ser	Thr	Tyr	Gln	Ser	Ala	Leu
				165				170						175	
Arg	Ile	Lys	Glu	Ala	Gln	Glu	Ala	Gly	Leu	Gly	Gly	Ile	Asp	Leu	Ile
			180					185					190		
Ile	Cys	Asp	Glu	Ala	His	Arg	Thr	Val	Gly	Ala	Met	Tyr	Ser	Ser	Asn
	195						200					205			
Glu	Arg	Asp	Asp	Lys	Asn	Ala	Phe	Thr	Leu	Cys	His	Ser	Asp	Lys	Asn
	210				215						220				
Ile	Lys	Ala	Lys	Lys	Arg	Leu	Tyr	Met	Thr	Ala	Thr	Pro	Lys	Val	Tyr
225					230					235					240
Ser	Glu	Ser	Ser	Lys	Ala	Lys	Ala	Lys	Glu	Ser	Asp	Asn	Val	Ile	Tyr
				245					250					255	
Ser	Met	Asp	Asp	Ala	Glu	Ile	Phe	Gly	Glu	Glu	Ile	Tyr	Thr	Leu	Asn
		260						265					270		
Phe	Ser	Lys	Ala	Ile	Ala	Leu	Asp	Leu	Leu	Thr	Asp	Tyr	Lys	Val	Ile
	275						280					285			
Ile	Leu	Ala	Val	Arg	Lys	Glu	Asn	Leu	Ser	Gly	Val	Thr	Asn	Ser	Val
	290				295						300				
Asn	Lys	Lys	Ile	Ser	Gln	Leu	Lys	Ala	Glu	Gly	Thr	Lys	Leu	Asp	Lys
305					310					315					320
Lys	Leu	Ile	Asn	Asn	Glu	Phe	Val	Cys	Lys	Ile	Ile	Gly	Thr	His	Lys
				325					330					335	
Gly	Leu	Ala	Lys	Gln	Asp	Leu	Ile	Val	Leu	Asn	Glu	Lys	Asn	Lys	Glu
			340					345					350		
Asp	His	Asn	Leu	Gln	Asn	Gln	Tyr	Asp	Thr	Ala	Pro	Ser	Gln	Arg	Ala
	355						360					365			
Ile	Asn	Phe	Cys	Lys	Ser	Ile	Asn	Thr	Ser	Lys	Asn	Ile	Lys	Asp	Ser
	370					375					380				
Phe	Glu	Thr	Ile	Met	Glu	Cys	Tyr	Asp	Glu	Glu	Leu	Lys	Lys	Lys	Ser
385					390					395					400
Phe	Lys	Asn	Leu	Lys	Ile	Ser	Ile	Asp	His	Ile	Asp	Gly	Thr	Met	Asn
				405					410					415	
Cys	Lys	Asp	Arg	Leu	Glu	Lys	Leu	Glu	Glu	Leu	Asn	Gln	Phe	Glu	Pro
		420						425					430		
Asn	Thr	Cys	Lys	Val	Leu	Ser	Asn	Ala	Arg	Cys	Leu	Ser	Glu	Gly	Val
	435						440					445			
Asp	Val	Pro	Ala	Leu	Asp	Ser	Ile	Val	Phe	Phe	Asp	Gly	Lys	Ser	Ala
	450					455					460				
Met	Val	Asp	Ile	Ile	Gln	Ala	Val	Gly	Arg	Val	Met	Arg	Lys	Ala	Lys
465					470					475					480
Arg	Lys	Lys	Arg	Gly	Tyr	Ile	Ile	Leu	Pro	Ile	Ala	Leu	Glu	Glu	Ser
				485					490					495	
Glu	Ile	Gln	Asn	Leu	Asp	Glu	Ala	Val	Asn	Asn	Thr	Asn	Phe	Lys	Asn
			500					505					510		

```

GAG CCC AAC ACT TGC AAG GTT TTA AGC AAC GCC AGG TGT TTG AGC GAA      1406
Glu Pro Asn Thr Cys Lys Val Leu Ser Asn Ala Arg Cys Leu Ser Glu
                     435                     440                     445

GGG GTG GAT GTC CCA GCG TTA GAT AGC ATC GTC TTT TTT GAT GGC AAA      1454
Gly Val Asp Val Pro Ala Leu Asp Ser Ile Val Phe Phe Asp Gly Lys
                     450                     455                     460

AGC GCT ATG GTG GAT ATT ATC CAA GCG GTG GGT AGG GTG ATG CGA AAA      1502
Ser Ala Met Val Asp Ile Ile Gln Ala Val Gly Arg Val Met Arg Lys
                     465                     470                     475

GCC AAA CGC AAG AAA AGA GGC TAT ATC ATT TTG CCT ATC GCT TTA GAA      1550
Ala Lys Arg Lys Lys Arg Gly Tyr Ile Ile Leu Pro Ile Ala Leu Glu
                     480                     485                     490

GAG AGT GAA ATC CAA AAC CTG GAT GAA GCC GTC AAT AAC ACC AAT TTC      1598
Glu Ser Glu Ile Gln Asn Leu Asp Glu Ala Val Asn Asn Thr Asn Phe
495                     500                     505                     510

AAA AAC ATT TGG AAA GTG ATA AAA GCC TTA AGA AGC CAT GAC CCA AGC      1646
Lys Asn Ile Trp Lys Val Ile Lys Ala Leu Arg Ser His Asp Pro Ser
                     515                     520                     525

CTG GTT GAT GAA GCC ACT TTT AAA GAA AAA ATC AAA ATC TTT GGA AGC      1694
Leu Val Asp Glu Ala Thr Phe Lys Glu Lys Ile Lys Ile Phe Gly Ser
                     530                     535                     540

GAT GAT GGC AAC CAA TCA CAA CGA TGAAAAAACC CTTTTTGACG CTATCTTACT      1748
Asp Asp Gly Asn Gln Ser Gln Arg
                     545                     550

GCAAGATCTA GCGGACGCTA TGTATAATGT CATGCCCACT AAATTAGGGG AC      1800

```

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

```

Met Gly Ile Asp Ile Asp Glu Ile Thr Glu Glu Asp Phe Ile Tyr Ser
 1             5             10             15
Arg Ile Asp Trp Glu Lys Phe Asp Pro Thr Lys Thr Gln Asp Glu Ile
      20             25             30
Pro Leu Cys Asp Lys Lys Lys Pro Arg Ser His Gln Thr Glu Ala Ile
      35             40             45
Asn Ala Thr Lys Glu Tyr Phe Ser Asp Pro Lys Asn Ala Arg Gly Lys
      50             55             60
Leu Ile Met Ala Cys Gly Thr Gly Lys Thr Tyr Thr Ser Leu Lys Ile

```

AGT AAT GAA AGG GAC GAT AAA AAC GCT TTC ACG CTT TGC CAT AGC GAT	734
Ser Asn Glu Arg Asp Asp Lys Asn Ala Phe Thr Leu Cys His Ser Asp	
210 215 220	
AAA AAT ATC AAA GCG AAA AAA CGC CTG TAT ATG ACC GCC ACG CCT AAA	782
Lys Asn Ile Lys Ala Lys Lys Arg Leu Tyr Met Thr Ala Thr Pro Lys	
225 230 235	
GTT TAT AGC GAA AGC TCC AAA GCT AAA GCC AAA GAG AGC GAT AAT GTT	830
Val Tyr Ser Glu Ser Ser Lys Ala Lys Ala Lys Glu Ser Asp Asn Val	
240 245 250	
ATC TAT TCT ATG GAC GAT GCA GAG ATT TTT GGC GAA GAA ATC TAT ACG	878
Ile Tyr Ser Met Asp Asp Ala Glu Ile Phe Gly Glu Glu Ile Tyr Thr	
255 260 265 270	
CTC AAT TTT TCA AAA GCG ATC GCT TTG GAT CTC TTA ACC GAT TAT AAA	926
Leu Asn Phe Ser Lys Ala Ile Ala Leu Asp Leu Leu Thr Asp Tyr Lys	
275 280 285	
GTC ATC ATT TTA GCG GTG CGA AAA GAA AAT TTA AGC GGC GTT ACT AAC	974
Val Ile Ile Leu Ala Val Arg Lys Glu Asn Leu Ser Gly Val Thr Asn	
290 295 300	
AGC GTG AAT AAA AAG ATC AGC CAG CTC AAA GCC GAA GGC ACT AAA TTA	1022
Ser Val Asn Lys Lys Ile Ser Gln Leu Lys Ala Glu Gly Thr Lys Leu	
305 310 315	
GAT AAA AAG CTC ATC AAT AAC GAA TTT GTT TGT AAG ATC ATC GGC ACT	1070
Asp Lys Lys Leu Ile Asn Asn Glu Phe Val Cys Lys Ile Ile Gly Thr	
320 325 330	
CAT AAA GGG TTA GCC AAG CAG GAT TTA ATC GTT TTA AAC GAG AAA AAC	1118
His Lys Gly Leu Ala Lys Gln Asp Leu Ile Val Leu Asn Glu Lys Asn	
335 340 345 350	
AAA GAA GAT CAC AAC TTG CAA AAC CAA TAC GAC ACC GCT CCC TCT CAA	1166
Lys Glu Asp His Asn Leu Gln Asn Gln Tyr Asp Thr Ala Pro Ser Gln	
355 360 365	
AGA GCC ATA AAC TTT TGT AAA AGC ATT AAC ACG AGC AAG AAC ATT AAA	1214
Arg Ala Ile Asn Phe Cys Lys Ser Ile Asn Thr Ser Lys Asn Ile Lys	
370 375 380	
GAC TCC TTT GAA ACG ATT ATG GAA TGC TAT GAT GAA GAG TTG AAG AAA	1262
Asp Ser Phe Glu Thr Ile Met Glu Cys Tyr Asp Glu Glu Leu Lys Lys	
385 390 395	
AAG AGT TTT AAA AAC CTA AAA ATC AGC ATC GAT CAC ATT GAT GGC ACC	1310
Lys Ser Phe Lys Asn Leu Lys Ile Ser Ile Asp His Ile Asp Gly Thr	
400 405 410	
ATG AAT TGT AAG GAT AGG CTT GAA AAA TTA GAA GAG CTC AAT CAA TTT	1358
Met Asn Cys Lys Asp Arg Leu Glu Lys Leu Glu Glu Leu Asn Gln Phe	
415 420 425 430	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

TCATCATCTC CACTTCTAAT TTAACCTCTA ACGCCCTTAA CGCAATTGAG CAAATCAGAA	60
GCACAGGA ATG GGG ATT GAC ATT GAT GAA ATC ACT GAA GAG GAT TTT ATC	110
Met Gly Ile Asp Ile Asp Glu Ile Thr Glu Glu Asp Phe Ile	
1 5 10	
TAT TCT CGC ATT GAT TGG GAA AAG TTT GAT CCC ACA AAA ACG CAA GAC	158
Tyr Ser Arg Ile Asp Trp Glu Lys Phe Asp Pro Thr Lys Thr Gln Asp	
15 20 25 30	
GAA ATC CCC TTA TGC GAT AAG AAA AAG CCG CGC TCG CAT CAA ACA GAA	206
Glu Ile Pro Leu Cys Asp Lys Lys Lys Pro Arg Ser His Gln Thr Glu	
35 40 45	
GCC ATA AAC GCC ACT AAA GAG TAT TTT TCT GAC CCT AAA AAC GCT AGA	254
Ala Ile Asn Ala Thr Lys Glu Tyr Phe Ser Asp Pro Lys Asn Ala Arg	
50 55 60	
GGC AAG CTC ATT ATG GCA TGC GGG ACA GGC AAA ACC TAC ACT TCT TTA	302
Gly Lys Leu Ile Met Ala Cys Gly Thr Gly Lys Thr Tyr Thr Ser Leu	
65 70 75	
AAA ATC ATG GAA GCT TTA GAC TCT AAG ATC ACG CTT TTT CTA GCA CCC	350
Lys Ile Met Glu Ala Leu Asp Ser Lys Ile Thr Leu Phe Leu Ala Pro	
80 85 90	
AGC ATC GCT TTG CTT TCT CAA ACT TTT AGA GAA TAC GCG CAA GAA AAA	398
Ser Ile Ala Leu Leu Ser Gln Thr Phe Arg Glu Tyr Ala Gln Glu Lys	
95 100 105 110	
AGT GAG CCG TTT TAC GCT TCT ATC GTG TGC AGC GAT GAT AAA GTC GGG	446
Ser Glu Pro Phe Tyr Ala Ser Ile Val Cys Ser Asp Asp Lys Val Gly	
115 120 125	
AAA AGT AAA GAC GAA GAC AAT GAT GAT ATT AAA TTT TCT GAG CTC CCT	494
Lys Ser Lys Asp Glu Asp Asn Asp Asp Ile Lys Phe Ser Glu Leu Pro	
130 135 140	
TTA AAG CCC TCC ACT CGC CTT GAA GAC ATT TTA AGC GTT CGA AAA AAA	542
Leu Lys Pro Ser Thr Arg Leu Glu Asp Ile Leu Ser Val Arg Lys Lys	
145 150 155	
GCG CAA AAA GAA AAC AAG CGC TTC ATT ATT TTT TCA ACC TAT CAA AGC	590
Ala Gln Lys Glu Asn Lys Arg Phe Ile Ile Phe Ser Thr Tyr Gln Ser	
160 165 170	
GCG TTG CGT ATT AAA GAA GCG CAA GAA GCG GGT TTG GGC GGA ATC GAT	638
Ala Leu Arg Ile Lys Glu Ala Gln Glu Ala Gly Leu Gly Gly Ile Asp	
175 180 185 190	
CTT ATT ATT TGC GAT GAA GCC CAC AGA ACG GTA GGG GCT ATG TAT TCT	686
Leu Ile Ile Cys Asp Glu Ala His Arg Thr Val Gly Ala Met Tyr Ser	
195 200 205	

```

TTG GTG TCT ATG ATT TCT TTA GCC CTA AGA AGC CCC ACT TTT AAA GAA      245
Leu Val Ser Met Ile Ser Leu Ala Leu Arg Ser Pro Thr Phe Lys Glu
           60                      65                      70

AAT CCC GCC TTT TGT GTT TGC ATC GTA ATC CCC CCA AAA CCG CAA CAA      293
Asn Pro Ala Phe Cys Val Cys Ile Val Ile Pro Pro Lys Pro Gln Gln
           75                      80                      85

TTG TCC GGC ATT TCT TTA ATT TCA TAATGCAAAT TGAGCAACCT TTTGCATTCT      347
Leu Ser Gly Ile Ser Leu Ile Ser
           90                      95

TAC                                                                    350

```

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

```

Met Leu Glu Asn Gly Val Lys Lys Ala Phe Tyr Ser Ala Leu Phe Lys
 1           5           10           15
Ala Leu Ala Met Ser Ser Lys Gly Cys Lys Asn Gly Gly Val Leu Gly
 20           25           30
Ser Ser Lys Asp Phe Lys Ala Leu Phe Asn Cys Ile Trp His Ala Pro
 35           40           45
His Ser Ala Leu Lys Ile Ala Ala Leu Val Ser Met Ile Ser Leu Ala
 50           55           60
Leu Arg Ser Pro Thr Phe Lys Glu Asn Pro Ala Phe Cys Val Cys Ile
 65           70           75           80
Val Ile Pro Pro Lys Pro Gln Gln Leu Ser Gly Ile Ser Leu Ile Ser
           85           90           95

```

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 69...1718
- (D) OTHER INFORMATION:

```

Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu Lys Ile Thr Pro Lys
      20              25              30
Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His Thr Pro Leu Lys Ser
      35              40              45
Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu Thr Ile Thr Tyr His
      50              55              60
Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala His Lys Glu Val Arg
      65              70              75              80
Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu Met Pro Asp Asn Cys
      85              90              95
Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln Lys Ala Gly Phe Ser
      100             105             110
Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile Ile Asp Thr Lys Ala
      115             120             125
Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His Met Gln Leu Asn Asn
      130             135             140
Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro Pro Phe Leu His Pro
      145             150             155             160
Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala Glu
      165             170

```

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...317
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

```

GGCGTTAAAG CTCTGTATTA TATAAAAAG ATG TTG GAG AAT GGG GTT AAA AAG      53
                               Met Leu Glu Asn Gly Val Lys Lys
                               1              5

GCT TTT TAT TCA GCG CTT TTT AAG GCT TTA GCG ATG AGT TCT AAA GGG      101
Ala Phe Tyr Ser Ala Leu Phe Lys Ala Leu Ala Met Ser Ser Lys Gly
      10              15              20

TGC AAA AAT GGC GGA GTG TTA GGG TCG TCT AAA GAC TTT AAA GCG TTG      149
Cys Lys Asn Gly Gly Val Leu Gly Ser Ser Lys Asp Phe Lys Ala Leu
      25              30              35              40

TTT AAT TGC ATA TGG CAT GCC CCG CAT TCA GCG CTC AAA ATT GCA GCT      197
Phe Asn Cys Ile Trp His Ala Pro His Ser Ala Leu Lys Ile Ala Ala
      45              50              55

```

AAA ATC ACG CCT AAA ATC TAT CTG GCG AGC GTG TTT TTA GAG AAA CAC	148
Lys Ile Thr Pro Lys Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His	
30 35 40	
ACC CCT TTA AAA AGT CTT TTA GAA AAA ATC CCT AAG GGA AAA AAA GAG	196
Thr Pro Leu Lys Ser Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu	
45 50 55	
ACT ATC ACC TAT CAT AAC CCT TGT CAT GCC AAA AAA ACC CTA AAC GCT	244
Thr Ile Thr Tyr His Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala	
60 65 70 75	
CAC AAA GAA GTG CGC AAC TTG CTC AAT TTG CAT TAT GAA ATT AAA GAA	292
His Lys Glu Val Arg Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu	
80 85 90	
ATG CCG GAC AAT TGT TGC GGT TTT GGG GGG ATT ACG ATG CAA ACA CAA	340
Met Pro Asp Asn Cys Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln	
95 100 105	
AAG GCG GGA TTT TCT TTA AAA GTG GGG CTT CTT AGG GCT AAA GAA ATC	388
Lys Ala Gly Phe Ser Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile	
110 115 120	
ATA GAC ACC AAA GCT GCA ATT TTG AGC GCT GAA TGC GGG GCA TGC CAT	436
Ile Asp Thr Lys Ala Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His	
125 130 135	
ATG CAA TTA AAC AAC GCT TTA AAG TCT TTA GAC GAC CCT AAC ACT CCG	484
Met Gln Leu Asn Asn Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro	
140 145 150 155	
CCA TTT TTG CAC CCT TTA GAA CTC ATC GCT AAA GCC TTA AAA AGC GCT	532
Pro Phe Leu His Pro Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala	
160 165 170	
GAA TAAAAAGCCT TTTTAACCCC ATTCTCCAAC ATCTTTTAT ATAATACAGA GCT	588
Glu	

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys Val Phe Leu Gly Glu
1 5 10 15

				165					170					175					
Asn	Tyr	Asp	Phe	Asn	His	Ala	Leu	Lys	Ser	Glu	Ile	Phe	Ala	Leu	Asp				
			180					185					190						
Glu	Glu	Gln	Glu	Glu	Ala	Gln	Lys	Thr	Ala	Ile	Gln	Asn	Ala	Ile	Lys				
		195					200					205							
Asn	His	Asp	Ser	Ile	Gly	Gly	Val	Ala	Leu	Ile	Arg	Ala	Arg	Ser	Ile				
	210				215					220									
Lys	Thr	Asn	Gln	Lys	Leu	Pro	Ile	Gly	Leu	Gly	Gln	Gly	Leu	Tyr	Ala				
225				230					235					240					
Lys	Leu	Asp	Ala	Lys	Ile	Ala	Glu	Ala	Met	Met	Gly	Leu	Asn	Gly	Val				
			245					250					255						
Lys	Ala	Val	Glu	Ile	Gly	Lys	Gly	Val	Glu	Ser	Ser	Leu	Leu	Lys	Gly				
		260					265						270						
Ser	Glu	Tyr	Asn	Asp	Leu	Met	Asp	Gln	Lys	Gly	Phe	Leu	Ser	Asn	Arg				
	275					280						285							
Ser	Gly	Gly	Val	Leu	Gly	Gly	Met	Ser	Asn	Gly	Glu	Glu	Ile	Ile	Val				
	290				295					300									
Arg	Val	His	Phe	Lys	Pro	Thr	Pro	Ser	Ile	Phe	Gln	Pro	Gln	Arg	Thr				
305				310						315				320					
Ile	Asp	Ile	Asn	Gly	Asn	Glu	Cys	Glu	Cys	Leu	Leu	Lys	Gly	Arg	His				
			325					330					335						
Asp	Pro	Cys	Ile	Ala	Ile	Arg	Gly	Ser	Val	Val	Cys	Glu	Ser	Leu	Leu				
		340					345					350							
Ala	Leu	Val	Leu	Ala	Asp	Met	Val	Leu	Leu	Asn	Leu	Thr	Ser	Lys	Ile				
	355				360						365								
Glu	Tyr	Leu	Lys	Thr	Ile	Tyr	Asn	Glu	Asn										
370					375														

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 20...535
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

TCATTGTGCC	TGAAGCCAC	ATG	CGC	TAC	ATG	CTC	ATC	AAC	GAT	TAT	TAC	AAG	52			
	Met	Arg	Tyr	Met	Leu	Ile	Asn	Asp	Tyr	Tyr	Lys					
	1				5					10						
GTG	TTT	TTG	GGC	GAA	AAA	GAT	AAG	GAT	TTG	TAT	GTG	AAG	CGC	TTG	GAA	100
Val	Phe	Leu	Gly	Glu	Lys	Asp	Lys	Asp	Leu	Tyr	Val	Lys	Arg	Leu	Glu	
	15					20					25					


```

TTC AAA CCC ACG CCA AGC ATT TTC CAA CCT CAA CGA ACC ATA GAC ATT      1016
Phe Lys Pro Thr Pro Ser Ile Phe Gln Pro Gln Arg Thr Ile Asp Ile
      310                      315                      320

AAT GGC AAT GAG TGC GAA TGC TTG TTA AAG GGC AGG CAT GAT CCT TGC      1064
Asn Gly Asn Glu Cys Glu Cys Leu Leu Lys Gly Arg His Asp Pro Cys
      325                      330                      335

ATT GCG ATT AGA GGG AGC GTG GTG TGC GAG AGT TTG TTA GCG TTG GTG      1112
Ile Ala Ile Arg Gly Ser Val Val Cys Glu Ser Leu Leu Ala Leu Val
      340                      345                      350                      355

TTG GCT GAT ATG GTA TTA CTC AAT TTG ACT TCA AAA ATA GAG TAT TTA      1160
Leu Ala Asp Met Val Leu Leu Asn Leu Thr Ser Lys Ile Glu Tyr Leu
      360                      365                      370

AAA ACG ATT TAT AAT GAG AAT TAAACGAAAT TGGATACAAT CAGCTTAAAA AGGA      1215
Lys Thr Ile Tyr Asn Glu Asn
      375

TA                                                                    1217

```

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

```

Met Arg Leu Ser Ser Ala Ser Lys Thr Glu Gly Ser Gln Met Asn Thr
 1           5           10           15
Leu Gly Arg Phe Leu Arg Leu Thr Thr Phe Gly Glu Ser His Gly Asp
      20           25           30
Val Ile Gly Gly Val Leu Asp Gly Met Pro Ser Gly Ile Lys Ile Asp
      35           40           45
Tyr Ala Leu Leu Glu Asn Glu Met Lys Arg Arg Gln Gly Gly Arg Asn
      50           55           60
Val Phe Ile Thr Pro Arg Lys Glu Asp Asp Lys Val Glu Ile Thr Ser
      65           70           75           80
Gly Val Phe Glu Asp Phe Ser Thr Gly Thr Pro Ile Gly Phe Leu Ile
      85           90           95
His Asn Gln Arg Ala Arg Ser Lys Asp Tyr Asp Asn Ile Lys Asn Leu
      100          105          110
Phe Arg Pro Ser His Ala Asp Phe Thr Tyr Phe His Lys Tyr Gly Ile
      115          120          125
Arg Asp Phe Arg Gly Gly Gly Arg Ser Ser Ala Arg Glu Ser Ala Ile
      130          135          140
Arg Val Ala Ala Gly Ala Phe Ala Lys Met Leu Leu Arg Glu Ile Gly
      145          150          155          160
Ile Val Cys Glu Ser Gly Ile Ile Glu Ile Gly Gly Ile Lys Ala Lys

```

GAA GAT TTT AGC ACA GGG ACT CCT ATA GGG TTT TTA ATC CAC AAC CAA	344
Glu Asp Phe Ser Thr Gly Thr Pro Ile Gly Phe Leu Ile His Asn Gln	
85 90 95	
AGG GCT AGG AGC AAG GAT TAC GAT AAC ATT AAA AAC CTT TTT AGG CCT	392
Arg Ala Arg Ser Lys Asp Tyr Asp Asn Ile Lys Asn Leu Phe Arg Pro	
100 105 110 115	
AGC CAT GCG GAT TTC ACT TAT TTT CAT AAA TAC GGC ATT AGG GAT TTT	440
Ser His Ala Asp Phe Thr Tyr Phe His Lys Tyr Gly Ile Arg Asp Phe	
120 125 130	
AGG GGT GGG GGG AGG AGT TCG GCC AGA GAG AGT GCT ATA AGA GTG GCT	488
Arg Gly Gly Gly Arg Ser Ser Ala Arg Glu Ser Ala Ile Arg Val Ala	
135 140 145	
GCT GGG GCG TTT GCT AAA ATG CTT TTA AGA GAA ATC GGT ATT GTT TGT	536
Ala Gly Ala Phe Ala Lys Met Leu Leu Arg Glu Ile Gly Ile Val Cys	
150 155 160	
GAA AGC GGG ATT ATA GAA ATT GGG GGT ATT AAA GCC AAA AAT TAT GAT	584
Glu Ser Gly Ile Ile Glu Ile Gly Gly Ile Lys Ala Lys Asn Tyr Asp	
165 170 175	
TTT AAT CAC GCC TTA AAA AGC GAG ATT TTT GCC CTA GAT GAA GAA CAA	632
Phe Asn His Ala Leu Lys Ser Glu Ile Phe Ala Leu Asp Glu Glu Gln	
180 185 190 195	
GAA GAA GCG CAA AAA ACA GCC ATT CAA AAC GCT ATC AAA AAC CAC GAT	680
Glu Glu Ala Gln Lys Thr Ala Ile Gln Asn Ala Ile Lys Asn His Asp	
200 205 210	
AGC ATA GGG GGT GTG GCT TTG ATT AGA GCG AGG AGC ATA AAA ACC AAT	728
Ser Ile Gly Gly Val Ala Leu Ile Arg Ala Arg Ser Ile Lys Thr Asn	
215 220 225	
CAA AAG CTC CCC ATT GGC TTA GGT CAA GGG CTA TAC GCT AAA TTA GAC	776
Gln Lys Leu Pro Ile Gly Leu Gly Gln Gly Leu Tyr Ala Lys Leu Asp	
230 235 240	
GCT AAA ATC GCT GAA GCG ATG ATG GGG CTT AAT GGG GTG AAA GCG GTT	824
Ala Lys Ile Ala Glu Ala Met Met Gly Leu Asn Gly Val Lys Ala Val	
245 250 255	
GAA ATA GGC AAG GGG GTA GAA AGC TCT TTA TTA AAA GGC TCA GAG TAT	872
Glu Ile Gly Lys Gly Val Glu Ser Ser Leu Leu Lys Gly Ser Glu Tyr	
260 265 270 275	
AAT GAT TTA ATG GAT CAA AAG GGG TTT TTG AGC AAT CGT AGC GGA GGG	920
Asn Asp Leu Met Asp Gln Lys Gly Phe Leu Ser Asn Arg Ser Gly Gly	
280 285 290	
GTT TTA GGG GGC ATG AGC AAT GGG GAA GAA ATC ATT GTT AGA GTG CAT	968
Val Leu Gly Gly Met Ser Asn Gly Glu Glu Ile Ile Val Arg Val His	
295 300 305	

```

Arg Ala Leu Asn Glu Ala Leu Lys Ile Leu Lys Arg Pro Cys Arg Ile
 50                      55                      60
Thr Leu Tyr Ser Asp Ser Gln Tyr Val Cys Gln Ala Ile Asn Val Trp
 65                      70                      75                      80
Leu Ala Asn Trp Gln Lys Lys Asn Phe Ser Lys Val Lys Asn Val Asp
                      85                      90                      95
Leu Trp Lys Glu Phe Leu Glu Val Ser Lys Gly His Ser Ile Val Ala
                      100                      105                      110
Val Trp Ile Lys Gly His Asn Gly His Ala Glu Asn Glu Arg Cys Asp
                      115                      120                      125
Ser Leu Ala Lys Leu Glu Ala Gln Lys Arg Val Lys Thr Thr Thr
 130                      135                      140

```

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...1181
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

```

ATGTATGCGA CCGCTAAAGG CAAAAGCAAA AAAGAAGCCG AACAGCA ATG CGC TTA      56
                                     Met Arg Leu
                                     1

TCA AGC GCT TCA AAA ACT GAA GGA AGC CAA ATG AAC ACT TTG GGG CGT      104
Ser Ser Ala Ser Lys Thr Glu Gly Ser Gln Met Asn Thr Leu Gly Arg
 5                      10                      15

TTT TTA AGG CTC ACG ACT TTT GGG GAA TCG CAT GGG GAT GTG ATA GGG      152
Phe Leu Arg Leu Thr Thr Phe Gly Glu Ser His Gly Asp Val Ile Gly
 20                      25                      30                      35

GGG GTA TTA GAC GGC ATG CCT AGC GGG ATT AAA ATA GAC TAT GCG CTA      200
Gly Val Leu Asp Gly Met Pro Ser Gly Ile Lys Ile Asp Tyr Ala Leu
                      40                      45                      50

TTA GAA AAT GAA ATG AAG CGC CGC CAA GGG GGG AGG AAC GTT TTC ATT      248
Leu Glu Asn Glu Met Lys Arg Arg Gln Gly Gly Arg Asn Val Phe Ile
                      55                      60                      65

ACG CCA CGA AAA GAA GAC GAT AAA GTG GAA ATA ACA AGC GGG GTT TTT      296
Thr Pro Arg Lys Glu Asp Asp Lys Val Glu Ile Thr Ser Gly Val Phe
 70                      75                      80

```

```

TTA GGC AAT CCC GGG CCA GGC GGT TAT GCG GCG ATT TTA CGC TAT AAA      99
Leu Gly Asn Pro Gly Pro Gly Gly Tyr Ala Ala Ile Leu Arg Tyr Lys
      15                      20                      25

GAT AAA GAA AAA ACC ATC AGT GGG GGC GAA GAA TTC ACC ACG AAT AAC      147
Asp Lys Glu Lys Thr Ile Ser Gly Gly Glu Glu Phe Thr Thr Asn Asn
      30                      35                      40

CGC ATG GAA TTA AGA GCG CTC AAT GAA GCG TTA AAA ATT TTG AAA CGC      195
Arg Met Glu Leu Arg Ala Leu Asn Glu Ala Leu Lys Ile Leu Lys Arg
      45                      50                      55                      60

CCA TGC CGT ATC ACG CTT TAT AGC GAT TCG CAA TAC GTG TGC CAA GCG      243
Pro Cys Arg Ile Thr Leu Tyr Ser Asp Ser Gln Tyr Val Cys Gln Ala
      65                      70                      75

ATC AAT GTG TGG CTA GCT AAC TGG CAA AAA AAG AAT TTT TCT AAA GTT      291
Ile Asn Val Trp Leu Ala Asn Trp Gln Lys Lys Asn Phe Ser Lys Val
      80                      85                      90

AAA AAT GTG GAT TTA TGG AAA GAA TTT TTA GAA GTC TCT AAA GGG CAT      339
Lys Asn Val Asp Leu Trp Lys Glu Phe Leu Glu Val Ser Lys Gly His
      95                      100                      105

TCT ATT GTG GCT GTT TGG ATC AAG GGG CAT AAC GGG CAT GCC GAG AAT      387
Ser Ile Val Ala Val Trp Ile Lys Gly His Asn Gly His Ala Glu Asn
      110                      115                      120

GAA CGA TGC GAT AGC CTC GCT AAA TTA GAG GCG CAA AAA CGG GTC AAA      435
Glu Arg Cys Asp Ser Leu Ala Lys Leu Glu Ala Gln Lys Arg Val Lys
      125                      130                      135                      140

ACG ACC ACT TAAAGGGAAA AATGATGAAA AACAAACGCT CTCAAAACAG CCC      487
Thr Thr Thr

```

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

```

Met Gln Glu Ile Glu Ile Phe Cys Asp Gly Ser Ser Leu Gly Asn Pro
  1                      5                      10                      15
Gly Pro Gly Gly Tyr Ala Ala Ile Leu Arg Tyr Lys Asp Lys Glu Lys
      20                      25                      30
Thr Ile Ser Gly Gly Glu Glu Phe Thr Thr Asn Asn Arg Met Glu Leu
      35                      40                      45

```

```

Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val His Val Gln Leu
 1           5           10           15
Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr Ser Phe Gly Glu
          20           25           30
Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly Leu Pro Gly Ala
          35           40           45
Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala Ile Gln Leu Gly
 50           55           60
Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile Phe Ala Arg Lys
65           70           75           80
Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln Ile Ser Gln Phe
          85           90           95
Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile Asp Thr Lys Glu
          100          105          110
Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met Glu Glu Asp Ala
          115          120          125
Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val Asp Leu Asn Arg
          130          135          140
Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro Asp Met Arg Asn
145          150          155          160
Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His Ala Ile Val Arg
          165          170          175
Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly Asn Phe Arg Cys
          180          185          190
Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu Lys Leu Tyr Thr
          195          200          205
Arg Val Glu Ile Lys Asn Leu Asn Ser Phe Arg Phe Ile Ala Lys Ala
          210          215          220
Ile Glu Tyr Glu Ile Glu Arg Gln Ser Ala Asp Val Gly Glu Arg Ala
225          230          235          240
Leu

```

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...444
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

```

ATGGGAGTGG ATTGA ATG CAA GAA ATT GAA ATT TTT TGC GAT GGC TCT TCT      51
      Met Gln Glu Ile Glu Ile Phe Cys Asp Gly Ser Ser
        1           5           10

```

80										85					90					
ATT	TCG	CAG	TTT	GAA	GTC	CCT	ATT	GTG	AGC	GAT	GGG	AAA	TTA	GAG	ATT	339				
Ile	Ser	Gln	Phe	Glu	Val	Pro	Ile	Val	Ser	Asp	Gly	Lys	Leu	Glu	Ile					
95						100					105									
GAC	ACT	AAA	GAG	GGT	GCA	AAA	ATC	GTG	CGT	ATT	GAA	AGG	GCC	CAC	ATG	387				
Asp	Thr	Lys	Glu	Gly	Ala	Lys	Ile	Val	Arg	Ile	Glu	Arg	Ala	His	Met					
110						115					120									
GAA	GAA	GAC	GCC	GGT	AAA	AAT	ATC	CAT	GAG	GGC	AGT	TAT	TCT	TTA	GTG	435				
Glu	Glu	Asp	Ala	Gly	Lys	Asn	Ile	His	Glu	Gly	Ser	Tyr	Ser	Leu	Val					
125						130					135					140				
GAT	TTG	AAC	CGC	GCT	TGC	ACC	CCT	TTA	TTA	GAA	ATT	GTC	AGT	AAG	CCG	483				
Asp	Leu	Asn	Arg	Ala	Cys	Thr	Pro	Leu	Leu	Glu	Ile	Val	Ser	Lys	Pro					
145						150					155									
GAC	ATG	CGA	AAT	AGT	GAA	GAA	GCT	ATA	GCG	TAT	TTG	AAA	AAG	CTC	CAT	531				
Asp	Met	Arg	Asn	Ser	Glu	Glu	Ala	Ile	Ala	Tyr	Leu	Lys	Lys	Leu	His					
160						165					170									
GCT	ATC	GTG	CGT	TTT	ATA	GGG	ATT	TCT	GAT	GCG	AAC	ATG	CAA	GAG	GGG	579				
Ala	Ile	Val	Arg	Phe	Ile	Gly	Ile	Ser	Asp	Ala	Asn	Met	Gln	Glu	Gly					
175						180					185									
AAT	TTC	AGG	TGC	GAT	GCG	AAC	GTG	TCC	ATT	AGA	CCC	AAA	GGC	GAT	GAA	627				
Asn	Phe	Arg	Cys	Asp	Ala	Asn	Val	Ser	Ile	Arg	Pro	Lys	Gly	Asp	Glu					
190						195					200									
AAG	CTT	TAT	ACG	AGA	GTA	GAG	ATT	AAA	AAT	CTA	AAT	AGC	TTT	AGA	TTC	675				
Lys	Leu	Tyr	Thr	Arg	Val	Glu	Ile	Lys	Asn	Leu	Asn	Ser	Phe	Arg	Phe					
205						210					215					220				
ATT	GCT	AAA	GCG	ATT	GAA	TAC	GAG	ATA	GAG	CGC	CAA	AGC	GCG	GAC	GTG	723				
Ile	Ala	Lys	Ala	Ile	Glu	Tyr	Glu	Ile	Glu	Arg	Gln	Ser	Ala	Asp	Val					
225						230					235									
GGA	GAA	CGG	GCG	CTA	TAATGAAGAG	GTGGTTCAAG	AAACGCGCCT	TT								770				
Gly	Glu	Arg	Ala	Leu																
240																				

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

450	455	460
Asn Tyr Tyr Leu Asn His Leu Lys Lys Glu Phe Asn His Pro Leu Phe		
465	470	475
Val Ala Tyr Ala Tyr Asn Ala Gly Pro Gly Phe Leu Arg Arg Trp Leu		480
	485	490
Glu Ser Ser Lys Arg Phe Lys Glu Lys Asn His Phe Glu Pro Trp Leu		495
	500	505
Ser Met Glu Leu Met Pro Tyr Ser Glu Thr Arg Met Tyr Gly Phe Arg		510
	515	520
Val Met Leu Asn Tyr Leu Ile Tyr Gln Glu Ile Phe Gly Asn Phe Ile		525
	530	535
Pro Ile Asp Gly Phe Leu Glu Gln Thr Leu Asn Ser Lys Asp Lys Pro		540
545	550	555
		560

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...738
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

TAAAAAGAAG GACAA ATG ATG CCA TTT GAA GCT GTA ATC GGG CTA GAA GTC	51
Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val	
1 5 10	
CAT GTC CAA CTC AAC ACC AAA ACC AAA ATC TTT TGC TCT TGC TCT ACA	99
His Val Gln Leu Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr	
15 20 25	
AGC TTT GGA GAA TCC CCT AAT TCT AAC ACC TGC CCT GTG TGT TTG GGT	147
Ser Phe Gly Glu Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly	
30 35 40	
TTA CCG GGA GCT TTG CCG GTA TTG AAT AAA GAA GTG GTT AAA AAA GCC	195
Leu Pro Gly Ala Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala	
45 50 55 60	
ATC CAA TTA GGC ACA GCC ATT GAA GCC AAT ATC AAC CAA TAT TCT ATT	243
Ile Gln Leu Gly Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile	
65 70 75	
TTT GCG AGG AAA AAT TAT TTT TAC CCT GAT TTG CCT AAG GCT TAT CAA	291
Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln	

```

Ser Gln Thr Glu Leu Asn Leu Lys Asp Leu Glu Lys Lys Pro Ala Gly
      20                      25                      30
Ile Val Arg Asp Tyr Tyr Leu Trp Arg Tyr Ile Ser Asp Lys Lys Thr
      35                      40                      45
Ser Leu Glu Asn Ala Lys Lys Ala Tyr Glu Leu Thr Gln Asn Lys Asn
      50                      55                      60
Asn Ala Leu Gln Lys Ala Met Gln Glu Lys Gly Ser Asp Asn Ala Glu
      65                      70                      75                      80
Lys Asn Pro Asp Val Lys Leu Pro Glu Asp Ile Tyr Cys Lys Gln Thr
      85                      90                      95
Ala Leu Glu Ser Met Leu Glu Thr Thr Asp Thr Phe Gln Ala Ser Cys
      100                     105                     110
Ile Ala Ile Ala Leu Lys Ser Lys Ile Arg Asp Phe Asp Lys Ile Pro
      115                     120                     125
Ile Glu Thr Leu Lys Pro Leu Gln Ile Lys Ile Lys Glu Ala Tyr Pro
      130                     135                     140
Val Leu Tyr Glu Glu Leu Glu Ile Leu Gln Ser Lys His Val Ser Ala
      145                     150                     155                     160
Ser Leu Phe Lys Ala Asn Ala Gln Val Phe Ser Ala Leu Phe Asn His
      165                     170                     175
Leu Ser Tyr Glu Lys Lys Leu Gln Ile Phe Glu Lys His Ile Pro Ile
      180                     185                     190
Lys Glu Leu Asn Arg Leu Leu Asp Glu Asn Tyr Pro Ala Phe Asn Arg
      195                     200                     205
Leu Ile Tyr Gln Val Ile Leu Asp Pro Lys Leu Asp His Phe Lys Asp
      210                     215                     220
Ala Leu Thr Lys Ser Asn Ala Thr His Ser Asn Ala Gln Thr Phe Phe
      225                     230                     235                     240
Ile Leu Gly Ile Asn Glu Ile Leu Arg Lys Lys Pro Ser Lys Ala Leu
      245                     250                     255
Lys Tyr Phe Glu Arg Ser Glu Ala Val Val Lys Asp Asp Asp Phe Ser
      260                     265                     270
Lys Asp Arg Ala Ile Phe Trp Gln Tyr Leu Val Ser Lys Lys Lys Lys
      275                     280                     285
Thr Leu Glu Arg Leu Ser Gln Ser Pro Ala Leu Asn Leu Tyr Ser Leu
      290                     295                     300
Tyr Ala Ser Arg Lys Leu Lys Thr Thr Pro Ser Tyr Arg Ile Ile Ser
      305                     310                     315                     320
Arg Ile Gln Asn Leu Ser Gln Glu Asp Pro Pro Phe Asn Thr Tyr Asp
      325                     330                     335
Pro Phe Ser Trp Gln Ile Phe Lys Glu Lys Thr Leu Ser Leu Lys Asp
      340                     345                     350
Glu Gly Ala Phe Asn Ala Met Leu Lys Ser Leu Tyr Tyr Glu Lys Ser
      355                     360                     365
Ala Pro Glu Leu Thr Tyr Leu Leu Ser Gln Arg Asn Lys Asp Lys Ile
      370                     375                     380
Tyr Tyr Tyr Leu Ser Pro Tyr Glu Gly Ile Ile Glu Trp Gln Asn Thr
      385                     390                     395                     400
Asp Glu Lys Ala Met Ala Tyr Ala Ile Ala Arg Gln Glu Ser Phe Leu
      405                     410                     415
Leu Pro Ala Val Ile Ser Arg Ser Phe Ala Leu Gly Leu Met Gln Ile
      420                     425                     430
Met Pro Phe Asn Val Gly Pro Phe Ala Lys Ser Leu Gly Met Asp Asn
      435                     440                     445
Ile Asp Leu Asn Asp Met Phe Asn Pro Asn Ile Ala Leu Lys Phe Gly

```


Arg	Gln	Glu	Ser	Phe	Leu	Leu	Pro	Ala	Val	Ile	Ser	Arg	Ser	Phe	Ala	
				415					420					425		
CTG	GGG	CTT	ATG	CAA	ATC	ATG	CCC	TTT	AAT	GTA	GGG	CCT	TTC	GCT	AAA	1347
Leu	Gly	Leu	Met	Gln	Ile	Met	Pro	Phe	Asn	Val	Gly	Pro	Phe	Ala	Lys	
			430				435				440					
AGC	CTT	GGC	ATG	GAT	AAC	ATT	GAT	CTA	AAC	GAC	ATG	TTT	AAC	CCC	AAC	1395
Ser	Leu	Gly	Met	Asp	Asn	Ile	Asp	Leu	Asn	Asp	Met	Phe	Asn	Pro	Asn	
		445				450				455						
ATC	GCT	CTC	AAA	TTT	GGC	AAT	TAT	TAC	TTG	AAC	CAT	TTG	AAA	AAA	GAA	1443
Ile	Ala	Leu	Lys	Phe	Gly	Asn	Tyr	Tyr	Leu	Asn	His	Leu	Lys	Lys	Glu	
	460				465				470							
TTC	AAC	CAC	CCC	CTT	TTT	GTC	GCC	TAC	GCT	TAT	AAC	GCT	GGG	CCT	GGG	1491
Phe	Asn	His	Pro	Leu	Phe	Val	Ala	Tyr	Ala	Tyr	Asn	Ala	Gly	Pro	Gly	
475				480				485				490				
TTT	TTA	AGG	AGG	TGG	TTA	GAA	AGT	TCC	AAA	CGA	TTT	AAA	GAA	AAA	AAT	1539
Phe	Leu	Arg	Arg	Trp	Leu	Glu	Ser	Ser	Lys	Arg	Phe	Lys	Glu	Lys	Asn	
			495					500				505				
CAT	TTT	GAG	CCA	TGG	CTT	AGC	ATG	GAG	CTT	ATG	CCT	TAT	AGC	GAG	ACT	1587
His	Phe	Glu	Pro	Trp	Leu	Ser	Met	Glu	Leu	Met	Pro	Tyr	Ser	Glu	Thr	
			510				515					520				
CGC	ATG	TAT	GGC	TTT	AGG	GTC	ATG	CTC	AAT	TAC	TTG	ATT	TAT	CAA	GAA	1635
Arg	Met	Tyr	Gly	Phe	Arg	Val	Met	Leu	Asn	Tyr	Leu	Ile	Tyr	Gln	Glu	
		525				530					535					
ATT	TTT	GGG	AAT	TTC	ATC	CCT	ATT	GAT	GGA	TTT	TTA	GAA	CAA	ACT	CTT	1683
Ile	Phe	Gly	Asn	Phe	Ile	Pro	Ile	Asp	Gly	Phe	Leu	Glu	Gln	Thr	Leu	
	540				545				550							
AAC	TCA	AAG	GAC	AAA	CCA	TGATTAAAAA	ATGCCTTTTT	CCTGCTGCGG	GCTATGGC							1739
Asn	Ser	Lys	Asp	Lys	Pro											
555				560												
A																1740

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

Met	Arg	Phe	Phe	Thr	Leu	Phe	Phe	Ile	Gly	Met	Leu	Gly	Val	Gly	Phe
1				5				10				15			

190										195										200									
TAT	CCG	GCG	TTT	AAC	CGC	TTG	ATC	TAT	CAG	GTT	ATT	TTA	GAT	CCT	AAA														
Tyr	Pro	Ala	Phe	Asn	Arg	Leu	Ile	Tyr	Gln	Val	Ile	Leu	Asp	Pro	Lys														675
		205																											
TTG	GAT	CAT	TTT	AAA	GAC	GCT	CTC	ACT	AAA	AGT	AAC	GCT	ACC	CAC	AGC														
Leu	Asp	His	Phe	Lys	Asp	Ala	Leu	Thr	Lys	Ser	Asn	Ala	Thr	His	Ser														723
		220																											
AAC	GCG	CAA	ACC	TTT	TTT	ATT	CTA	GGG	ATT	AAT	GAA	ATC	TTG	CGC	AAA														
Asn	Ala	Gln	Thr	Phe	Phe	Ile	Leu	Gly	Ile	Asn	Glu	Ile	Leu	Arg	Lys														771
		235																											
AAA	CCC	TCT	AAA	GCG	CTC	AAG	TAT	TTT	GAA	CGA	TCA	GAA	GCG	GTT	GTC														
Lys	Pro	Ser	Lys	Ala	Leu	Lys	Tyr	Phe	Glu	Arg	Ser	Glu	Ala	Val	Val														819
AAA	GAC	GAT	GAT	TTT	TCA	AAA	GAC	AGA	GCG	ATT	TTT	TGG	CAG	TAT	TTA														
Lys	Asp	Asp	Asp	Phe	Ser	Lys	Asp	Arg	Ala	Ile	Phe	Trp	Gln	Tyr	Leu														867
GTT	TCT	AAA	AAG	AAA	AAA	ACT	TTA	GAA	CGC	CTT	TCA	CAA	AGC	CCA	GCT														
Val	Ser	Lys	Lys	Lys	Lys	Thr	Leu	Glu	Arg	Leu	Ser	Gln	Ser	Pro	Ala														915
TTA	AAT	CTC	TAT	AGT	CTT	TAT	GCG	AGC	CGC	AAA	CTC	AAA	ACC	ACG	CCC														
Leu	Asn	Leu	Tyr	Ser	Leu	Tyr	Ala	Ser	Arg	Lys	Leu	Lys	Thr	Thr	Pro														963
AGT	TAC	CGC	ATC	ATT	TCA	CGC	ATC	CAG	AAT	TTA	AGC	CAA	GAA	GAT	CCT														
Ser	Tyr	Arg	Ile	Ile	Ser	Arg	Ile	Gln	Asn	Leu	Ser	Gln	Glu	Asp	Pro														1011
CCT	TTT	AAC	ACT	TAT	GAC	CCT	TTT	TCG	TGG	CAA	ATT	TTT	AAG	GAA	AAA														
Pro	Phe	Asn	Thr	Tyr	Asp	Pro	Phe	Ser	Trp	Gln	Ile	Phe	Lys	Glu	Lys														1059
ACC	TTG	AGT	TTG	AAA	GAT	GAG	GGC	GCG	TTT	AAT	GCG	ATG	CTA	AAA	AGC														
Thr	Leu	Ser	Leu	Lys	Asp	Glu	Gly	Ala	Phe	Asn	Ala	Met	Leu	Lys	Ser														1107
CTG	TAT	TAT	GAA	AAA	AGC	GCT	CCT	GAA	TTG	ACC	TAT	CTT	TTA	AGC	CAA														
Leu	Tyr	Tyr	Glu	Lys	Ser	Ala	Pro	Glu	Leu	Thr	Tyr	Leu	Leu	Ser	Gln														1155
CGC	AAT	AAA	GAC	AAG	ATT	TAT	TAT	TAT	TTA	TCC	CCT	TAT	GAG	GGC	ATT														
Arg	Asn	Lys	Asp	Lys	Ile	Tyr	Tyr	Tyr	Leu	Ser	Pro	Tyr	Glu	Gly	Ile														1203
ATT	GAA	TGG	CAA	AAT	ACT	GAT	GAA	AAG	GCT	ATG	GCG	TAT	GCG	ATC	GCT														
Ile	Glu	Trp	Gln	Asn	Thr	Asp	Glu	Lys	Ala	Met	Ala	Tyr	Ala	Ile	Ala														1251
AGG	CAA	GAA	AGC	TTT	TTG	CTC	CCG	GCA	GTC	ATT	TCG	CGC	TCG	TTC	GCT														
																													1299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

TAAAAACCTT TAAAGAAAAT C ATG CGT TTT TTT ACC TTG TTT TTT ATC GGT	51
Met Arg Phe Phe Thr Leu Phe Phe Ile Gly	
1 5 10	
ATG CTT GGC GTT GGT TTT TCT CAA ACC GAG TTA AAT TTA AAA GAT TTA	99
Met Leu Gly Val Gly Phe Ser Gln Thr Glu Leu Asn Leu Lys Asp Leu	
15 20 25	
GAA AAA AAG CCC GCC GGG ATC GTT AGG GAT TAT TAT TTG TGG CGT TAT	147
Glu Lys Lys Pro Ala Gly Ile Val Arg Asp Tyr Tyr Leu Trp Arg Tyr	
30 35 40	
ATT AGC GAT AAA AAA ACC AGT TTA GAA AAC GCT AAA AAA GCC TAT GAA	195
Ile Ser Asp Lys Lys Thr Ser Leu Glu Asn Ala Lys Lys Ala Tyr Glu	
45 50 55	
TTG ACT CAA AAT AAA AAC AAC GCC CTA CAA AAG GCC ATG CAA GAA AAA	243
Leu Thr Gln Asn Lys Asn Asn Ala Leu Gln Lys Ala Met Gln Glu Lys	
60 65 70	
GGC TCA GAC AAT GCA GAA AAA AAC CCT GAT GTT AAA TTG CCT GAA GAT	291
Gly Ser Asp Asn Ala Glu Lys Asn Pro Asp Val Lys Leu Pro Glu Asp	
75 80 85 90	
ATT TAT TGC AAG CAA ACG GCT TTA GAA AGC ATG CTA GAA ACA ACA GAC	339
Ile Tyr Cys Lys Gln Thr Ala Leu Glu Ser Met Leu Glu Thr Thr Asp	
95 100 105	
ACT TTC CAA GCA AGC TGC ATC GCT ATC GCT TTA AAA TCA AAG ATC AGA	387
Thr Phe Gln Ala Ser Cys Ile Ala Ile Ala Leu Lys Ser Lys Ile Arg	
110 115 120	
GAT TTT GAT AAA ATC CCT ATT GAA ACC CTT AAG CCC TTA CAA ATT AAA	435
Asp Phe Asp Lys Ile Pro Ile Glu Thr Leu Lys Pro Leu Gln Ile Lys	
125 130 135	
ATC AAA GAG GCT TAC CCC GTT CTT TAT GAA GAA TTA GAA ATT TTG CAA	483
Ile Lys Glu Ala Tyr Pro Val Leu Tyr Glu Glu Leu Glu Ile Leu Gln	
140 145 150	
AGT AAG CAT GTG AGC GCT TCT TTG TTT AAG GCT AAC GCG CAA GTG TTT	531
Ser Lys His Val Ser Ala Ser Leu Phe Lys Ala Asn Ala Gln Val Phe	
155 160 165 170	
AGC GCG CTT TTC AAT CAT TTG AGT TAT GAA AAA AAG CTC CAA ATT TTT	579
Ser Ala Leu Phe Asn His Leu Ser Tyr Glu Lys Lys Leu Gln Ile Phe	
175 180 185	
GAA AAG CAT ATC CCC ATT AAA GAG TTA AAC CGT CTT TTA GAC GAA AAT	627
Glu Lys His Ile Pro Ile Lys Glu Leu Asn Arg Leu Leu Asp Glu Asn	

```

CCG GTG TTT TAT TTT TTA CGC TCT AGA TTC AAG CTG GTG TTT AAC GGG      250
Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val Phe Asn Gly
          55                      60                      65

TTG GAT TTC TCT CCT TTA GTG GTG GTC ATT GTT TTG AAA TTC TTG GAT      298
Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys Phe Leu Asp
          70                      75                      80

CTC ACG CTC ATT CAG TGG CTT TTC ATG CTC GCT AAA AAC CTT TAAAGAAAA    349
Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn Leu
          85                      90                      95

TCATGCGTTT T                                                              360

```

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

```

Met Ile Phe Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser
 1             5             10             15
Leu Ile Thr Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser
          20             25             30
Phe Val Gln Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg
          35             40             45
Leu Cys Glu Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val
          50             55             60
Phe Asn Gly Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys
65             70             75             80
Phe Leu Asp Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn
          85             90             95
Leu

```

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1701
- (D) OTHER INFORMATION:

```

225          230          235          240
Ala Lys Glu Cys His Lys Ser Phe Leu Asn Ile His Asn Lys Thr Glu
          245          250          255
Leu Lys Phe Leu Leu Lys Asn Tyr Asp Leu Glu Pro Phe Asn Leu Ala
          260          265          270
Leu Asp Phe Tyr Ala Leu Lys Asn Pro Lys His Ala Leu Lys Ile Lys
          275          280          285
Gly Leu Leu Lys Glu Ile Phe Asp Ser Asn Glu Pro Phe Lys Lys Glu
          290          295          300
His Leu Ala Leu Lys Gly Gly Ala Leu Gln Ser Leu Gly Tyr Gln His
305          310          315          320
Gln Lys Ile Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala
          325          330          335
Asn Pro Lys Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly
          340          345          350
His Tyr Leu Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg
          355          360          365
Asn

```

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...340
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

```

TTTTCCCCTA TATCCAAAGC CATCATCAAG AAGTTTAAAG GCTCAAAGC ATG ATT TTT      58
                                     Met Ile Phe
                                     1

TCC ACT CTT ATT AAT GCG ATA GCG GTG ATT TTA AGC TCG CTC ATT ACG      106
Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser Leu Ile Thr
      5              10              15

ATT TAT ATG TGG ATA GTA ATC ATT TAT TCG CTT ATC AGT TTC GTG CAG      154
Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser Phe Val Gln
      20              25              30              35

CCT AAC CCC AAT AAC CCC ATC ATG CAA ATT CTC GCT CGC TTG TGT GAG      202
Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg Leu Cys Glu
          40              45              50

```

GGC GAA ATT TTA AAC GCA TGC TTA GAT TTA GTC ATC GCT AAC CCT AAA 1065
 Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala Asn Pro Lys
 325 330 335

AAT AAC GCT TTA GAA TGG CTG ATT GAA TGG GTT AAG GGT CAT TAT TTA 1113
 Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly His Tyr Leu
 340 345 350 355

CCT AAT GAT ACT ATA AAT CTT TCG CCA ATA GGC AGA AGA AAT TAAAAACAG 1164
 Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg Asn
 360 365

AGAAAACATG ATAACGATGA ATGCGATTCA ATGGCCT 1201

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

Met Gly Ile Thr Pro Lys Asp Tyr Asp Leu Thr Ser Asn Ala Leu Val
 1 5 10 15
 Asn Glu Ser Lys Glu Leu Leu Leu Lys Arg His Phe Arg Val Leu Glu
 20 25 30
 Thr Gly Ile Lys His Gly Thr Ile Thr Ala Leu Lys Asn His Gln Ser
 35 40 45
 Tyr Glu Ile Thr Thr Phe Arg Ile Glu Lys Gly His Ile Lys His Arg
 50 55 60
 Lys Pro Lys Glu Leu Val Phe Ser Val His Leu Thr Asp Asp Leu Lys
 65 70 75 80
 Arg Arg Asp Phe Ser Met Asn Ala Ile Ala Tyr Ser Pro Thr Lys Gly
 85 90 95
 Leu Ile Asp Pro Phe Lys Gly Gln Asn Ala Ile Glu Asn Gln Met Ile
 100 105 110
 Glu Cys Val Gly Glu Ala Arg Leu Arg Phe Phe Glu Asp Ala Leu Arg
 115 120 125
 Ile Leu Arg Ser Leu Arg Phe Ser Ala Thr Leu Gly Phe Lys Ile Ala
 130 135 140
 Pro Asn Thr Lys Glu Ala Val Phe Ala Cys Lys Asp Leu Leu Lys His
 145 150 155 160
 Leu Ser Lys Glu Arg Leu Gln Ser Glu Leu Asn Lys Leu Leu Met Gly
 165 170 175
 Lys Asn Ala Tyr Glu Val Ala Lys Glu Tyr Gln Glu Ile Leu Glu Leu
 180 185 190
 Val Ile Gln Glu Lys Ile Glu Asn Leu Gly Phe Leu Lys Asn Ala Pro
 195 200 205
 Phe Asn Leu Glu Leu Arg Leu Leu Gly Phe Phe Lys His Gln Lys Ser
 210 215 220
 Leu Glu Ser Leu Arg Tyr Pro Lys Lys Thr Ile Val Leu Phe Ser Lys

Pro	Phe	Lys	Gly	Gln	Asn	Ala	Ile	Glu	Asn	Gln	Met	Ile	Glu	Cys	Val	
100					105					110					115	
GGG	GAA	GCG	CGA	TTA	AGG	TTT	TTT	GAA	GAC	GCT	TTA	AGG	ATT	TTA	AGA	441
Gly	Glu	Ala	Arg	Leu	Arg	Phe	Phe	Glu	Asp	Ala	Leu	Arg	Ile	Leu	Arg	
				120					125					130		
TCG	CTG	CGA	TTC	AGT	GCA	ACT	TTA	GGC	TTT	AAG	ATA	GCG	CCA	AAC	ACC	489
Ser	Leu	Arg	Phe	Ser	Ala	Thr	Leu	Gly	Phe	Lys	Ile	Ala	Pro	Asn	Thr	
				135				140					145			
AAA	GAA	GCG	GTT	TTT	GCG	TGT	AAG	GAT	TTG	TTA	AAA	CAC	CTT	TCT	AAA	537
Lys	Glu	Ala	Val	Phe	Ala	Cys	Lys	Asp	Leu	Leu	Lys	His	Leu	Ser	Lys	
		150					155					160				
GAA	CGC	TTA	CAA	AGT	GAA	TTG	AAT	AAG	CTT	CTT	ATG	GGG	AAA	AAC	GCC	585
Glu	Arg	Leu	Gln	Ser	Glu	Leu	Asn	Lys	Leu	Leu	Met	Gly	Lys	Asn	Ala	
	165					170					175					
TAT	GAA	GTG	GCT	AAA	GAA	TAT	CAA	GAA	ATT	TTA	GAG	TTG	GTT	ATT	CAA	633
Tyr	Glu	Val	Ala	Lys	Glu	Tyr	Gln	Glu	Ile	Leu	Glu	Leu	Val	Ile	Gln	
180					185					190					195	
GAA	AAA	ATA	GAA	AAT	TTA	GGG	TTT	TTA	AAA	AAC	GCG	CCT	TTC	AAT	CTG	681
Glu	Lys	Ile	Glu	Asn	Leu	Gly	Phe	Leu	Lys	Asn	Ala	Pro	Phe	Asn	Leu	
				200					205					210		
GAA	TTA	AGA	TTG	TTA	GGG	TTT	TTT	AAG	CAT	CAA	AAA	AGT	TTA	GAA	AGT	729
Glu	Leu	Arg	Leu	Leu	Gly	Phe	Phe	Lys	His	Gln	Lys	Ser	Leu	Glu	Ser	
			215					220					225			
TTA	CGC	TAC	CCT	AAA	AAA	ACG	ATC	GTT	TTA	TTT	TCC	AAA	GCT	AAA	GAA	777
Leu	Arg	Tyr	Pro	Lys	Lys	Thr	Ile	Val	Leu	Phe	Ser	Lys	Ala	Lys	Glu	
		230					235						240			
TGC	CAT	AAA	TCT	TTT	TTA	AAT	ATT	CAT	AAC	AAA	ACA	GAG	TTA	AAA	TTT	825
Cys	His	Lys	Ser	Phe	Leu	Asn	Ile	His	Asn	Lys	Thr	Glu	Leu	Lys	Phe	
	245					250					255					
TTA	TTG	AAA	AAC	TAC	GAT	TTA	GAG	CCT	TTT	AAT	TTG	GCT	TTA	GAT	TTT	873
Leu	Leu	Lys	Asn	Tyr	Asp	Leu	Glu	Pro	Phe	Asn	Leu	Ala	Leu	Asp	Phe	
260					265					270					275	
TAT	GCG	CTC	AAA	AAC	CCC	AAA	CAT	GCT	TTA	AAA	ATT	AAA	GGC	TTG	TTA	921
Tyr	Ala	Leu	Lys	Asn	Pro	Lys	His	Ala	Leu	Lys	Ile	Lys	Gly	Leu	Leu	
				280					285					290		
AAA	GAA	ATC	TTT	GAT	TCT	AAC	GAG	CCT	TTT	AAA	AAA	GAA	CAC	TTG	GCC	969
Lys	Glu	Ile	Phe	Asp	Ser	Asn	Glu	Pro	Phe	Lys	Lys	Glu	His	Leu	Ala	
		295						300					305			
CTT	AAG	GGC	GGT	GCG	CTT	CAA	AGC	TTG	GGT	TAC	CAG	CAC	CAA	AAA	ATC	1017
Leu	Lys	Gly	Gly	Ala	Leu	Gln	Ser	Leu	Gly	Tyr	Gln	His	Gln	Lys	Ile	
		310					315					320				

Gly Glu Arg Lys Ile Leu His Ala Tyr Gly Tyr Gly Cys Asp Lys Cys
 195 200 205
 Pro Ala Cys Gln Leu Arg Lys Lys Gly Phe Glu Glu Phe Gln Ala Asn
 210 215 220
 Lys Lys
 225

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1155
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

TCCTCTCATG AGCTTTACTT GGTAGGGGGG TCGTGCGCG ATTATTTA ATG GGC ATT	57
Met Gly Ile	
1	
ACC CCA AAA GAT TAC GAT TTA ACC TCA AAC GCT TTA GTC AAT GAA AGC	105
Thr Pro Lys Asp Tyr Asp Leu Thr Ser Asn Ala Leu Val Asn Glu Ser	
5 10 15	
AAA GAG CTT CTT TTA AAG CGC CAT TTT AGG GTG CTA GAA ACC GGT ATC	153
Lys Glu Leu Leu Leu Lys Arg His Phe Arg Val Leu Glu Thr Gly Ile	
20 25 30 35	
AAA CAT GGT ACG ATC ACG GCT CTT AAA AAC CAT CAA AGC TAT GAA ATC	201
Lys His Gly Thr Ile Thr Ala Leu Lys Asn His Gln Ser Tyr Glu Ile	
40 45 50	
ACA ACT TTT AGA ATT GAA AAG GGG CAT ATC AAA CAC CGA AAG CCT AAA	249
Thr Thr Phe Arg Ile Glu Lys Gly His Ile Lys His Arg Lys Pro Lys	
55 60 65	
GAA TTG GTT TTT AGC GTT CAT TTA ACA GAC GAT TTA AAG CGG CGC GAT	297
Glu Leu Val Phe Ser Val His Leu Thr Asp Asp Leu Lys Arg Arg Asp	
70 75 80	
TTT AGC ATG AAT GCG ATC GCT TAT AGC CCT ACA AAA GGG CTG ATT GAT	345
Phe Ser Met Asn Ala Ile Ala Tyr Ser Pro Thr Lys Gly Leu Ile Asp	
85 90 95	
CCT TTT AAA GGG CAG AAT GCG ATT GAA AAT CAA ATG ATT GAA TGC GTG	393

	160	165	170	
ATG GCT AAA GAT TTG GGC GTC TTG GAT TTA GTC ATC AAA GAA ACG CAC				580
Met Ala Lys Asp Leu Gly Val Leu Asp Leu Val Ile Lys Glu Thr His				
	175	180	185	
ACC TGC TAT CAA GGA GAG CGA AAG ATT TTG CAT GCT TAT GGT TAT GGT				628
Thr Cys Tyr Gln Gly Glu Arg Lys Ile Leu His Ala Tyr Gly Tyr Gly				
	190	195	200	
TGC GAT AAA TGC CCG GCA TGC CAA TTG AGA AAA AAA GGC TTT GAA GAG				676
Cys Asp Lys Cys Pro Ala Cys Gln Leu Arg Lys Lys Gly Phe Glu Glu				
	205	210	215	220
TTT CAA GCT AAT AAA AAA TAAGGTTTTT TAAAAAACCA A				715
Phe Gln Ala Asn Lys Lys				
	225			

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

Met	Glu	Gln	Lys	Ile	Cys	Val	Ile	Gly	Phe	Ser	Gly	Gly	Gln	Asp	Ser
1				5					10					15	
Thr	Thr	Leu	Ala	Val	Trp	Ala	Lys	Lys	Arg	Phe	Lys	Lys	Val	Cys	Leu
			20					25					30		
Val	Gly	Phe	Asp	Tyr	Ala	Gln	Lys	His	Ser	Val	Glu	Leu	Glu	Cys	Ala
		35					40					45			
Gln	Lys	Ile	Ala	Ser	Leu	Leu	Gln	Leu	Pro	Tyr	Glu	Ile	Ile	Pro	Leu
	50					55					60				
Asp	Phe	Leu	Glu	Asn	Ile	Thr	Arg	Ser	Ala	Leu	Phe	Lys	Asn	Ser	Asn
65				70					75					80	
Asp	Leu	Ile	Gly	His	Ser	His	Ala	Gln	Asn	Lys	Asp	Leu	Pro	Asn	Ser
				85					90					95	
Phe	Val	Pro	Asn	Arg	Asn	Ala	Ile	Phe	Ile	Thr	Leu	Leu	His	Ser	Tyr
			100					105					110		
Ala	Gln	Lys	Leu	Gly	Ala	Ser	Asn	Ile	Ala	Leu	Gly	Val	Ser	Gln	Ala
		115					120					125			
Asp	Phe	Ser	Gly	Tyr	Pro	Asp	Cys	Lys	Glu	Asp	Phe	Ile	Lys	Ser	Ile
	130					135					140				
Glu	His	Ala	Leu	Asn	Leu	Gly	Ser	Asn	Thr	Ala	Ile	Lys	Ile	Leu	Thr
145				150					155					160	
Pro	Leu	Met	Phe	Leu	Asn	Lys	Ala	Gln	Glu	Phe	Gln	Met	Ala	Lys	Asp
			165						170					175	
Leu	Gly	Val	Leu	Asp	Leu	Val	Ile	Lys	Glu	Thr	His	Thr	Cys	Tyr	Gln
		180						185					190		

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 17...694

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

```

TTTTTAAGGA ATTTTG ATG GAA CAA AAA ATT TGC GTG ATC GGT TTT AGC GGC      52
      Met Glu Gln Lys Ile Cys Val Ile Gly Phe Ser Gly
              1              5              10

GGG CAA GAC AGC ACC ACT TTA GCC GTG TGG GCG AAA AAG CGT TTT AAA      100
Gly Gln Asp Ser Thr Thr Leu Ala Val Trp Ala Lys Lys Arg Phe Lys
      15              20              25

AAA GTC TGT TTA GTG GGG TTT GAT TAT GCG CAA AAA CAC TCT GTG GAA      148
Lys Val Cys Leu Val Gly Phe Asp Tyr Ala Gln Lys His Ser Val Glu
      30              35              40

TTA GAA TGC GCT CAA AAA ATC GCT TCT CTT TTA CAA CTC CCT TAT GAA      196
Leu Glu Cys Ala Gln Lys Ile Ala Ser Leu Leu Gln Leu Pro Tyr Glu
      45              50              55              60

ATC ATC CCA TTA GAT TTT TTA GAA AAT ATC ACC CGC TCT GCG CTT TTT      244
Ile Ile Pro Leu Asp Phe Leu Glu Asn Ile Thr Arg Ser Ala Leu Phe
      65              70              75

AAA AAC TCT AAC GAT TTA ATA GGG CAT TCG CAT GCG CAA AAT AAA GAT      292
Lys Asn Ser Asn Asp Leu Ile Gly His Ser His Ala Gln Asn Lys Asp
      80              85              90

TTA CCC AAT TCT TTT GTG CCT AAT CGT AAC GCT ATT TTT ATC ACC CTT      340
Leu Pro Asn Ser Phe Val Pro Asn Arg Asn Ala Ile Phe Ile Thr Leu
      95              100              105

TTG CAT TCT TAC GCG CAA AAA CTA GGG GCT AGC AAT ATC GCT TTA GGA      388
Leu His Ser Tyr Ala Gln Lys Leu Gly Ala Ser Asn Ile Ala Leu Gly
      110              115              120

GTT TCG CAA GCG GAT TTT AGC GGC TAT CCG GAT TGT AAA GAA GAT TTT      436
Val Ser Gln Ala Asp Phe Ser Gly Tyr Pro Asp Cys Lys Glu Asp Phe
      125              130              135              140

ATT AAA AGC ATC GAG CAT GCC TTA AAT TTA GGA TCA AAC ACG GCG ATT      484
Ile Lys Ser Ile Glu His Ala Leu Asn Leu Gly Ser Asn Thr Ala Ile
      145              150              155

AAA ATC CTA ACG CCT TTA ATG TTT TTG AAT AAA GCG CAA GAA TTT CAA      532
Lys Ile Leu Thr Pro Leu Met Phe Leu Asn Lys Ala Gln Glu Phe Gln

```

```

Leu Ile Asp Cys Leu Thr Gln Leu Lys Gly Met Leu Lys Thr Gln Asp
115 120 125
Phe Ile Pro Ile Phe Thr Ser Arg Glu Ala Leu Ser Leu Ser Leu Lys
130 135 140
Asn Pro Ser Pro Ser Val Ile Phe Ser Asp Leu Ser Ser Val Leu Ser
145 150 155 160
Cys Thr Lys Leu Pro Leu Glu Asp Ala Lys Tyr Leu Ala Ser Leu Glu
165 170 175
Lys Pro Ser Ile Lys Ala Pro Leu Lys Ser Val Phe Lys Asp Thr Phe
180 185 190
Lys Asn Asp Glu Ile Ile Ala Gln Leu Pro Tyr Asp Pro Ile Leu Asn
195 200 205
Leu Leu Cys His Ile Leu Gln Asp Glu Gly Ile Glu Phe Val Phe Met
210 215 220
His Glu Ser Arg Ser Cys Glu Ala Leu Leu Tyr Tyr Glu Ala Leu Phe
225 230 235 240
Lys Thr Pro Lys Arg Leu Ile Thr Pro Thr Lys Lys Phe Val Leu Glu
245 250 255
Asn Asn Phe Ser Thr Phe Pro Phe Lys Asp Glu Leu Glu Phe Leu Ser
260 265 270
Ala Thr Pro Asn Ser Ile Val Leu Tyr Leu Ser Phe Lys Arg Pro Thr
275 280 285
Arg Leu Leu Leu His Ala Asn Gly Ser Leu Lys Thr Leu Leu Ser Val
290 295 300
Ser Phe Asp Phe Asn Lys Met Phe Asn Ala Leu Lys Gln Asp Glu Lys
305 310 315 320
Ala Ser Arg Met Leu Gln Asn Tyr Ala Thr Lys Phe Pro Asp Phe Tyr
325 330 335
Ala Arg Ile Val Glu Leu Ser Lys Tyr Asp Leu Gly Gly Ala Asn Leu
340 345 350
Leu Asp Phe Phe Cys Ile Leu Gly Phe Val Leu Gly Tyr Ser Glu Asp
355 360 365
Phe Cys Thr Gln Ser Val Ile Pro Leu Ala Lys Glu Cys Leu Arg Pro
370 375 380
Lys Gly Pro Arg Ile Asp Tyr Lys Ile Leu Lys Asp Asn Ser Leu Lys
385 390 395 400
Met Ala Leu Asn Phe Ser Lys Ile Met His Ser Ala Met Ser Phe Arg
405 410 415
Leu Ala Gly Val Glu Asn Glu Ile Leu Ser Leu Gly Ile Leu Asp Ser
420 425 430
Leu Ala Glu Phe Leu Gly Asn Phe Ile Trp Asp Asn Ala Gln Asn Phe
435 440 445
Ser Val Gln Glu Val Thr Ile Ala Gly Asp Phe Phe Gly Glu Lys Val
450 455 460
Phe Leu Asp Leu Phe Val Arg Tyr Phe Pro Lys Thr Leu Ala Leu Lys
465 470 475 480
Thr His Ala Phe Leu Asp Tyr Glu
485

```

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

```

AAA ATC CTT AAA GAC AAT TCT TTG AAA ATG GCT TTA AAC TTT TCA AAG      1252
Lys Ile Leu Lys Asp Asn Ser Leu Lys Met Ala Leu Asn Phe Ser Lys
      395                      400                      405

ATC ATG CAC AGT GCG ATG AGT TTC AGG CTC GCA GGC GTG GAA AAT GAA      1300
Ile Met His Ser Ala Met Ser Phe Arg Leu Ala Gly Val Glu Asn Glu
      410                      415                      420

ATT TTG AGT TTG GGG ATT TTG GAT TCT TTA GCG GAG TTT TTA GGG AAT      1348
Ile Leu Ser Leu Gly Ile Leu Asp Ser Leu Ala Glu Phe Leu Gly Asn
      425                      430                      435

TTC ATT TGG GAT AAC GCG CAA AAT TTT AGC GTT CAA GAA GTA ACG ATC      1396
Phe Ile Trp Asp Asn Ala Gln Asn Phe Ser Val Gln Glu Val Thr Ile
      440                      445                      450                      455

GCT GGG GAT TTC TTT GGC GAA AAA GTG TTT TTG GAT TTG TTT GTG CGG      1444
Ala Gly Asp Phe Phe Gly Glu Lys Val Phe Leu Asp Leu Phe Val Arg
      460                      465                      470

TAT TTC CCT AAA ACC CTA GCC CTT AAA ACG CAT GCA TTT TTG GAT TAT      1492
Tyr Phe Pro Lys Thr Leu Ala Leu Lys Thr His Ala Phe Leu Asp Tyr
      475                      480                      485

GAA TAAGGGCTTA AAAGCGGATG TGCATCATCA GCCCGCCGTC CATGTATT      1543
Glu

```

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

```

Met Ala Cys Asn Leu Gln Ala Arg Phe Tyr Ser Val Tyr Lys Asp Asn
 1           5           10           15
Thr Thr Ser Phe Tyr Leu Gln Ala Ser Ala Glu Thr Thr Leu Glu Phe
      20           25           30
Ala Gln Lys Leu Ser Glu Ile Leu Pro Phe Ser Leu Asp Phe Ser Phe
      35           40           45
Leu Ser Leu Lys Glu Ile Thr Glu Pro Leu Asp Glu Asn Leu Phe Gln
      50           55           60
Thr Ala Ser Leu Ser Lys Pro Leu Phe Met Asn Ala Lys Glu His Gln
      65           70           75           80
Asp Phe Leu Asp Lys Asn Ser Ser Leu Tyr Ala Asp Thr Leu Gly Leu
      85           90           95
Ile Lys Asn Thr Ala Phe Lys Gly Asp Ile Ile His Ser Pro Lys Glu
      100          105          110

```

GAC GCT AAA TAT TTG GCC AGT TTG GAA AAA CCC TCC ATC AAA GCC CCA	580
Asp Ala Lys Tyr Leu Ala Ser Leu Glu Lys Pro Ser Ile Lys Ala Pro	
170 175 180	
TTA AAA AGC GTG TTT AAA GAC ACT TTC AAA AAC GAT GAA ATC ATC GCC	628
Leu Lys Ser Val Phe Lys Asp Thr Phe Lys Asn Asp Glu Ile Ile Ala	
185 190 195	
CAG CTA CCC TAT GAC CCC ATA TTG AAT TTA TTG TGC CAT ATT TTA CAA	676
Gln Leu Pro Tyr Asp Pro Ile Leu Asn Leu Leu Cys His Ile Leu Gln	
200 205 210 215	
GAT GAG GGG ATA GAA TTT GTT TTT ATG CAT GAA AGC CGT TCT TGT GAA	724
Asp Glu Gly Ile Glu Phe Val Phe Met His Glu Ser Arg Ser Cys Glu	
220 225 230	
GCG CTT TTG TAT TAT GAA GCG CTT TTT AAA ACC CCT AAA CGC TTG ATC	772
Ala Leu Leu Tyr Tyr Glu Ala Leu Phe Lys Thr Pro Lys Arg Leu Ile	
235 240 245	
ACA CCC ACT AAA AAA TTC GTG CTA GAA AAT AAT TTT TCT ACC TTT CCC	820
Thr Pro Thr Lys Lys Phe Val Leu Glu Asn Asn Phe Ser Thr Phe Pro	
250 255 260	
TTT AAA GAT GAA TTA GAG TTT TTA AGC GCA ACC CCC AAT TCT ATC GTT	868
Phe Lys Asp Glu Leu Glu Phe Leu Ser Ala Thr Pro Asn Ser Ile Val	
265 270 275	
TTG TAT CTC AGT TTC AAG CGC CCT ACA AGG TTG TTA TTG CAT GCT AAT	916
Leu Tyr Leu Ser Phe Lys Arg Pro Thr Arg Leu Leu Leu His Ala Asn	
280 285 290 295	
GGT TCT TTA AAA ACG CTT TTA AGC GTC AGT TTT GAT TTT AAC AAA ATG	964
Gly Ser Leu Lys Thr Leu Leu Ser Val Ser Phe Asp Phe Asn Lys Met	
300 305 310	
TTT AAC GCG CTC AAA CAA GAT GAA AAA GCC TCC AGA ATG CTA CAA AAC	1012
Phe Asn Ala Leu Lys Gln Asp Glu Lys Ala Ser Arg Met Leu Gln Asn	
315 320 325	
TAC GCC ACT AAA TTC CCT GAT TTT TAC GCG CGC ATT GTA GAG CTT TCT	1060
Tyr Ala Thr Lys Phe Pro Asp Phe Tyr Ala Arg Ile Val Glu Leu Ser	
330 335 340	
AAA TAC GAT CTA GGG GGC GCG AAT TTA TTG GAT TTT TTT TGC ATT TTA	1108
Lys Tyr Asp Leu Gly Gly Ala Asn Leu Leu Asp Phe Phe Cys Ile Leu	
345 350 355	
GGG TTT GTT TTG GGC TAT AGC GAG GAT TTT TGC ACA CAG AGC GTT ATT	1156
Gly Phe Val Leu Gly Tyr Ser Glu Asp Phe Cys Thr Gln Ser Val Ile	
360 365 370 375	
CCT TTG GCT AAA GAA TGC TTA CGC CCT AAA GGC CCT AGG ATT GAT TAT	1204
Pro Leu Ala Lys Glu Cys Leu Arg Pro Lys Gly Pro Arg Ile Asp Tyr	
380 385 390	

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 32...1495

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

AAGCCTGAAT TTTACGCCCC TTTTAGAGCG A ATG GCA TGC AAT TTG CAA GCG	52
Met Ala Cys Asn Leu Gln Ala	
1 5	
CGT TTT TAT AGC GTT TAT AAG GAT AAT ACC ACT TCT TTC TAC CTC CAA	100
Arg Phe Tyr Ser Val Tyr Lys Asp Asn Thr Thr Ser Phe Tyr Leu Gln	
10 15 20	
GCG AGC GCT GAA ACC ACT TTA GAG TTC GCG CAA AAA CTC AGC GAA ATT	148
Ala Ser Ala Glu Thr Thr Leu Glu Phe Ala Gln Lys Leu Ser Glu Ile	
25 30 35	
CTG CCC TTT TCT TTA GAT TTT AGC TTT TTG TCT TTA AAG GAA ATC ACA	196
Leu Pro Phe Ser Leu Asp Phe Ser Phe Leu Ser Leu Lys Glu Ile Thr	
40 45 50 55	
GAG CCT TTA GAT GAA AAT CTT TTC CAA ACA GCA AGC CTT TCA AAG CCC	244
Glu Pro Leu Asp Glu Asn Leu Phe Gln Thr Ala Ser Leu Ser Lys Pro	
60 65 70	
CTT TTT ATG AAC GCT AAA GAG CAT CAA GAT TTT TTA GAC AAA AAT TCA	292
Leu Phe Met Asn Ala Lys Glu His Gln Asp Phe Leu Asp Lys Asn Ser	
75 80 85	
TCT TTG TAT GCC GAT ACT CTG GGC TTG ATT AAA AAC ACC GCT TTT AAG	340
Ser Leu Tyr Ala Asp Thr Leu Gly Leu Ile Lys Asn Thr Ala Phe Lys	
90 95 100	
GGG GAT ATA ATC CAT AGC CCT AAA GAG CTT ATA GAT TGC TTA ACC CAA	388
Gly Asp Ile Ile His Ser Pro Lys Glu Leu Ile Asp Cys Leu Thr Gln	
105 110 115	
TTA AAA GGC ATG CTC AAA ACG CAA GAT TTT ATC CCT ATT TTC ACT TCT	436
Leu Lys Gly Met Leu Lys Thr Gln Asp Phe Ile Pro Ile Phe Thr Ser	
120 125 130 135	
AGA GAG GCG TTA TCC CTT TCT TTA AAA AAT CCC TCT CCA AGC GTT ATT	484
Arg Glu Ala Leu Ser Leu Ser Leu Lys Asn Pro Ser Pro Ser Val Ile	
140 145 150	
TTT AGC GAT CTT TCT AGC GTT TTG AGC TGC ACT AAA TTG CCT TTA GAG	532
Phe Ser Asp Leu Ser Ser Val Leu Ser Cys Thr Lys Leu Pro Leu Glu	
155 160 165	

ATG ATT AAT GGC TAT GGT TAT ACC AAA GAA TGAGTCAAAA AATCCTAATT CTA 733
 Met Ile Asn Gly Tyr Gly Tyr Thr Lys Glu
 215 220

GGTATTGGCA ATATCCTTTT TGGCGATGAA GGGATTGGGG TGCATTTAGC CCACTACCTC 793
 AAAAAAATT TTTCTTT 810

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

Met	Asp	Lys	Met	Asn	Lys	Val	Val	Leu	His	Lys	Glu	Tyr	Ser	Gly	Phe	1	5	10	15
Val	Arg	Phe	Phe	His	Trp	Val	Arg	Ala	Leu	Ser	Ile	Phe	Ala	Leu	Ile	20	25	30	
Ala	Thr	Gly	Phe	Tyr	Ile	Ala	Tyr	Pro	Phe	Leu	Gln	Pro	Asn	Ser	Ser	35	40	45	
Phe	Tyr	Lys	Gly	Val	Tyr	Leu	Leu	Gln	Ala	Tyr	Val	Arg	Ser	Phe	His	50	55	60	
Val	Met	Phe	Gly	Phe	Leu	Ile	Ser	Ala	Leu	Ile	Phe	Arg	Thr	Tyr		65	70	75	80
Leu	Phe	Phe	Thr	Lys	Glu	Ser	Leu	Met	Glu	Arg	Lys	Ser	Phe	Ser	Gln	85	90	95	
Leu	Leu	Ser	Pro	Lys	Ala	Trp	Ile	Asp	Gln	Met	Lys	Ala	Tyr	Phe	Leu	100	105	110	
Ile	Ser	Gly	Lys	Pro	His	Thr	Lys	Gly	Ala	Tyr	Asn	Pro	Ile	Gln	Leu	115	120	125	
Val	Ala	Tyr	Ser	Thr	Leu	Ile	Val	Leu	Ile	Val	Leu	Met	Ser	Leu	Ser	130	135	140	
Gly	Met	Val	Leu	Tyr	Tyr	Asn	Val	Tyr	His	Ala	Gly	Leu	Gly	Ala	Phe	145	150	155	160
Leu	Gly	Ser	Ala	Phe	Lys	Trp	Phe	Glu	Thr	Leu	Cys	Gly	Gly	Leu	Ala	165	170	175	
Asn	Val	Arg	Phe	Ile	His	His	Leu	Ala	Thr	Trp	Gly	Phe	Ile	Leu	Phe	180	185	190	
Val	Pro	Val	His	Val	Tyr	Met	Val	Phe	Phe	His	Ser	Ile	Arg	Tyr	Glu	195	200	205	
Ser	Ser	Gly	Ala	Asp	Ser	Met	Ile	Asn	Gly	Tyr	Gly	Tyr	Thr	Lys	Glu	210	215	220	

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

TAGAGCCTAA TTTCGCTAAA TTCTAAAAAG GGTTACGC ATG GAT AAA ATG AAT AAG	56
Met Asp Lys Met Asn Lys	
1 5	
GTC GTT TTA CAC AAA GAA TAT TCC GGT TTT GTG CGC TTT TTC CAT TGG	104
Val Val Leu His Lys Glu Tyr Ser Gly Phe Val Arg Phe Phe His Trp	
10 15 20	
GTT AGG GCT TTG AGT ATT TTC GCT TTA ATC GCT ACA GGG TTT TAC ATC	152
Val Arg Ala Leu Ser Ile Phe Ala Leu Ile Ala Thr Gly Phe Tyr Ile	
25 30 35	
GCT TAC CCT TTT TTG CAG CCT AAT TCC AGC TTT TAT AAA GGG GTG TAT	200
Ala Tyr Pro Phe Leu Gln Pro Asn Ser Ser Phe Tyr Lys Gly Val Tyr	
40 45 50	
CTT TTA CAA GCT TAT GTG CGT TCT TTT CAT GTC ATG TTT GGG TTT TTG	248
Leu Leu Gln Ala Tyr Val Arg Ser Phe His Val Met Phe Gly Phe Leu	
55 60 65 70	
CTC ATT AGC GCA TTA ATC TTT AGA ACC TAT CTT TTT TTC ACT AAA GAA	296
Leu Ile Ser Ala Leu Ile Phe Arg Thr Tyr Leu Phe Phe Thr Lys Glu	
75 80 85	
AGC TTG ATG GAA CGC AAG AGT TTT AGC CAA CTT TTA AGC CCA AAA GCC	344
Ser Leu Met Glu Arg Lys Ser Phe Ser Gln Leu Leu Ser Pro Lys Ala	
90 95 100	
TGG ATT GAT CAG ATG AAA GCG TAT TTT CTT ATC AGC GGC AAA CCC CAC	392
Trp Ile Asp Gln Met Lys Ala Tyr Phe Leu Ile Ser Gly Lys Pro His	
105 110 115	
ACT AAA GGA GCG TAT AAC CCT ATC CAA CTC GTG GCT TAT TCC ACT TTG	440
Thr Lys Gly Ala Tyr Asn Pro Ile Gln Leu Val Ala Tyr Ser Thr Leu	
120 125 130	
ATT GTT TTG ATC GTG TTG ATG AGT TTG AGC GGG ATG GTG CTG TAT TAT	488
Ile Val Leu Ile Val Leu Met Ser Leu Ser Gly Met Val Leu Tyr Tyr	
135 140 145 150	
AAT GTC TAT CAT GCG GGG CTT GGA GCG TTT TTA GGA AGC GCT TTT AAG	536
Asn Val Tyr His Ala Gly Leu Gly Ala Phe Leu Gly Ser Ala Phe Lys	
155 160 165	
TGG TTT GAA ACG CTT TGT GGA GGG TTA GCG AAT GTT CGT TTC ATC CAC	584
Trp Phe Glu Thr Leu Cys Gly Gly Leu Ala Asn Val Arg Phe Ile His	
170 175 180	
CAC TTA GCG ACT TGG GGG TTT ATT TTG TTT GTC CCT GTG CAT GTT TAT	632
His Leu Ala Thr Trp Gly Phe Ile Leu Phe Val Pro Val His Val Tyr	
185 190 195	
ATG GTG TTT TTC CAT TCT ATC AGG TAT GAA AGT TCG GGG GCG GAT TCT	680
Met Val Phe Phe His Ser Ile Arg Tyr Glu Ser Ser Gly Ala Asp Ser	
200 205 210	


```

Ala Asp Pro Thr Ile Asp Ser Ile Ile Phe Asp Tyr Ile Asn Leu Glu
      100                      105                      110
Tyr His Glu Thr Ile Met Val Ala Ser Gly Phe Gln Ala Glu Lys Ser
      115                      120                      125
Leu His Asp Ala Ile Glu Lys His Lys Asn Asn Tyr Ile Leu Met Val
      130                      135                      140
Glu Gly Gly Ile Pro Gln Gly Thr Glu Tyr Phe Leu Thr Gln Gly Pro
      145                      150                      155                      160
Asn Ala Glu Thr Gly Ala Glu Glu Cys Arg Lys Ala Ala Gln Tyr Ala
      165                      170                      175
Ala Ala Ile Phe Ala Ile Gly Thr Cys Ser Ser Phe Gly Gly Val Gln
      180                      185                      190
Ala Ala Tyr Pro Asn Pro Ser Asn Ala Gln Pro Leu His Lys Ile Ile
      195                      200                      205
Asp Lys Pro Val Ile Asn Val Pro Gly Cys Pro Pro Ser Glu Lys Asn
      210                      215                      220
Ile Val Gly Asn Val Leu Tyr Tyr Leu Met Phe Gly Ala Leu Pro Lys
      225                      230                      235                      240
Leu Asp Ala Tyr Asn Arg Pro Ser Trp Ala Tyr Gly Asn Arg Ile His
      245                      250                      255
Asp Leu Cys Glu Arg Arg Gly His Phe Asp Ala Gly Glu Phe Val Glu
      260                      265                      270
His Phe Gly Asp Glu Asn Ala Lys Arg Gly Phe Cys Leu Tyr Lys Met
      275                      280                      285
Gly Cys Lys Gly Pro Tyr Thr Phe Asn Asn Cys Ser Lys Leu Arg Phe
      290                      295                      300
Asn Ser His Thr Ser Trp Pro Ile Gly Ala Gly His Gly Cys Ile Gly
      305                      310                      315                      320
Cys Ser Glu Pro Asn Phe Trp Asp Thr Met Ser Pro Phe Glu Glu Pro
      325                      330                      335
Leu Ala Asn Arg Ser Ile Lys Thr Ala Phe Asp Gly Leu Gly Ala Asp
      340                      345                      350
Lys Val Ala Asp Lys Val Gly Thr Thr Leu Leu Ser Ala Thr Ala Ile
      355                      360                      365
Gly Ile Val Ala His Ala Leu Leu Ser Lys Ala Ile Lys Asn Lys Glu
      370                      375                      380

```

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...710
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

```

GAT GAA AAC GCT AAA AGG GGC TTT TGT TTG TAT AAA ATG GGC TGT AAA      922
Asp Glu Asn Ala Lys Arg Gly Phe Cys Leu Tyr Lys Met Gly Cys Lys
                280                      285                      290

GGG CCT TAC ACT TTC AAC AAT TGC TCC AAA CTC CGC TTC AAT TCA CAC      970
Gly Pro Tyr Thr Phe Asn Asn Cys Ser Lys Leu Arg Phe Asn Ser His
                295                      300                      305

ACC TCT TGG CCC ATA GGT GCA GGG CAT GGG TGT ATA GGG TGT TCT GAG     1018
Thr Ser Trp Pro Ile Gly Ala Gly His Gly Cys Ile Gly Cys Ser Glu
                310                      315                      320

CCT AAT TTT TGG GAT ACG ATG AGT CCT TTT GAA GAG CCT TTA GCG AAT     1066
Pro Asn Phe Trp Asp Thr Met Ser Pro Phe Glu Glu Pro Leu Ala Asn
                325                      330                      335

CGT TCC ATT AAA ACC GCT TTT GAC GGA TTA GGG GCT GAT AAA GTA GCG     1114
Arg Ser Ile Lys Thr Ala Phe Asp Gly Leu Gly Ala Asp Lys Val Ala
                340                      345                      350                      355

GAT AAA GTA GGC ACG ACT TTG CTG AGC GCA ACC GCT ATT GGC ATT GTT     1162
Asp Lys Val Gly Thr Thr Leu Leu Ser Ala Thr Ala Ile Gly Ile Val
                360                      365                      370

GCG CAT GCG CTC CTT TCT AAA GCG ATC AAA AAC AAA GAG TAAGGGATTA AC   1213
Ala His Ala Leu Leu Ser Lys Ala Ile Lys Asn Lys Glu
                375                      380

ATGTCAAAAA AAATCGTAGT CGATCCTATC ACTAGGATTG AGGGGCATTT AAGGATTGAA   1273
GTGATCGTAG ATGATGATAA CGTGATCACT G                                  1304

```

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

```

Met Phe Tyr Asp Glu Lys Lys Thr Tyr Gln Lys Ile Glu Glu Arg Leu
 1           5           10           15
Asp Ile Val Arg Ser Phe Asn Ala His Asn Glu His Lys Asn Leu Gln
 20           25           30
Asp Glu Phe Lys Gly Ala Gly Ile Ser Arg Arg Asp Leu Leu Lys Trp
 35           40           45
Ala Gly Met Met Ser Thr Ala Leu Ala Leu Pro Ala Ser Phe Ala Pro
 50           55           60
Leu Thr Leu Lys Ala Val Glu Val Ala Asn Arg Leu Pro Val Ile Trp
 65           70           75           80
Leu His Met Ala Glu Cys Thr Gly Cys Ser Glu Ser Leu Leu Arg Ser
 85           90           95

```

ATG	AGC	ACA	GCG	TTA	GCC	TTG	CCG	GCT	AGT	TTT	GCT	CCC	TTG	ACT	TTG	250
Met	Ser	Thr	Ala	Leu	Ala	Leu	Pro	Ala	Ser	Phe	Ala	Pro	Leu	Thr	Leu	
			55					60					65			
AAG	GCG	GTG	GAA	GTG	GCT	AAC	AGA	TTG	CCC	GTG	ATT	TGG	TTG	CAC	ATG	298
Lys	Ala	Val	Glu	Val	Ala	Asn	Arg	Leu	Pro	Val	Ile	Trp	Leu	His	Met	
		70					75					80				
GCA	GAA	TGC	ACC	GGT	TGT	AGC	GAA	AGT	TTG	TTA	AGG	AGC	GCA	GAC	CCC	346
Ala	Glu	Cys	Thr	Gly	Cys	Ser	Glu	Ser	Leu	Leu	Arg	Ser	Ala	Asp	Pro	
		85				90					95					
ACC	ATT	GAT	AGC	ATT	ATC	TTT	GAT	TAC	ATC	AAC	CTA	GAA	TAC	CAT	GAG	394
Thr	Ile	Asp	Ser	Ile	Ile	Phe	Asp	Tyr	Ile	Asn	Leu	Glu	Tyr	His	Glu	
100					105					110					115	
ACC	ATC	ATG	GTA	GCG	AGC	GGT	TTT	CAA	GCT	GAA	AAA	AGC	TTG	CAT	GAC	442
Thr	Ile	Met	Val	Ala	Ser	Gly	Phe	Gln	Ala	Glu	Lys	Ser	Leu	His	Asp	
				120					125					130		
GCC	ATA	GAA	AAG	CAT	AAA	AAC	AAT	TAC	ATT	TTA	ATG	GTA	GAA	GGG	GGT	490
Ala	Ile	Glu	Lys	His	Lys	Asn	Asn	Tyr	Ile	Leu	Met	Val	Glu	Gly	Gly	
			135					140					145			
ATC	CCC	CAA	GGC	ACG	GAA	TAC	TTC	CTC	ACT	CAA	GGC	CCA	AAC	GCT	GAA	538
Ile	Pro	Gln	Gly	Thr	Glu	Tyr	Phe	Leu	Thr	Gln	Gly	Pro	Asn	Ala	Glu	
		150					155					160				
ACG	GGA	GCT	GAA	GAG	TGT	AGG	AAA	GCC	GCT	CAA	TAC	GCA	GCC	GCT	ATT	586
Thr	Gly	Ala	Glu	Glu	Cys	Arg	Lys	Ala	Ala	Gln	Tyr	Ala	Ala	Ala	Ile	
	165					170					175					
TTT	GCC	ATA	GGC	ACA	TGC	TCA	AGT	TTT	GGG	GGC	GTT	CAA	GCG	GCT	TAC	634
Phe	Ala	Ile	Gly	Thr	Cys	Ser	Ser	Phe	Gly	Gly	Val	Gln	Ala	Ala	Tyr	
180					185					190					195	
CCT	AAC	CCC	TCT	AAC	GCG	CAA	CCC	TTG	CAT	AAA	ATC	ATT	GAT	AAA	CCC	682
Pro	Asn	Pro	Ser	Asn	Ala	Gln	Pro	Leu	His	Lys	Ile	Ile	Asp	Lys	Pro	
				200					205					210		
GTG	ATC	AAT	GTT	CCT	GGT	TGC	CCG	CCT	AGT	GAA	AAA	AAT	ATC	GTG	GGT	730
Val	Ile	Asn	Val	Pro	Gly	Cys	Pro	Pro	Ser	Glu	Lys	Asn	Ile	Val	Gly	
			215					220					225			
AAT	GTG	CTT	TAT	TAC	TTG	ATG	TTT	GGG	GCT	CTC	CCT	AAA	TTG	GAT	GCG	778
Asn	Val	Leu	Tyr	Tyr	Leu	Met	Phe	Gly	Ala	Leu	Pro	Lys	Leu	Asp	Ala	
		230					235					240				
TAT	AAC	CGC	CCC	TCT	TGG	GCT	TAT	GGG	AAC	AGG	ATC	CAT	GAT	TTG	TGC	826
Tyr	Asn	Arg	Pro	Ser	Trp	Ala	Tyr	Gly	Asn	Arg	Ile	His	Asp	Leu	Cys	
	245					250					255					
GAA	AGG	AGA	GGG	CAT	TTT	GAT	GCG	GGC	GAA	TTT	GTG	GAG	CAT	TTT	GGC	874
Glu	Arg	Arg	Gly	His	Phe	Asp	Ala	Gly	Glu	Phe	Val	Glu	His	Phe	Gly	
260					265					270					275	

```

Asn Phe Asn Ala Gly Ala Met Gly Val Cys Met Asn Glu Gly Arg Ile
      260                      265                      270
Ser Ser Ser Val Val Val Gly Ala Gly Thr Asp Ile Gly Gly Gly Ala
      275                      280                      285
Ser Val Leu Gly Val Leu Ser Gly Gly Asn Asn Asn Pro Ile Ser Ile
      290                      295                      300
Gly Lys Asn Cys Leu Leu Gly Ala Asn Ser Val Thr Gly Ile Ser Leu
      305                      310                      315                      320
Gly Asp Gly Cys Ile Val Asp Ala Gly Val Ala Ile Leu Ala Gly Ser
      325                      330                      335
Val Ile Glu Ile Glu Glu Asn Glu Phe Lys Lys Leu Leu Glu Val Asn
      340                      345                      350
Ser Ala Leu Glu Lys His Ala Asn Leu Tyr Lys Gly Lys Glu Leu
      355                      360                      365
Ser Gly Lys Asn Gly Val His Phe Arg Ser Asn Ser Gln Asn Gly Lys
      370                      375                      380
Leu Ile Ala Phe Arg Ser Val Lys Lys Ile Glu Leu Asn Gln Asn Leu
      385                      390                      395                      400
His

```

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...1201
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

```

TTATTTTAT TATGTTAAGA TAATGAAAT TTCTAATTAA GGAGTGGTC ATG TTC TAC      58
                                     Met Phe Tyr
                                     1

GAT GAA AAA AAG ACC TAT CAA AAG ATT GAA GAA CGC CTT GAT ATA GTC      106
Asp Glu Lys Lys Thr Tyr Gln Lys Ile Glu Glu Arg Leu Asp Ile Val
   5                      10                      15

CGT TCG TTT AAC GCT CAC AAC GAG CAT AAA AAC TTG CAA GAC GAG TTT      154
Arg Ser Phe Asn Ala His Asn Glu His Lys Asn Leu Gln Asp Glu Phe
  20                      25                      30                      35

AAA GGG GCG GGC ATT TCT AGG CGC GAT TTA TTG AAG TGG GCG GGC ATG      202
Lys Gly Ala Gly Ile Ser Arg Arg Asp Leu Leu Lys Trp Ala Gly Met
      40                      45                      50

```

```

AAT GGC GTG CAT TTT CGT TCC AAT AGT CAG AAT GGC AAG CTG ATT GCT 1210
Asn Gly Val His Phe Arg Ser Asn Ser Gln Asn Gly Lys Leu Ile Ala
      375                      380                      385

TTT AGG AGC GTG AAA AAA ATT GAG TTG AAT CAA AAC CTG CAT TAAGGATTA 1261
Phe Arg Ser Val Lys Lys Ile Glu Leu Asn Gln Asn Leu His
      390                      395                      400

AAAGAATGCT CAAAAAAAGT TTGTTATTGC TTGTTTTTTTT AGTCTTACAG CTTAGCGGCG 1321
CTGAAGAAAA CAATCAAGCC CCAAAAAAC 1350

```

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

```

Met Ile Asn Lys Phe Lys Asn Phe Val Ser Asn Tyr Gln Gln Ser Asn
 1           5           10           15
His Tyr Lys Glu Pro Leu Gly Phe Gly Ile Ala Arg Val Asp Ile Ala
      20           25           30
Pro Ile Ser Lys Lys Ile Leu Cys Ala Thr Tyr Pro Val Leu Asn Trp
      35           40           45
Lys Asp Glu Asn Leu Gly Ser Tyr Ala Val Phe Cys Asn Ser Leu Ser
      50           55           60
Lys Glu Lys Ile Leu Lys Glu Ser Ala Ser Glu Arg Val Ile Glu Ile
      65           70           75           80
Asp Glu Ser Phe Val Leu Lys Ala Leu Asp Phe Tyr Thr Pro Phe Leu
      85           90           95
Asn Glu Ala Tyr Ser Asn Lys Met Ala His Lys Asn Ile Gln Val Val
      100          105          110
Leu Glu Leu Leu Lys Ala Leu Glu Glu Asn Arg Leu Lys Asn Ser Asp
      115          120          125
Gly Glu Ser Leu Tyr Arg Leu Val Ile Leu Tyr Glu Asp Lys Pro Cys
      130          135          140
Glu Ser Val Glu Ser Ala Tyr Met Lys Leu Leu Ala Leu Ser Leu Gly
      145          150          155          160
Lys Ala Pro Leu Arg Ser Leu Asn Leu Glu Gly Ile Phe Asn Gln Leu
      165          170          175
Ser Asn Ala Ala Trp Ser Gly Asn Lys Pro Tyr Glu Leu Glu Trp Leu
      180          185          190
Arg Met Asn Glu Val Ala Leu Lys Met Arg Asp His Phe Pro Ser Ile
      195          200          205
Asp Phe Ile Asp Lys Phe Pro Arg Tyr Leu Met Gln Leu Ile Pro Glu
      210          215          220
Phe Asp Asn Ile Arg Leu Leu Asp Ser Ser Lys Thr Arg Phe Gly Ala
      225          230          235          240
Tyr Leu Gly Thr Gly Gly Tyr Thr Gln Met Pro Gly Ala Ser Tyr Val
      245          250          255

```

GAG AGC GCG TAT ATG AAA CTT TTA GCG CTC TCT TTA GGT AAA GCC CCT	538
Glu Ser Ala Tyr Met Lys Leu Leu Ala Leu Ser Leu Gly Lys Ala Pro	
150 155 160	
TTG AGG AGT TTG AAT TTA GAG GGT ATT TTT AAC CAG CTT TCT AAT GCG	586
Leu Arg Ser Leu Asn Leu Glu Gly Ile Phe Asn Gln Leu Ser Asn Ala	
165 170 175	
GCC TGG AGC GGT AAC AAG CCC TAT GAA TTA GAA TGG CTT AGA ATG AAC	634
Ala Trp Ser Gly Asn Lys Pro Tyr Glu Leu Glu Trp Leu Arg Met Asn	
180 185 190 195	
GAA GTG GCT TTA AAA ATG CGA GAC CAT TTC CCT AGC ATT GAT TTC ATA	682
Glu Val Ala Leu Lys Met Arg Asp His Phe Pro Ser Ile Asp Phe Ile	
200 205 210	
GAT AAA TTC CCA CGC TAT TTG ATG CAA TTA ATC CCT GAG TTT GAT AAT	730
Asp Lys Phe Pro Arg Tyr Leu Met Gln Leu Ile Pro Glu Phe Asp Asn	
215 220 225	
ATC CGC TTA TTG GAT AGC TCA AAA ACG CGC TTT GGG GCG TAT TTA GGG	778
Ile Arg Leu Leu Asp Ser Ser Lys Thr Arg Phe Gly Ala Tyr Leu Gly	
230 235 240	
ACT GGA GGT TAT ACC CAA ATG CCT GGG GCT AGT TAT GTG AAT TTT AAC	826
Thr Gly Gly Tyr Thr Gln Met Pro Gly Ala Ser Tyr Val Asn Phe Asn	
245 250 255	
GCA GGG GCT ATG GGA GTG TGC ATG AAT GAG GGG CGT ATT TCT TCA TCG	874
Ala Gly Ala Met Gly Val Cys Met Asn Glu Gly Arg Ile Ser Ser Ser	
260 265 270 275	
GTG GTG GTT GGA GCA GGC ACT GAT ATT GGT GGG GGA GCG AGC GTG TTA	922
Val Val Val Gly Ala Gly Thr Asp Ile Gly Gly Gly Ala Ser Val Leu	
280 285 290	
GGC GTT TTA AGT GGA GGG AAT AAC AAC CCC ATT AGC ATC GGG AAA AAT	970
Gly Val Leu Ser Gly Gly Asn Asn Asn Pro Ile Ser Ile Gly Lys Asn	
295 300 305	
TGT TTG CTA GGG GCT AAT AGC GTT ACT GGA ATT AGT CTA GGC GAT GGC	1018
Cys Leu Leu Gly Ala Asn Ser Val Thr Gly Ile Ser Leu Gly Asp Gly	
310 315 320	
TGT ATC GTG GAT GCA GGC GTT GCG ATA CTA GCC GGG AGC GTG ATA GAA	1066
Cys Ile Val Asp Ala Gly Val Ala Ile Leu Ala Gly Ser Val Ile Glu	
325 330 335	
ATT GAA GAA AAT GAG TTT AAA AAG CTT TTA GAA GTG AAT AGC GCT TTA	1114
Ile Glu Glu Asn Glu Phe Lys Lys Leu Leu Glu Val Asn Ser Ala Leu	
340 345 350 355	
GAA AAA CAT GCC AAC AAC CTT TAC AAA GGC AAA GAA CTT TCC GGA AAA	1162
Glu Lys His Ala Asn Asn Leu Tyr Lys Gly Lys Glu Leu Ser Gly Lys	
360 365 370	

(A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 50...1252
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

```

AAGTGGAAAA TTTAGCTAAA GAAAGAGAAA AAAGTTTAAA GGATTAGGC ATG ATC AAT      58
                                   Met Ile Asn
                                   1

AAG TTT AAA AAT TTT GTG AGC AAC TAC CAG CAA TCT AAC CAC TAT AAA      106
Lys Phe Lys Asn Phe Val Ser Asn Tyr Gln Gln Ser Asn His Tyr Lys
   5                               10                               15

GAG CCT TTA GGT TTT GGC ATT GCC AGA GTG GAT ATT GCC CCT ATT TCC      154
Glu Pro Leu Gly Phe Gly Ile Ala Arg Val Asp Ile Ala Pro Ile Ser
 20                               25                               30                               35

AAA AAG ATT TTA TGC GCC ACT TAC CCT GTT TTG AAT TGG AAA GAT GAA      202
Lys Lys Ile Leu Cys Ala Thr Tyr Pro Val Leu Asn Trp Lys Asp Glu
          40                               45                               50

AAT TTA GGC TCT TAT GCG GTG TTT TGC AAC TCG CTT TCA AAA GAA AAA      250
Asn Leu Gly Ser Tyr Ala Val Phe Cys Asn Ser Leu Ser Lys Glu Lys
          55                               60                               65

ATC CTA AAA GAG AGC GCG AGC GAG CGC GTT ATT GAG ATT GAT GAA AGT      298
Ile Leu Lys Glu Ser Ala Ser Glu Arg Val Ile Glu Ile Asp Glu Ser
          70                               75                               80

TTT GTG TTA AAA GCG TTG GAT TTT TAT ACG CCC TTT TTG AAT GAA GCC      346
Phe Val Leu Lys Ala Leu Asp Phe Tyr Thr Pro Phe Leu Asn Glu Ala
          85                               90                               95

TAT TCT AAT AAA ATG GCT CAT AAA AAC ATC CAA GTG GTT TTA GAG CTT      394
Tyr Ser Asn Lys Met Ala His Lys Asn Ile Gln Val Val Leu Glu Leu
100                               105                               110                               115

TTA AAG GCT TTA GAA GAA AAT CGT TTG AAA AAT AGC GAT GGG GAG TCT      442
Leu Lys Ala Leu Glu Glu Asn Arg Leu Lys Asn Ser Asp Gly Glu Ser
          120                               125                               130

CTT TAT CGC TTG GTG ATC TTG TAT GAA GAT AAG CCT TGC GAG AGC GTG      490
Leu Tyr Arg Leu Val Ile Leu Tyr Glu Asp Lys Pro Cys Glu Ser Val
          135                               140                               145

```

Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220

AAA TAC AGC AGA CGA TAC GCT CCT TTA AAA ACC CCT AAA GAG GTT TAAAA 722
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

AGAGCGGGCT TTATGTTAGA ATAAGTCTTT TTATTCAAAG GAGATTGCAA TGAAT 777

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

Ser Tyr Pro Pro Pro Pro Asn Pro Thr Gln Glu Thr Gln Gln Asp Phe
 1 5 10 15
 Ile Ile Glu Ala Gln Gln Asp Leu Ile Ile Glu Thr Gln Gln Asp Pro
 20 25 30
 Lys Glu Leu Pro Glu Ser Cys Lys Ile Thr Pro Gln Lys Ile Ser Phe
 35 40 45
 Asn Gln Val Val Phe Lys Lys Ile Lys Arg Lys Leu Asn Arg Phe Ile
 50 55 60
 Gly Ser Ile Leu Ala Arg Thr Glu Val Tyr Lys Asn Leu Val Ala Lys
 65 70 75 80
 Tyr Asp Glu Leu Thr Gly Lys Tyr Glu Ser Leu Leu Ala Lys Glu Ala
 85 90 95
 Asn Ile Lys Glu Thr Phe Trp Glu Arg Arg Ala Asp Ser Glu Lys Glu
 100 105 110
 Ala Phe Phe Leu Glu His Phe Tyr Leu Thr Ser Val Tyr Val Ala Ser
 115 120 125
 Thr Ala Gly Tyr Tyr Ile Thr Pro Lys Gly Ala Lys Thr Phe Ile Glu
 130 135 140
 Ala Thr Glu Arg Phe Lys Ile Ile Glu Pro Val Asp Met Phe Ile Asn
 145 150 155 160
 Asn Pro Thr Tyr His Asp Val Ala Asn Phe Thr Tyr Leu Pro Cys Pro
 165 170 175
 Val Ser Leu Asn Lys His Ala Phe Asn Ser Thr Ile Gln Asn Ala Lys
 180 185 190
 Lys Pro Asp Ile Ser Leu Lys Pro Pro Arg Lys Ser Tyr Phe Asp Asn
 195 200 205
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

AGT TAC CCC CCC CCC CCC AAT CCC ACA CAA GAA ACG CAA CAA GAT TTT	48
Ser Tyr Pro Pro Pro Pro Asn Pro Thr Gln Glu Thr Gln Gln Asp Phe	
1 5 10 15	
ATT ATT GAA GCA CAA CAA GAT TTG ATT ATT GAA ACG CAA CAA GAC CCC	96
Ile Ile Glu Ala Gln Gln Asp Leu Ile Ile Glu Thr Gln Gln Asp Pro	
20 25 30	
AAA GAA CTA CCT GAG TCT TGC AAA ATA ACG CCC CAA AAA ATC TCT TTT	144
Lys Glu Leu Pro Glu Ser Cys Lys Ile Thr Pro Gln Lys Ile Ser Phe	
35 40 45	
AAC CAA GTG GTT TTT AAA AAA ATT AAA AGA AAA CTC AAC CGC TTC ATT	192
Asn Gln Val Val Phe Lys Lys Ile Lys Arg Lys Leu Asn Arg Phe Ile	
50 55 60	
GGA AGC ATT TTA GCT CGG ACA GAA GTG TAT AAG AAT CTC GTG GCA AAA	240
Gly Ser Ile Leu Ala Arg Thr Glu Val Tyr Lys Asn Leu Val Ala Lys	
65 70 75 80	
TAC GAT GAA CTC ACA GGA AAA TAC GAA TCA TTA TTG GCA AAA GAG GCA	288
Tyr Asp Glu Leu Thr Gly Lys Tyr Glu Ser Leu Leu Ala Lys Glu Ala	
85 90 95	
AAC ATC AAA GAG ACC TTT TGG GAA AGG CGT GCT GAT AGC GAA AAA GAA	336
Asn Ile Lys Glu Thr Phe Trp Glu Arg Arg Ala Asp Ser Glu Lys Glu	
100 105 110	
GCC TTT TTT TTA GAG CAT TTT TAC CTC ACT AGC GTG TAT GTG GCT TCT	384
Ala Phe Phe Leu Glu His Phe Tyr Leu Thr Ser Val Tyr Val Ala Ser	
115 120 125	
ACA GCA GGA TAC TAT ATC ACG CCT AAG GGC GCT AAA ACC TTT ATA GAA	432
Thr Ala Gly Tyr Tyr Ile Thr Pro Lys Gly Ala Lys Thr Phe Ile Glu	
130 135 140	
GCC ACG GAG CGT TTT AAA ATC ATA GAG CCG GTG GAT ATG TTC ATA AAC	480
Ala Thr Glu Arg Phe Lys Ile Ile Glu Pro Val Asp Met Phe Ile Asn	
145 150 155 160	
AAC CCC ACT TAC CAT GAT GTG GCT AAT TTT ACC TAT TTG CCT TGC CCT	528
Asn Pro Thr Tyr His Asp Val Ala Asn Phe Thr Tyr Leu Pro Cys Pro	
165 170 175	
GTT TCT TTA AAC AAG CAT GCT TTC AAT AGC ACC ATT CAA AAT GCA AAA	576
Val Ser Leu Asn Lys His Ala Phe Asn Ser Thr Ile Gln Asn Ala Lys	
180 185 190	
AAG CCT GAC ATT TCA TTA AAA CCC CCT AGA AAA TCC TAT TTT GAT AAT	624
Lys Pro Asp Ile Ser Leu Lys Pro Pro Arg Lys Ser Tyr Phe Asp Asn	
195 200 205	
CTT TTT TAT GAT CAA TTA AAC ACT AGA AAG TGC TTA AAA GCC TTT CAC	672

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

```

Met Lys Gln Leu Phe Leu Ile Ile Gly Ala Pro Gly Ser Gly Lys Thr
 1             5             10             15
Thr Asp Ala Glu Leu Ile Ala Lys Asn Asn Ser Glu Thr Ile Ala His
      20             25             30
Phe Ser Thr Gly Asp Leu Leu Arg Ala Glu Ser Ala Lys Lys Thr Glu
      35             40             45
Arg Gly Leu Leu Ile Glu Lys Phe Thr Ser Gln Gly Glu Leu Val Pro
      50             55             60
Leu Glu Ile Val Val Glu Thr Ile Leu Ser Ala Ile Lys Ser Ser Gly
      65             70             75             80
Lys Gly Ile Ile Leu Ile Asp Gly Tyr Pro Arg Ser Val Glu Gln Met
      85             90             95
Gln Ala Leu Asp Lys Glu Leu Asn Ala Gln Asn Glu Val Ile Leu Lys
      100            105            110
Ser Val Ile Glu Val Glu Val Ser Glu Asn Thr Ala Lys Glu Arg Val
      115            120            125
Leu Gly Arg Ser Arg Gly Ala Asp Asp Asn Glu Lys Val Phe His Asn
      130            135            140
Arg Met Arg Val Phe Leu Asp Pro Leu Gly Glu Ile Gln Asn Phe Tyr
      145            150            155            160
Lys Asn Lys Lys Val Tyr Lys Ala Ile Asp Gly Glu Arg Ser Ile Glu
      165            170            175
Glu Ile Val Gly Glu Met Gln Glu Tyr Ile Leu Ser Phe Gly Asn
      180            185            190

```

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...717
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

ATAATTAAAA AGGATACGAT	ATG AAA CAA CTA TTT TTG ATC ATT GGA GCC	50
	Met Lys Gln Leu Phe Leu Ile Ile Gly Ala	
	1 5 10	
CCA GGG AGT GGT AAA ACC ACT GAT GCA GAG CTT ATC GCT AAA AAT AAC		98
Pro Gly Ser Gly Lys Thr Thr Asp Ala Glu Leu Ile Ala Lys Asn Asn		
	15 20 25	
AGC GAA ACA ATC GCT CAT TTT TCT ACC GGG GAT TTA CTC AGG GCT GAG		146
Ser Glu Thr Ile Ala His Phe Ser Thr Gly Asp Leu Leu Arg Ala Glu		
	30 35 40	
AGC GCT AAA AAG ACC GAG CGA GGC TTA TTG ATT GAA AAA TTC ACT TCT		194
Ser Ala Lys Lys Thr Glu Arg Gly Leu Leu Ile Glu Lys Phe Thr Ser		
	45 50 55	
CAA GGC GAA TTA GTG CCT TTA GAA ATT GTG GTA GAA ACG ATC CTT TCA		242
Gln Gly Glu Leu Val Pro Leu Glu Ile Val Val Glu Thr Ile Leu Ser		
	60 65 70	
GCG ATT AAA AGC TCT GGT AAA GGG ATC ATT TTA ATT GAT GGT TAT CCT		290
Ala Ile Lys Ser Ser Gly Lys Gly Ile Ile Leu Ile Asp Gly Tyr Pro		
	75 80 85 90	
AGG AGC GTG GAA CAA ATG CAG GCT TTG GAT AAG GAA TTG AAC GCT CAA		338
Arg Ser Val Glu Gln Met Gln Ala Leu Asp Lys Glu Leu Asn Ala Gln		
	95 100 105	
AAC GAA GTG ATC TTA AAA AGC GTG ATT GAA GTA GAA GTG AGT GAA AAC		386
Asn Glu Val Ile Leu Lys Ser Val Ile Glu Val Glu Val Ser Glu Asn		
	110 115 120	
ACT GCT AAA GAA AGG GTT TTA GGG CGC TCT AGG GGG GCT GAT GAT AAT		434
Thr Ala Lys Glu Arg Val Leu Gly Arg Ser Arg Gly Ala Asp Asp Asn		
	125 130 135	
GAA AAG GTG TTT CAT AAC CGC ATG CGG GTG TTT TTG GAT CCG TTG GGC		482
Glu Lys Val Phe His Asn Arg Met Arg Val Phe Leu Asp Pro Leu Gly		
	140 145 150	
GAG ATC CAA AAT TTT TAC AAG AAT AAG AAG GTG TAT AAA GCG ATC GAT		530
Glu Ile Gln Asn Phe Tyr Lys Asn Lys Lys Val Tyr Lys Ala Ile Asp		
	155 160 165 170	
GGG GAG AGG AGC ATT GAA GAG ATT GTG GGC GAA ATG CAA GAG TAT ATC		578
Gly Glu Arg Ser Ile Glu Glu Ile Val Gly Glu Met Gln Glu Tyr Ile		
	175 180 185	
TTG TCT TTC GGT AAT TAAAATGCAC TCTCAAGGAG AATAGCTGTG ATTTCTG		630
Leu Ser Phe Gly Asn		
	190	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

```

Met Asn Ile Phe Lys Ile Arg Glu Ile Ile His Tyr Asp Gly Glu Val
 1           5           10           15
Thr Glu Ile Leu Gly Gly Ser Asp Gly Val Met Leu Gly Phe Leu Ser
      20           25           30
Val Arg Gly Glu Ser Ile Pro Leu Val Asp Val Lys Arg Trp Leu His
      35           40           45
Tyr Asn Ala Asn Asp Pro Ser Arg Asp Leu Lys Glu Cys Ser Val Lys
      50           55           60
Asp Asp His Asn Leu Val Ile Val Cys His Phe Ser Asn His Ser Ile
      65           70           75           80
Ala Leu Lys Val Leu Lys Ile Glu Arg Ile Ile His Lys Asn Trp Thr
      85           90           95
Glu Ile Ser Ala Gly Asp Lys Gln Gly Ile Asn Glu Glu Gly Lys Leu
      100          105          110
Ser Ala Ile Thr Arg Phe Asp Glu Glu Arg Val Val Gln Ile Leu Asp
      115          120          125
Val Glu Lys Met Ile Ser Asp Val Phe Pro Ser Leu Lys Asp Leu Asp
      130          135          140
Asp Leu Thr Leu Arg Cys Ile Glu Ala Ile Gln Ser Gln Lys Leu Ile
      145          150          155          160
Leu Ile Ala Glu Asp Ser Leu Ser Ala Leu Lys Thr Leu Glu Lys Ile
      165          170          175
Val Gln Thr Leu Glu Leu Arg Tyr Leu Ala Phe Pro Asn Gly Arg Glu
      180          185          190
Leu Leu Asp Tyr Leu Tyr Glu Lys Glu His Tyr Gln Gln Val Gly Val
      195          200          205
Val Ile Thr Asp Leu Glu Met Pro Asn Ile Ser Gly Phe Glu Val Leu
      210          215          220
Lys Thr Ile Lys Ala Asp His Arg Thr Glu His Leu Pro Val Ile Ile
      225          230          235          240
Asn Ser Ser Met Ser Ser Asp Ser Asn Arg Gln Leu Ala Gln Ser Leu
      245          250          255
Glu Ala Asp Gly Phe Val Val Lys Ser Asn Ile Leu Glu Ile His Glu
      260          265          270
Met Leu Lys Lys Thr Leu Ser
      275

```

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...593
- (D) OTHER INFORMATION:

CGT TTT GAT GAA GAA CGA GTG GTG CAG ATC TTA GAT GTG GAA AAA ATG	439
Arg Phe Asp Glu Glu Arg Val Val Gln Ile Leu Asp Val Glu Lys Met	
120 125 130	
ATT AGC GAT GTT TTC CCT AGC TTG AAA GAT TTA GAC GAT TTG ACT TTG	487
Ile Ser Asp Val Phe Pro Ser Leu Lys Asp Leu Asp Asp Leu Thr Leu	
135 140 145	
CGT TGC ATA GAA GCC ATT CAA AGC CAA AAA CTC ATT TTA ATC GCT GAA	535
Arg Cys Ile Glu Ala Ile Gln Ser Gln Lys Leu Ile Leu Ile Ala Glu	
150 155 160	
GAC TCC CTA AGC GCT CTT AAA ACC TTA GAA AAG ATC GTT CAA ACT TTA	583
Asp Ser Leu Ser Ala Leu Lys Thr Leu Glu Lys Ile Val Gln Thr Leu	
165 170 175 180	
GAA TTG CGT TAT TTA GCT TTT CCA AAC GGG AGG GAA TTG TTG GAT TAT	631
Glu Leu Arg Tyr Leu Ala Phe Pro Asn Gly Arg Glu Leu Leu Asp Tyr	
185 190 195	
TTG TAT GAA AAA GAA CAT TAC CAA CAA GTT GGC GTG GTC ATT ACG GAT	679
Leu Tyr Glu Lys Glu His Tyr Gln Gln Val Gly Val Val Ile Thr Asp	
200 205 210	
TTA GAA ATG CCT AAC ATT TCA GGG TTT GAA GTG TTA AAA ACC ATT AAA	727
Leu Glu Met Pro Asn Ile Ser Gly Phe Glu Val Leu Lys Thr Ile Lys	
215 220 225	
GCT GAT CAT AGA ACT GAG CAT CTT CCT GTG ATT ATC AAT TCG TCC ATG	775
Ala Asp His Arg Thr Glu His Leu Pro Val Ile Ile Asn Ser Ser Met	
230 235 240	
AGC AGC GAT TCT AAC CGC CAG TTA GCC CAA TCT TTA GAA GCG GAT GGT	823
Ser Ser Asp Ser Asn Arg Gln Leu Ala Gln Ser Leu Glu Ala Asp Gly	
245 250 255 260	
TTT GTG GTA AAA TCT AAC ATT CTT GAA ATC CAT GAA ATG CTT AAA AAA	871
Phe Val Val Lys Ser Asn Ile Leu Glu Ile His Glu Met Leu Lys Lys	
265 270 275	
ACG CTT TCA TAAATTTAAT TTTTGTTTTA ATTTAAAGGG ATAAAACATG CGAAGTCAT	929
Thr Leu Ser	
TTTTGCAC	937

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

290
Ile Asn Ser Arg Leu
305

295

300

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 44...880
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GTGCTTTAGA	TTAGATGCAG	AAAAAGACGC	CCAACCTTTAT	GGC	ATG	AAT	ATT	TTT									55
												Met	Asn	Ile	Phe		
												1					
AAG	ATC	CGA	GAA	ATT	ATC	CAT	TAT	GAC	GGG	GAG	GTT	ACA	GAG	ATT	CTT		103
Lys	Ile	Arg	Glu	Ile	Ile	His	Tyr	Asp	Gly	Glu	Val	Thr	Glu	Ile	Leu		
5					10					15					20		
GGG	GGG	AGC	GAT	GGC	GTG	ATG	CTC	GGG	TTT	CTT	AGC	GTT	AGG	GGC	GAG		151
Gly	Gly	Ser	Asp	Gly	Val	Met	Leu	Gly	Phe	Leu	Ser	Val	Arg	Gly	Glu		
				25					30					35			
TCT	ATC	CCT	TTA	GTG	GAT	GTG	AAA	AGG	TGG	TTG	CAT	TAT	AAC	GCT	AAT		199
Ser	Ile	Pro	Leu	Val	Asp	Val	Lys	Arg	Trp	Leu	His	Tyr	Asn	Ala	Asn		
			40					45					50				
GAT	CCG	AGC	CGT	GAT	CTA	AAA	GAA	TGC	AGC	GTT	AAA	GAT	GAC	CAT	AAT		247
Asp	Pro	Ser	Arg	Asp	Leu	Lys	Glu	Cys	Ser	Val	Lys	Asp	Asp	His	Asn		
		55					60					65					
TTG	GTG	ATT	GTG	TGC	CAT	TTT	TCT	AAC	CAT	TCC	ATC	GCT	CTA	AAG	GTT		295
Leu	Val	Ile	Val	Cys	His	Phe	Ser	Asn	His	Ser	Ile	Ala	Leu	Lys	Val		
	70					75					80						
TTA	AAA	ATT	GAA	AGG	ATC	ATC	CAT	AAA	AAT	TGG	ACT	GAG	ATT	AGC	GCT		343
Leu	Lys	Ile	Glu	Arg	Ile	Ile	His	Lys	Asn	Trp	Thr	Glu	Ile	Ser	Ala		
85					90					95					100		
GGG	GAC	AAA	CAA	GGC	ATT	AAT	GAA	GAG	GGT	AAG	CTT	AGC	GCT	ATC	ACT		391
Gly	Asp	Lys	Gln	Gly	Ile	Asn	Glu	Glu	Gly	Lys	Leu	Ser	Ala	Ile	Thr		
				105					110					115			

AAA TNG CTT GCG CTT ATA AAT TCC CGG CTT TAGAAAAACA CACCAAAATT GTA 968
 Lys Xaa Leu Ala Leu Ile Asn Ser Arg Leu
 300 305

GGAGTCATTA ACCAAGTGGG GCGCASSGGG CGATCACAC 1007

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

Met	Ile	Lys	Ser	Gln	Lys	Glu	Tyr	Leu	Glu	Arg	Ile	Ala	Tyr	Leu	Asn	1	5	10	15
Thr	Leu	Ser	His	His	Tyr	Tyr	Asn	Leu	Asp	Glu	Pro	Ile	Val	Ser	Asp	20	25	30	
Ala	Ile	Tyr	Asp	Glu	Leu	Tyr	Gln	Glu	Leu	Lys	Ala	Tyr	Glu	Glu	Lys	35	40	45	
Asn	Pro	Asn	Gly	Ile	Gln	Ala	Asn	Ser	Pro	Thr	Gln	Lys	Val	Gly	Ala	50	55	60	
Thr	Thr	Thr	Asn	Ser	Phe	Asn	Lys	Asn	Pro	His	Leu	Met	Arg	Met	Trp	65	70	75	80
Ser	Leu	Asp	Asp	Val	Phe	Asn	Gln	Ser	Glu	Leu	Gln	Ala	Trp	Leu	Gln	85	90	95	
Arg	Ile	Leu	Lys	Ala	Tyr	Pro	Ser	Ala	Ser	Phe	Val	Cys	Ser	Pro	Lys	100	105	110	
Leu	Asp	Gly	Val	Ser	Leu	Asn	Leu	Leu	Tyr	Gln	His	Gly	Lys	Leu	Val	115	120	125	
Lys	Ala	Thr	Thr	Arg	Gly	Asn	Gly	Leu	Glu	Gly	Glu	Leu	Val	Ser	Ala	130	135	140	
Asn	Ala	Lys	His	Ile	Ala	Asn	Ile	Pro	His	Ala	Ile	Ala	Tyr	Asn	Gly	145	150	155	160
Glu	Ile	Glu	Ile	Arg	Gly	Glu	Val	Ile	Ile	Ser	Lys	Lys	Asp	Phe	Asp	165	170	175	
Ala	Leu	Asn	Gln	Glu	Arg	Leu	Asn	Ala	Asn	Glu	Pro	Leu	Phe	Ala	Asn	180	185	190	
Pro	Arg	Asn	Ala	Ala	Ser	Gly	Ser	Leu	Arg	Gln	Leu	Asp	Ser	Glu	Ile	195	200	205	
Thr	Lys	Lys	Arg	Lys	Leu	Gln	Phe	Ile	Pro	Trp	Gly	Val	Gly	Lys	His	210	215	220	
Ser	Leu	Asn	Phe	Leu	Ser	Phe	Lys	Glu	Cys	Leu	Asp	Phe	Ile	Val	Ser	225	230	235	240
Leu	Gly	Phe	Ser	Ala	Ile	Gln	Tyr	Leu	Ser	Leu	Asn	Lys	Asn	His	Gln	245	250	255	
Glu	Ile	Glu	Asp	Asn	Tyr	His	Thr	Leu	Ile	Arg	Glu	Arg	Glu	Gly	Phe	260	265	270	
Phe	Ala	Leu	Leu	Asp	Gly	Met	Val	Ile	Val	Val	Asn	Glu	Leu	Asn	Ile	275	280	285	
Gln	Lys	Glu	Leu	Gly	Tyr	Thr	Gln	Lys	Ser	Pro	Lys	Xaa	Leu	Ala	Leu				

TTA ATG CGG ATG TGG AGC TTA GAT GAT GTG TTC AAT CAA AGC GAA TTG	291
Leu Met Arg Met Trp Ser Leu Asp Asp Val Phe Asn Gln Ser Glu Leu	
80 85 90	
CAA GCG TGG TTG CAA CGC ATT TTA AAA GCC TAT CCT AGT GCT TCG TTC	339
Gln Ala Trp Leu Gln Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe	
95 100 105	
GTG TGT TCG CCC AAA CTT GAT GGG GTT TCG CTC AAT CTT TTG TAT CAA	387
Val Cys Ser Pro Lys Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln	
110 115 120	
CAT GGC AAG CTA GTG AAG GCG ACC ACT AGG GGC AAC GGC TTA GAA GGA	435
His Gly Lys Leu Val Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly	
125 130 135	
GAA TTA GTT AGC GCA AAC GCT AAA CAC ATC GCT AAT ATC CCC CAC GCT	483
Glu Leu Val Ser Ala Asn Ala Lys His Ile Ala Asn Ile Pro His Ala	
140 145 150 155	
ATC GCT TAT AAT GGA GAA ATA GAA ATC AGG GGC GAA GTG ATC ATT TCT	531
Ile Ala Tyr Asn Gly Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser	
160 165 170	
AAA AAG GAT TTT GAC GCT TTG AAT CAA GAG CGC TTA AAC GCT AAT GAA	579
Lys Lys Asp Phe Asp Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu	
175 180 185	
CCC CTA TTC GCT AAC CCC AGA AAC GCC GCA TCA GGG AGT TTG AGG CAA	627
Pro Leu Phe Ala Asn Pro Arg Asn Ala Ala Ser Gly Ser Leu Arg Gln	
190 195 200	
CTT GAT AGC GAA ATC ACT AAA AAG CGT AAA TTG CAA TTC ATT CCT TGG	675
Leu Asp Ser Glu Ile Thr Lys Lys Arg Lys Leu Gln Phe Ile Pro Trp	
205 210 215	
GGC GTG GGC AAG CAT TCT TTA AAT TTT TTA AGC TTT AAG GAG TGT TTG	723
Gly Val Gly Lys His Ser Leu Asn Phe Leu Ser Phe Lys Glu Cys Leu	
220 225 230 235	
GAT TTT ATC GTC TCG TTA GGT TTT AGC GCC ATT CAA TAC TTA AGC CTA	771
Asp Phe Ile Val Ser Leu Gly Phe Ser Ala Ile Gln Tyr Leu Ser Leu	
240 245 250	
AAC AAA AAC CAC CAA GAA ATA GAA GAC AAT TAC CAC ACC CTA ATT AGA	819
Asn Lys Asn His Gln Glu Ile Glu Asp Asn Tyr His Thr Leu Ile Arg	
255 260 265	
GAA AGG GAG GGC TTT TTT GCC CTT TTA GAC GGC ATG GTG ATC GTT GTG	867
Glu Arg Glu Gly Phe Phe Ala Leu Leu Asp Gly Met Val Ile Val Val	
270 275 280	
AAT GAA TTA AAT ATT CAA AAG GAG CTA GGC TAC ACG CAA AAA TCC CCT	915
Asn Glu Leu Asn Ile Gln Lys Glu Leu Gly Tyr Thr Gln Lys Ser Pro	
285 290 295	

50		55		60	
Asn	Glu	Glu	Arg	Lys	Lys
65		70		75	
Ala	Gly	Lys	Thr	Arg	Leu
		85		90	
Val	Cys	Gly	Met	Leu	Pro
		100		105	
Met	Lys	Ser	Pro	Ile	Gly
		115		120	
Met	Val	Leu	Ser	Leu	Leu
		130		135	
Pro	Ile	Asp	Asp	Lys	Ile
145				150	
Glu				155	

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...945
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

TAAAAGGTTT TTACAAAC ATG ATA AAA AGC CAA AAA GAA TAT TTA GAA AGA	51
Met Ile Lys Ser Gln Lys Glu Tyr Leu Glu Arg	
1 5 10	
ATT GCA TAT TTA AAC ACC CTA TCG CAC CAT TAT TAC AAC CTT GAT GAA	99
Ile Ala Tyr Leu Asn Thr Leu Ser His His Tyr Tyr Asn Leu Asp Glu	
15 20 25	
CCC ATC GTA AGC GAT GCG ATC TAT GAT GAA CTT TAC CAA GAA TTG AAA	147
Pro Ile Val Ser Asp Ala Ile Tyr Asp Glu Leu Tyr Gln Glu Leu Lys	
30 35 40	
GCT TAT GAA GAA AAA AAC CCT AAT GGC ATT CAA GCT AAT TCC CCT ACC	195
Ala Tyr Glu Glu Lys Asn Pro Asn Gly Ile Gln Ala Asn Ser Pro Thr	
45 50 55	
CAA AAA GTG GGG GCT ACT ACC ACC AAT TCG TTC AAT AAA AAC CCC CAT	243
Gln Lys Val Gly Ala Thr Thr Thr Asn Ser Phe Asn Lys Asn Pro His	
60 65 70 75	

35	40	45	
CTC ATT GGT ATG GTG GGT AAA AAC GCC ACG CTT TTA ATT GAT GTG GCG			253
Leu Ile Gly Met Val Gly Lys Asn Ala Thr Leu Leu Ile Asp Val Ala			
50	55	60	
AAT GAA GAG CGT AAA AAA GGT TTG AAT ATC CAA GAG GCC ATT TTA TTT			301
Asn Glu Glu Arg Lys Lys Gly Leu Asn Ile Gln Glu Ala Ile Leu Phe			
65	70	75	80
GCC GGC AAA ACC CGT CTA AGA CCG ATT TTA ATG ACG ACC ATT GCG ATG			349
Ala Gly Lys Thr Arg Leu Arg Pro Ile Leu Met Thr Thr Ile Ala Met			
85	90	95	
GTT TGC GGG ATG CTG CCT TTA GCG TTG GCG AGT GGG GAT GGA GCG GCG			397
Val Cys Gly Met Leu Pro Leu Ala Leu Ala Ser Gly Asp Gly Ala Ala			
100	105	110	
ATG AAA TCC CCT ATA GGG ATT GCG ATG AGT GGG GGC TTG ATG ATT TCT			445
Met Lys Ser Pro Ile Gly Ile Ala Met Ser Gly Gly Leu Met Ile Ser			
115	120	125	
ATG GTG TTA AGC TTA CTC ATT GTG CCG GTG TTT TAT CGT TTG CTC GCT			493
Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala			
130	135	140	
CCC ATA GAC GAC AAA ATC AAG CGG TTT TAT CAA AAC CAA AAA ACT TTA			541
Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu			
145	150	155	160
GAA TGAAAAAAAT TGCTTTCATT TTGGCTTTAT GGGTGGGCTT GTTAGGGGCG TTTGAG			600
Glu			
CCTAAAAAAA GTCATATTTA TTTTGGGGCT			630

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

Met	Ile	Leu	Ala	Ala	Leu	Tyr	Glu	Ser	Ile	Leu	Glu	Pro	Phe	Ile	Ile
1				5					10					15	
Met	Val	Thr	Met	Pro	Leu	Ser	Phe	Ser	Gly	Ala	Phe	Phe	Ala	Leu	Gly
				20					25				30		
Leu	Val	His	Gln	Pro	Leu	Ser	Met	Phe	Ser	Met	Ile	Gly	Leu	Ile	Leu
				35				40				45			
Leu	Ile	Gly	Met	Val	Gly	Lys	Asn	Ala	Thr	Leu	Leu	Ile	Asp	Val	Ala

```

Val Thr Glu Gly Ser Val Val Lys Lys Gly Asp Val Leu Leu Leu Leu
 50                      55                      60
Tyr Asn Gln Asp Lys Gln Ala Gln Ser Asp Ser Thr Glu Gln Gln Leu
 65                      70                      75                      80
Ile Phe Ala Lys Lys Gln Tyr Gln Arg Tyr Ser Lys Ile Gly Gly Ala
                      85                      90                      95
Val Asp Lys Asn Thr Leu Glu Gly Tyr Glu Phe Thr Tyr Arg Arg Leu
                      100                      105                      110
Glu Ser Asp Tyr Ala Tyr Ser Ile Ala Val Leu Asn Lys Thr Ile Leu
                      115                      120                      125
Arg Ala Pro Phe Asp Gly Val Ile Ala Ser Lys Asn Ile Gln Val Gly
                      130                      135                      140
Glu Gly Val Ser Ala Asn Asn Thr Val Leu Leu Arg Leu Val Ser His
 145                      150                      155                      160
Ala Arg Lys Leu Val Ile Glu Phe Asp Ser Lys Tyr Ile Asn Ala Val
                      165                      170                      175
Lys Val Gly Asp Thr Tyr Thr Tyr Ser Ile Asp Gly Asp Ser Asn Gln
                      180                      185                      190
His Glu Ala Lys Ile Thr Lys Ile Tyr Pro Thr Val Asp Glu Asn Thr
                      195                      200                      205
Arg Lys Val Ser Ala Glu Ala Leu Leu Ser Lys Pro Met Ala Val Gly
                      210                      215                      220
Leu Phe Gly Asp Gly Phe Ile Gln Thr Lys
 225                      230

```

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...544
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

```

ACGCCAAAGA GAGCAACGGG GAGTTTTTAG TCGCTTTAGC GNAGCGNTTG TGCTGATTTA      60
T ATG ATT TTA GCG GCG TTG TAT GAG TCC ATT TTA GAG CCT TTT ATC ATC      109
Met Ile Leu Ala Ala Leu Tyr Glu Ser Ile Leu Glu Pro Phe Ile Ile
  1              5              10              15

ATG GTT ACC ATG CCT TTA AGT TTT TCA GGG GCG TTT TTT GCT CTA GGT      157
Met Val Thr Met Pro Leu Ser Phe Ser Gly Ala Phe Phe Ala Leu Gly
          20              25              30

TTA GTC CAT CAG CCT TTG AGC ATG TTC TCT ATG ATA GGC TTG ATT TTG      205
Leu Val His Gln Pro Leu Ser Met Phe Ser Met Ile Gly Leu Ile Leu

```

TAT GAG TTC ACT TAC AGG CGC TTG GAG TCT GAT TAC GCT TAT TCT ATT	390
Tyr Glu Phe Thr Tyr Arg Arg Leu Glu Ser Asp Tyr Ala Tyr Ser Ile	
105 110 115 120	
GCG GTA TTG AAT AAA ACC ATT TTA AGA GCC CCT TTT GAT GGC GTG ATA	438
Ala Val Leu Asn Lys Thr Ile Leu Arg Ala Pro Phe Asp Gly Val Ile	
125 130 135	
GCG AGT AAA AAC ATT CAA GTG GGC GAA GGG GTG AGC GCG AAT AAC ACG	486
Ala Ser Lys Asn Ile Gln Val Gly Glu Gly Val Ser Ala Asn Asn Thr	
140 145 150	
GTG TTA TTG AGA TTA GTC AGC CAT GCT AGG AAA TTA GTT ATT GAA TTT	534
Val Leu Leu Arg Leu Val Ser His Ala Arg Lys Leu Val Ile Glu Phe	
155 160 165	
GAT TCT AAA TAT ATT AAT GCG GTC AAA GTA GGG GAC ACT TAC ACC TAT	582
Asp Ser Lys Tyr Ile Asn Ala Val Lys Val Gly Asp Thr Tyr Thr Tyr	
170 175 180	
TCT ATA GAC GGG GAT TCT AAT CAG CAT GAA GCT AAA ATC ACT AAG ATT	630
Ser Ile Asp Gly Asp Ser Asn Gln His Glu Ala Lys Ile Thr Lys Ile	
185 190 195 200	
TAC CCC ACG GTT GAT GAA AAC ACC AGG AAA GTG AGC GCT GAA GCC CTT	678
Tyr Pro Thr Val Asp Glu Asn Thr Arg Lys Val Ser Ala Glu Ala Leu	
205 210 215	
TTA TCT AAG CCT ATG GCA GTG GGG CTT TTT GGC GAT GGG TTT ATC CAA	726
Leu Ser Lys Pro Met Ala Val Gly Leu Phe Gly Asp Gly Phe Ile Gln	
220 225 230	
ACG AAA TAATAGGATA TTTTGATGTA TAAACAGCG ATTA	766
Thr Lys	

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

Met Ile Arg Lys Ile Leu Ile Gly Leu Phe Leu Ser Phe Leu Ser Met	
1 5 10 15	
Glu Ala Gly Glu Lys Val Tyr Ala Ile Phe Asn Val Lys Ala Thr Gln	
20 25 30	
Asp Ser Lys Leu Thr Leu Asp Ser Thr Gly Ile Val Asp Ser Ile Lys	
35 40 45	

```

      290              295              300
Met Gly Asn Gln Gly His Ile Phe Asn Leu Gly His Gly Met Leu Pro
305              310              315              320
Asp Leu Pro Arg Glu Asn Ala Lys Tyr Leu Val Gln Leu Val His Ala
      325              330              335
Lys Thr Arg Arg
      340

```

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...732
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

```

TAGACGACTA TGTGCATTAA GGGAATGAAA ATG ATA CGA AAA ATT TTA ATA GGA      54
                               Met Ile Arg Lys Ile Leu Ile Gly
                               1               5

CTT TTT TTG AGT TTT TTG AGC ATG GAA GCT GGC GAA AAA GTG TAT GCG      102
Leu Phe Leu Ser Phe Leu Ser Met Glu Ala Gly Glu Lys Val Tyr Ala
   10               15               20

ATT TTC AAT GTG AAA GCG ACA CAA GAT TCC AAA CTC ACC TTA GAC AGC      150
Ile Phe Asn Val Lys Ala Thr Gln Asp Ser Lys Leu Thr Leu Asp Ser
   25               30               35               40

ACA GGA ATT GTG GAT AGC ATT AAG GTT ACT GAG GGG AGC GTG GTC AAA      198
Thr Gly Ile Val Asp Ser Ile Lys Val Thr Glu Gly Ser Val Val Lys
           45               50               55

AAG GGC GAT GTT TTG TTG CTT TTA TAT AAT CAA GAC AAA CAG GCT CAA      246
Lys Gly Asp Val Leu Leu Leu Leu Tyr Asn Gln Asp Lys Gln Ala Gln
           60               65               70

AGC GAT TCC ACC GAA CAA CAA CTC ATT TTC GCT AAA AAG CAA TAC CAA      294
Ser Asp Ser Thr Glu Gln Gln Leu Ile Phe Ala Lys Lys Gln Tyr Gln
       75               80               85

CGA TAC AGC AAA ATT GGG GGC GCT GTG GAT AAA AAC ACT CTA GAG GGT      342
Arg Tyr Ser Lys Ile Gly Gly Ala Val Asp Lys Asn Thr Leu Glu Gly
   90               95               100

```

TAT TTA GTG CAA TTA GTG CAT GCT AAA ACC AGA CGA TAGGGGGATT GATGAA 1065
 Tyr Leu Val Gln Leu Val His Ala Lys Thr Arg Arg
 330 335 340

TACTATCATA AGATA

1080

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

Met	Met	Ile	Phe	Ile	Asp	Ala	Cys	Phe	Arg	Lys	Glu	Thr	Pro	Tyr	Thr
1				5					10					15	
Pro	Ile	Trp	Met	Met	Arg	Gln	Ala	Gly	Arg	Tyr	Leu	Ser	Glu	Tyr	Gln
			20					25					30		
Glu	Ser	Arg	Lys	Lys	Ala	Gly	Ser	Phe	Leu	Glu	Leu	Cys	Lys	Asn	Ser
			35				40					45			
Asp	Leu	Ala	Thr	Glu	Val	Thr	Leu	Gln	Pro	Val	Glu	Ile	Leu	Gly	Val
	50					55				60					
Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp	Ile	Leu	Val	Val	Pro	Leu	Glu	Met
65					70				75						80
Gly	Leu	Asn	Leu	Glu	Phe	Ile	Pro	Lys	Lys	Gly	Pro	His	Phe	Leu	Glu
				85				90						95	
Thr	Ile	Thr	Asp	Leu	Lys	Ser	Val	Glu	Ser	Leu	Lys	Val	Gly	Ala	Tyr
			100					105					110		
Lys	Gln	Leu	Asn	Tyr	Val	Tyr	Asp	Thr	Ile	Ser	Gln	Thr	Arg	Gln	Lys
			115				120					125			
Leu	Ser	Arg	Glu	Lys	Ala	Leu	Ile	Gly	Phe	Cys	Gly	Ser	Pro	Trp	Thr
	130					135					140				
Leu	Ala	Thr	Tyr	Met	Ile	Glu	Gly	Glu	Gly	Ser	Lys	Ser	Tyr	Ala	Lys
145					150					155					160
Ser	Lys	Lys	Met	Leu	Tyr	Ser	Glu	Pro	Glu	Val	Leu	Lys	Ala	Leu	Leu
			165					170					175		
Glu	Lys	Leu	Ser	Leu	Glu	Leu	Ile	Glu	Tyr	Leu	Ser	Leu	Gln	Ile	Gln
			180					185					190		
Ala	Gly	Val	Asn	Ala	Val	Met	Ile	Phe	Asp	Ser	Trp	Ala	Ser	Ala	Leu
		195				200						205			
Glu	Lys	Glu	Ala	Tyr	Leu	Lys	Phe	Ser	Trp	Asp	Tyr	Leu	Lys	Lys	Ile
	210					215					220				
Ser	Lys	Glu	Leu	Lys	Lys	Arg	Tyr	Ala	His	Ile	Pro	Val	Ile	Leu	Phe
225					230					235					240
Pro	Lys	Gly	Ile	Gly	Ala	Tyr	Leu	Asp	Ser	Ile	Asp	Gly	Glu	Phe	Asp
				245					250				255		
Val	Phe	Gly	Val	Asp	Trp	Gly	Thr	Pro	Leu	Thr	Ala	Ala	Lys	Lys	Ile
			260					265					270		
Leu	Gly	Gly	Lys	Tyr	Val	Leu	Gln	Gly	Asn	Leu	Glu	Pro	Thr	Arg	Leu
		275					280					285			
Tyr	Asp	Lys	Asn	Ala	Leu	Glu	Glu	Gly	Val	Glu	Thr	Ile	Leu	Lys	Val

GAA AGC CTA AAA GTA GGG GCT TAT AAA CAA CTA AAC TAT GTC TAT GAT	389
Glu Ser Leu Lys Val Gly Ala Tyr Lys Gln Leu Asn Tyr Val Tyr Asp	
105 110 115 120	
ACG ATT TCT CAA ACG CGC CAA AAG CTT TCT AGA GAG AAA GCG TTA ATC	437
Thr Ile Ser Gln Thr Arg Gln Lys Leu Ser Arg Glu Lys Ala Leu Ile	
125 130 135	
GGT TTT TGC GGA TCG CCT TGG ACT TTA GCG ACT TAC ATG ATA GAA GGC	485
Gly Phe Cys Gly Ser Pro Trp Thr Leu Ala Thr Tyr Met Ile Glu Gly	
140 145 150	
GAG GGG AGC AAA TCG TAT GCC AAA AGC AAG AAA ATG CTT TAT AGC GAG	533
Glu Gly Ser Lys Ser Tyr Ala Lys Ser Lys Lys Met Leu Tyr Ser Glu	
155 160 165	
CCT GAA GTT TTA AAA GCG CTT TTA GAA AAA TTA AGC CTT GAA TTG ATA	581
Pro Glu Val Leu Lys Ala Leu Leu Glu Lys Leu Ser Leu Glu Leu Ile	
170 175 180	
GAG TAT TTG AGC CTT CAA ATC CAA GCA GGG GTC AAT GCA GTG ATG ATC	629
Glu Tyr Leu Ser Leu Gln Ile Gln Ala Gly Val Asn Ala Val Met Ile	
185 190 195 200	
TTT GAC TCA TGG GCT AGC GCT TTA GAA AAA GAA GCG TAT TTG AAA TTC	677
Phe Asp Ser Trp Ala Ser Ala Leu Glu Lys Glu Ala Tyr Leu Lys Phe	
205 210 215	
AGT TGG GAT TAT TTG AAA AAA ATC TCT AAA GAG CTT AAA AAA CGC TAT	725
Ser Trp Asp Tyr Leu Lys Lys Ile Ser Lys Glu Leu Lys Lys Arg Tyr	
220 225 230	
GCG CAT ATC CCA GTT ATC CTT TTC CCT AAA GGG ATT GGC GCT TAT TTG	773
Ala His Ile Pro Val Ile Leu Phe Pro Lys Gly Ile Gly Ala Tyr Leu	
235 240 245	
GAT AGC ATA GAT GGG GAA TTT GAT GTG TTT GGC GTG GAT TGG GGC ACG	821
Asp Ser Ile Asp Gly Glu Phe Asp Val Phe Gly Val Asp Trp Gly Thr	
250 255 260	
CCT TTA ACT GCG GCA AAA AAG ATT TTA GGC GGT AAG TAT GTT TTG CAA	869
Pro Leu Thr Ala Ala Lys Lys Ile Leu Gly Gly Lys Tyr Val Leu Gln	
265 270 275 280	
GGG AAT TTA GAA CCC ACC CGC CTT TAT GAT AAA AAC GCT TTA GAA GAA	917
Gly Asn Leu Glu Pro Thr Arg Leu Tyr Asp Lys Asn Ala Leu Glu Glu	
285 290 295	
GGG GTT GAA ACG ATT CTA AAA GTC ATG GGC AAT CAA GGG CAT ATT TTT	965
Gly Val Glu Thr Ile Leu Lys Val Met Gly Asn Gln Gly His Ile Phe	
300 305 310	
AAT TTA GGG CAT GGG ATG TTG CCG GAT TTA CCC AGA GAA AAC GCC AAA	1013
Asn Leu Gly His Gly Met Leu Pro Asp Leu Pro Arg Glu Asn Ala Lys	
-315 320 325	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

```

Met Tyr Leu Gly Leu Asn Pro Lys Arg Thr Thr Lys Ser Ala Thr Ala
 1             5             10             15
Pro Ile Lys Ile Met Leu Met Arg Cys Ala Gln Gln Lys Ile Gln Gly
      20             25             30
Glu Ser Phe Lys Thr
      35

```

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...1049
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

```

ACCATAATTA GACAAACCTT TAAGGATTT ATG ATG ATT TTC ATT GAT GCA TGT      53
                               Met Met Ile Phe Ile Asp Ala Cys
                               1             5

TTT AGA AAG GAA ACG CCT TAC ACG CCC ATT TGG ATG ATG AGG CAA GCG      101
Phe Arg Lys Glu Thr Pro Tyr Thr Pro Ile Trp Met Met Arg Gln Ala
 10             15             20

GGG CGT TAC CTT AGC GAA TAC CAA GAG AGC CGT AAA AAA GCG GGG AGT      149
Gly Arg Tyr Leu Ser Glu Tyr Gln Glu Ser Arg Lys Lys Ala Gly Ser
 25             30             35             40

TTC TTG GAA TTG TGT AAA AAT AGC GAT CTA GCC ACA GAA GTT ACC TTA      197
Phe Leu Glu Leu Cys Lys Asn Ser Asp Leu Ala Thr Glu Val Thr Leu
      45             50             55

CAG CCG GTA GAG ATT TTA GGC GTG GAT GCG GCT ATT TTG TTT AGC GAT      245
Gln Pro Val Glu Ile Leu Gly Val Asp Ala Ala Ile Leu Phe Ser Asp
      60             65             70

ATT TTA GTA GTG CCT TTG GAA ATG GGC TTG AAT TTG GAG TTT ATC CCC      293
Ile Leu Val Val Pro Leu Glu Met Gly Leu Asn Leu Glu Phe Ile Pro
      75             80             85

AAA AAG GGG CCG CAT TTT TTA GAG ACG ATT ACG GAT TTA AAA AGC GTG      341
Lys Lys Gly Pro His Phe Leu Glu Thr Ile Thr Asp Leu Lys Ser Val
 90             95             100

```



```

Lys Glu Ile Gly Asp Lys Tyr Glu Lys Ile Leu Val Ile Glu Leu Asn
      325                      330                      335
Lys Gly Gln Tyr Leu Glu Glu Ile Glu Arg Ala Met Gln Arg Lys Val
      340                      345                      350
His Phe Leu Gly Gln Ala Asn Gly Arg Thr Ile Ser Pro Lys Gln Ile
      355                      360                      365
Ile Ala Lys Leu Lys Glu Leu
      370                      375

```

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 54...164
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

```

TATGATAAAA GCTCTCATAT AACCCGCTAC TAGCCATAAG CAACAGCAAG GCA ATG      56
                                         Met
                                         1

TAT TTA GGC TTA AAC CCA AAA CGC ACC ACC AAA AGC GCC ACA GCC CCT      104
Tyr Leu Gly Leu Asn Pro Lys Arg Thr Thr Lys Ser Ala Thr Ala Pro
      5                      10                      15

ATT AAA ATC ATG TTG ATG CGT TGC GCC CAG CAA AAA ATA CAA GGC GAA      152
Ile Lys Ile Met Leu Met Arg Cys Ala Gln Gln Lys Ile Gln Gly Glu
      20                      25                      30

TCT TTC AAA ACA TAGCCAAAAT AACCTTAAAA AACGCTTT      192
Ser Phe Lys Thr
      35

```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

TTTGC GTGTG GATAAAATAC CCACTTTGTG GTGTTGGGGC TGTGGCGATG GCGTGATTTT 1338
GAAATCCATT AT 1350

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEO ID NO:752:

Met 1	Arg	Glu	Ile	Ile 5	Ser	Asp	Gly	Asn 10	Glu	Leu	Val	Ala	Lys 15	Ala	
Ile	Glu	Val	Gly	Cys	Arg	Phe	Phe	Gly	Gly	Tyr	Pro	Ile	Thr	Pro	Ser
			20					25					30		
Ser	Asp	Ile	Met	His	Ala	Met	Ser	Val	Ala	Leu	Pro	Lys	Cys	Gly	Gly
			35					40					45		
His	Phe	Ile	Gln	Met	Glu	Asp	Glu	Ile	Ser	Gly	Ile	Ser	Val	Ser	Leu
						55						60			
Gly	Ala	Ser	Met	Ser	Gly	Thr	Lys	Ser	Met	Thr	Ala	Ser	Ser	Gly	Pro
65					70					75					80
Gly	Ile	Ser	Leu	Lys	Val	Glu	Gln	Ile	Gly	Tyr	Ser	Phe	Met	Ala	Glu
				85					90					95	
Ile	Pro	Leu	Val	Ile	Ala	Asp	Val	Met	Arg	Ser	Gly	Pro	Ser	Thr	Gly
			100					105					110		
Met	Pro	Thr	Arg	Val	Ala	Gln	Gly	Asp	Val	Asn	Phe	Leu	Arg	His	Pro
			115					120				125			
Ile	His	Gly	Asp	Phe	Lys	Ala	Val	Ala	Leu	Ala	Pro	Ala	Asn	Leu	Glu
						135					140				
Glu	Ala	Tyr	Thr	Glu	Thr	Val	Arg	Ala	Phe	Asn	Leu	Ala	Glu	Met	Leu
145					150					155					160
Met	Thr	Pro	Val	Phe	Leu	Leu	Met	Asp	Glu	Thr	Val	Gly	His	Met	Tyr
				165					170					175	
Gly	Lys	Val	Gln	Ile	Pro	Asp	Leu	Glu	Glu	Val	Gln	Lys	Met	Thr	Ile
			180					185					190		
Asn	Arg	Lys	Glu	Phe	Leu	Gly	Asp	Lys	Lys	Asp	Tyr	Lys	Pro	Tyr	Gly
			195				200					205			
Val	Ala	Gln	Asp	Glu	Pro	Ala	Val	Leu	Asn	Pro	Phe	Phe	Lys	Gly	Tyr
			210			215					220				
Arg	Tyr	His	Val	Ser	Gly	Leu	His	His	Gly	Pro	Ile	Gly	Phe	Pro	Thr
225					230					235					240
Glu	Asp	Ala	Lys	Ile	Gly	Gly	Asp	Leu	Ile	Asp	Arg	Leu	Phe	Asn	Lys
				245					250					255	
Ile	Glu	Ser	Lys	Gln	Asp	Ile	Ile	Asn	Glu	Asn	Glu	Glu	Met	Asp	Leu
			260					265					270		
Glu	Gly	Ala	Glu	Ile	Val	Val	Ile	Ala	Tyr	Gly	Ser	Val	Ser	Leu	Ala
			275				280					285			
Val	Lys	Glu	Ala	Leu	Lys	Asp	Tyr	His	Lys	Glu	Ser	Lys	Gln	Lys	Val
			290			295					300				
Gly	Phe	Phe	Arg	Pro	Lys	Thr	Leu	Trp	Pro	Ser	Pro	Ala	Lys	Arg	Leu
305					310					315					320

ATG CTC ATG ACT CCT GTA TTC TTG CTC ATG GAT GAA ACC GTG GGG CAT	648
Met Leu Met Thr Pro Val Phe Leu Leu Met Asp Glu Thr Val Gly His	
160 165 170	
ATG TAT GGC AAG GTG CAA ATC CCA GAT TTA GAA GAA GTG CAA AAG ATG	696
Met Tyr Gly Lys Val Gln Ile Pro Asp Leu Glu Glu Val Gln Lys Met	
175 180 185 190	
ACT ATT AAT CGT AAG GAA TTT CTG GGC GAT AAA AAA GAC TAC AAG CCT	744
Thr Ile Asn Arg Lys Glu Phe Leu Gly Asp Lys Lys Asp Tyr Lys Pro	
195 200 205	
TAT GGG GTC GCA CAA GAC GAG CCG GCT GTT TTG AAC CCT TTC TTT AAA	792
Tyr Gly Val Ala Gln Asp Glu Pro Ala Val Leu Asn Pro Phe Phe Lys	
210 215 220	
GGT TAT CGC TAC CAT GTT TCA GGC TTG CAC CAT GGG CCT ATT GGC TTT	840
Gly Tyr Arg Tyr His Val Ser Gly Leu His His Gly Pro Ile Gly Phe	
225 230 235	
CCT ACT GAA GAC GCT AAA ATT GGT GGG GAT TTG ATT GAC AGA TTA TTT	888
Pro Thr Glu Asp Ala Lys Ile Gly Gly Asp Leu Ile Asp Arg Leu Phe	
240 245 250	
AAT AAG ATT GAA TCC AAG CAA GAC ATT ATC AAC GAA AAT GAG GAA ATG	936
Asn Lys Ile Glu Ser Lys Gln Asp Ile Ile Asn Glu Asn Glu Glu Met	
255 260 265 270	
GAT TTA GAG GGT GCT GAA ATC GTT GTT ATC GCT TAC GGT TCG GTT TCT	984
Asp Leu Glu Gly Ala Glu Ile Val Val Ile Ala Tyr Gly Ser Val Ser	
275 280 285	
TTG GCG GTT AAA GAG GCC TTG AAA GAT TAC CAT AAA GAA AGC AAG CAA	1032
Leu Ala Val Lys Glu Ala Leu Lys Asp Tyr His Lys Glu Ser Lys Gln	
290 295 300	
AAA GTC GGC TTT TTC AGG CCT AAA ACC TTA TGG CCA AGC CCG GCT AAA	1080
Lys Val Gly Phe Phe Arg Pro Lys Thr Leu Trp Pro Ser Pro Ala Lys	
305 310 315	
CGC TTG AAA GAA ATA GGG GAT AAA TAC GAA AAA ATC CTT GTG ATT GAA	1128
Arg Leu Lys Glu Ile Gly Asp Lys Tyr Glu Lys Ile Leu Val Ile Glu	
320 325 330	
TTG AAT AAA GGG CAG TAT TTA GAA GAA ATT GAA AGG GCT ATG CAA AGA	1176
Leu Asn Lys Gly Gln Tyr Leu Glu Glu Ile Glu Arg Ala Met Gln Arg	
335 340 345 350	
AAG GTG CAT TTC TTG GGG CAA GCC AAT GGG CGC ACG ATT TCG CCT AAA	1224
Lys Val His Phe Leu Gly Gln Ala Asn Gly Arg Thr Ile Ser Pro Lys	
355 360 365	
CAA ATC ATC GCA AAA TTG AAG GAG CTT TAAAATGGCG TTTAATTATG ATGAATA	1278
Gln Ile Ile Ala Lys Leu Lys Glu Leu	
370 375	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 127...1251

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

TGTGGCTGAC AGGAAGGATT TCAAATTCGC TAAAGTTTCT AAAGAAGCCC AAGAAAGAAG	60
CGAAAAGGTT AAGGCCAATA AATACATGCT CTTAGAAGAG ACTATTTT TAG AAGGGAGAGA	120
CAAATA ATG CGT GAG ATT ATT TCT GAT GGG AAT GAA TTA GTC GCT AAA	168
Met Arg Glu Ile Ile Ser Asp Gly Asn Glu Leu Val Ala Lys	
1 5 10	
GCG GCG ATT GAA GTG GGG TGT CGG TTT TTT GGG GGC TAT CCT ATC ACG	216
Ala Ala Ile Glu Val Gly Cys Arg Phe Phe Gly Gly Tyr Pro Ile Thr	
15 20 25 30	
CCA AGT TCG GAT ATT ATG CAT GCG ATG AGC GTG GCT TTA CCC AAA TGC	264
Pro Ser Ser Asp Ile Met His Ala Met Ser Val Ala Leu Pro Lys Cys	
35 40 45	
GGC GGT CAT TTT ATC CAA ATG GAA GAT GAA ATC AGC GGG ATT AGC GTG	312
Gly Gly His Phe Ile Gln Met Glu Asp Glu Ile Ser Gly Ile Ser Val	
50 55 60	
TCT TTA GGA GCG AGC ATG AGC GGG ACG AAG TCT ATG ACA GCA AGC TCT	360
Ser Leu Gly Ala Ser Met Ser Gly Thr Lys Ser Met Thr Ala Ser Ser	
65 70 75	
GGG CCT GGT ATT TCA TTG AAA GTG GAG CAA ATC GGT TAT TCT TTC ATG	408
Gly Pro Gly Ile Ser Leu Lys Val Glu Gln Ile Gly Tyr Ser Phe Met	
80 85 90	
GCG GAA ATC CCT TTA GTG ATC GCT GAT GTG ATG CGT TCA GGC CCA TCA	456
Ala Glu Ile Pro Leu Val Ile Ala Asp Val Met Arg Ser Gly Pro Ser	
95 100 105 110	
ACC GGA ATG CCC ACT CGT GTG GCT CAA GGC GAT GTG AAT TTC TTA AGA	504
Thr Gly Met Pro Thr Arg Val Ala Gln Gly Asp Val Asn Phe Leu Arg	
115 120 125	
CAC CCC ATA CAT GGG GAT TTT AAA GCC GTC GCG CTC GCT CCT GCG AAT	552
His Pro Ile His Gly Asp Phe Lys Ala Val Ala Leu Ala Pro Ala Asn	
130 135 140	
TTA GAA GAA GCT TAC ACC GAA ACC GTT CGC GCG TTC AAT TTG GCT GAA	600
Leu Glu Glu Ala Tyr Thr Glu Thr Val Arg Ala Phe Asn Leu Ala Glu	
145 150 155	

35	40	45	
GTA GCC TAC CCA GAG AGC TGT ATC GGT TGC GTG CAA TGC GAG TTG CAC	250		
Val Ala Tyr Pro Glu Ser Cys Ile Gly Cys Val Gln Cys Glu Leu His			
50 55 60 65			
TGC CCG GAT TTT GCG ATT TAT GTG GCT GAC AGG AAG GAT TTC AAA TTC	298		
Cys Pro Asp Phe Ala Ile Tyr Val Ala Asp Arg Lys Asp Phe Lys Phe			
70 75 80			
GCT AAA GTT TCT AAA GAA GCC CAA GAA AGA AGC GAA AAG GTT AAG GCC	346		
Ala Lys Val Ser Lys Glu Ala Gln Glu Arg Ser Glu Lys Val Lys Ala			
85 90 95			
AAT AAA TAC ATG CTC TTA GAA GAG ACT ATT TTA GAA GGG AGA GAC AAA T	395		
Asn Lys Tyr Met Leu Leu Glu Glu Thr Ile Leu Glu Gly Arg Asp Lys			
100 105 110			
AATGCGTGAG ATTATTTCTG ATGGGAATGA ATTAGTCGCT AAAGCGGCGA TTGAA	450		

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

Met	Ala	Lys	Met	Ser	Ala	Pro	Asp	Gly	Val	Ala	Val	Trp	Val	Asn	Glu
1				5					10					15	
Asp	Arg	Cys	Lys	Gly	Cys	Asp	Ile	Cys	Val	Ser	Val	Cys	Pro	Ala	Gly
			20					25					30		
Val	Leu	Gly	Met	Gly	Ile	Glu	Lys	Glu	Arg	Val	Leu	Gly	Lys	Val	Ala
			35				40					45			
Lys	Val	Ala	Tyr	Pro	Glu	Ser	Cys	Ile	Gly	Cys	Val	Gln	Cys	Glu	Leu
			50				55				60				
His	Cys	Pro	Asp	Phe	Ala	Ile	Tyr	Val	Ala	Asp	Arg	Lys	Asp	Phe	Lys
65					70					75				80	
Phe	Ala	Lys	Val	Ser	Lys	Glu	Ala	Gln	Glu	Arg	Ser	Glu	Lys	Val	Lys
				85					90				95		
Ala	Asn	Lys	Tyr	Met	Leu	Leu	Glu	Glu	Thr	Ile	Leu	Glu	Gly	Arg	Asp
			100				105						110		
Lys															

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

```

Met Arg Ser Cys Leu Phe Leu Lys Thr Asn Ser Val Leu Ser Ile Leu
 1           5           10           15
Met Gly Asp Lys Pro Ser Leu Lys Thr Thr Glu Gly Phe Ile Lys Val
          20           25           30
Ala Leu Ile Thr Glu Phe Phe Lys Ser Asp Gly Thr Asn Ser Leu Gly
          35           40           45
Val Lys Leu Ala Leu Ile Glu Ala Leu Ser Ile Leu Lys Leu Ala Asn
          50           55           60
Trp Ile Leu Ser Lys Ile His Val Phe Lys Phe Phe Cys Asp Trp Arg
65           70           75           80
Trp Lys Arg Gly Phe Lys Asn Ala Arg Leu Phe Ile Thr Glu Val Leu
          85           90           95
Ile Phe Asn Ser Met Val Phe Lys Ser Val Ser Pro Cys Lys
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 56...394
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

```

GGCAAATTTT GATTGCTAGG GCTTTAAATG CAGCTTTTAG CACAAAGGAG AATGA ATG      58
                                     Met
                                     1

GCT AAA ATG AGC GCT CCA GAT GGG GTT GCC GTT TGG GTG AAT GAA GAC      106
Ala Lys Met Ser Ala Pro Asp Gly Val Ala Val Trp Val Asn Glu Asp
          5           10           15

AGG TGT AAG GGT TGT GAT ATT TGC GTA TCG GTA TGC CCT GCT GGG GTT      154
Arg Cys Lys Gly Cys Asp Ile Cys Val Ser Val Cys Pro Ala Gly Val
          20           25           30

CTT GGC ATG GGG ATT GAA AAA GAA AGG GTG CTT GGA AAA GTG GCC AAA      202
Leu Gly Met Gly Ile Glu Lys Glu Arg Val Leu Gly Lys Val Ala Lys

```

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...375
- (D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

```

GAGCCAGTTA ATTCCATGGT TTCATAAGTG ATTTTGTGGG GCTGT ATG AGG AGC TGT      57
                                     Met Arg Ser Cys
                                     1

TTG TTT TTG AAA ACT AAT TCG GTT TTA TCC ATT TTA ATG GGC GAT AAG      105
Leu Phe Leu Lys Thr Asn Ser Val Leu Ser Ile Leu Met Gly Asp Lys
  5                      10                      15                      20

CCA TCA TTA AAA ACG ACT GAA GGC TTC ATC AAA GTG GCT TTA ATT ACA      153
Pro Ser Leu Lys Thr Thr Glu Gly Phe Ile Lys Val Ala Leu Ile Thr
                25                      30                      35

GAA TTT TTT AAA AGC GAT GGG ACA AAC TCG CTA GGA GTG AAA TTG GCT      201
Glu Phe Phe Lys Ser Asp Gly Thr Asn Ser Leu Gly Val Lys Leu Ala
                40                      45                      50

TTG ATT GAA GCG TTA TCA ATC TTA AAG CTA GCG AAT TGG ATC TTA TCA      249
Leu Ile Glu Ala Leu Ser Ile Leu Lys Leu Ala Asn Trp Ile Leu Ser
                55                      60                      65

AAA ATC CAT GTT TTT AAA TTT TTT TGC GAT TGG CGT TGG AAA AGA GGC      297
Lys Ile His Val Phe Lys Phe Phe Cys Asp Trp Arg Trp Lys Arg Gly
                70                      75                      80

TTT AAA AAC GCC AGG CTT TTC ATT ACA GAA GTG TTA ATT TTT AAT TCT      345
Phe Lys Asn Ala Arg Leu Phe Ile Thr Glu Val Leu Ile Phe Asn Ser
                85                      90                      95                      100

ATG GTT TTT AAA TCG GTT AGC CCT TGC AAA TAAATTGCAG CGCTGGGTTC GAT      398
Met Val Phe Lys Ser Val Ser Pro Cys Lys
                105                      110

TAAGGGCTTG ACAATCAAAT TAAACGCCAT TTTCCTAGCT TTGGGTGAAT AG      450

```

- (2) INFORMATION FOR SEQ ID NO:748:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid

```

CATCAGATAT TATCCAAGCG CCTTTTAAAA TCTTGCGCCG TATTTTCACA CCTATTGACA      60
TCATCGTGG ATG AAG TCA AAA AAA ACA TTG ATT CAA AAA GGA AGT AAA ATG      111
      Met Lys Ser Lys Lys Thr Leu Ile Gln Lys Gly Ser Lys Met
        1              5              10

ACG CTC AAT GAA GCC ATT AAA GAC AAA GTT TAT GAA ATC GTA GAA ATC      159
Thr Leu Asn Glu Ala Ile Lys Asp Lys Val Tyr Glu Ile Val Glu Ile
15              20              25              30

GCT AAC TGC GAT GAA GCC CTT AAA AAA CGC TTT CTC TCT TTT GGT ATC      207
Ala Asn Cys Asp Glu Ala Leu Lys Lys Arg Phe Leu Ser Phe Gly Ile
              35              40              45

CAT GAA GGG GTT CAA TGC ATT CTT TTG CAT TAT TCC ATG AAA AAA GCC      255
His Glu Gly Val Gln Cys Ile Leu Leu His Tyr Ser Met Lys Lys Ala
              50              55              60

ACG CTT TCG GTT AAA ATC AAC CGC ATT CAA GTG GCT TTA AGA TCC CAT      303
Thr Leu Ser Val Lys Ile Asn Arg Ile Gln Val Ala Leu Arg Ser His
              65              70              75

GAA GCA CAA TAC CTT GTC ATC AAA GAA AGC GTG TGAAAATGGG TTAAAAACGC      356
Glu Ala Gln Tyr Leu Val Ile Lys Glu Ser Val
              80              85

GCTAAACGCT ATAATAA      373

```

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

```

Met Lys Ser Lys Lys Thr Leu Ile Gln Lys Gly Ser Lys Met Thr Leu
 1              5              10              15
Asn Glu Ala Ile Lys Asp Lys Val Tyr Glu Ile Val Glu Ile Ala Asn
              20              25              30
Cys Asp Glu Ala Leu Lys Lys Arg Phe Leu Ser Phe Gly Ile His Glu
              35              40              45
Gly Val Gln Cys Ile Leu Leu His Tyr Ser Met Lys Lys Ala Thr Leu
              50              55              60
Ser Val Lys Ile Asn Arg Ile Gln Val Ala Leu Arg Ser His Glu Ala
              65              70              75              80
Gln Tyr Leu Val Ile Lys Glu Ser Val
              85

```

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

```

Met Lys Ile Leu Ala Leu Leu Ile Ala Ile Ile Gly His Glu Ile Met
 1           5           10           15
His Gly Leu Ser Ala Phe Leu Phe Gly Asp Arg Ser Thr Lys Asp Ala
          20           25           30
Arg Arg Leu Ser Leu Asn Pro Ile Arg His Leu Asp Met Met Gly Ser
          35           40           45
Val Leu Leu Pro Ala Leu Leu Leu Ile Phe Gln Ala Pro Phe Leu Phe
          50           55           60
Gly Trp Ala Lys Pro Val Pro Val Asp Met Arg Tyr Ile Val Ser Gln
65           70           75           80
Lys Gly Ser Leu Ala Cys Val Val Val Ser Leu Ala Gly Val Ala Tyr
          85           90           95
Asn Phe Thr Leu Ala Val Leu Leu Ala Phe Ile Thr His Trp Ser Phe
          100          105          110
Gln Gln Leu Gly Ile Asn Ala Leu Ser Ile Asp Glu Leu Asn Leu Tyr
          115          120          125
Gln Leu Ala Leu Val Thr Phe Leu Ile Gln Gly Ile Leu Tyr Asn Leu
          130          135          140
Val Leu Gly Val Phe Asn Ser Leu Pro Ile Pro Pro Leu Asp Gly Ser
145          150          155          160
Lys Ala Leu Gly Phe Leu Ala Leu His Phe Lys Ser Ala Phe Leu Leu
          165          170          175
Glu Trp Phe Ser Lys Met Glu Arg Tyr Gly Leu Leu Val Val Phe Ile
          180          185          190
Phe Leu Phe Ile Pro Pro Leu Ser Glu Phe Phe Ile His Ala Pro Thr
          195          200          205
Arg Phe Leu Phe Ser Leu Leu Leu Ser
210          215

```

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 70...336

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

AGC ACT AAA GAC GCT AGG CGT TTG AGT TTA AAC CCT ATC AGG CAT TTA	206
Ser Thr Lys Asp Ala Arg Arg Leu Ser Leu Asn Pro Ile Arg His Leu	
30 35 40	
GAC ATG ATG GGT TCG GTG CTT TTA CCG GCT TTA TTA CTC ATT TTT CAA	254
Asp Met Met Gly Ser Val Leu Leu Pro Ala Leu Leu Leu Ile Phe Gln	
45 50 55	
GCC CCT TTT TTG TTT GGG TGG GCC AAA CCC GTG CCT GTT GAT ATG CGC	302
Ala Pro Phe Leu Phe Gly Trp Ala Lys Pro Val Pro Val Asp Met Arg	
60 65 70 75	
TAC ATT GTC TCT CAA AAA GGC TCT CTA GCA TGC GTA GTG GTG AGT TTA	350
Tyr Ile Val Ser Gln Lys Gly Ser Leu Ala Cys Val Val Val Ser Leu	
80 85 90	
GCC GGG GTG GCT TAT AAT TTC ACT CTG GCC GTT CTG CTC GCT TTC ATC	398
Ala Gly Val Ala Tyr Asn Phe Thr Leu Ala Val Leu Leu Ala Phe Ile	
95 100 105	
ACG CAT TGG AGC TTC CAA CAA CTA GGG ATC AAC GCT TTA AGC ATT GAT	446
Thr His Trp Ser Phe Gln Gln Leu Gly Ile Asn Ala Leu Ser Ile Asp	
110 115 120	
GAA TTG AAT CTT TAT CAG CTC GCT TTA GTA ACC TTT CTC ATT CAA GGC	494
Glu Leu Asn Leu Tyr Gln Leu Ala Leu Val Thr Phe Leu Ile Gln Gly	
125 130 135	
ATT CTT TAT AAT CTT GTC TTA GGC GTT TTC AAT AGC CTC CCT ATC CCG	542
Ile Leu Tyr Asn Leu Val Leu Gly Val Phe Asn Ser Leu Pro Ile Pro	
140 145 150 155	
CCC TTA GAC GGC TCC AAA GCG TTA GGC TTT TTA GCG TTG CAT TTT AAA	590
Pro Leu Asp Gly Ser Lys Ala Leu Gly Phe Leu Ala Leu His Phe Lys	
160 165 170	
AGT GCG TTT TTA TTG GAA TGG TTT TCT AAA ATG GAA CGC TAC GGC TTG	638
Ser Ala Phe Leu Leu Glu Trp Phe Ser Lys Met Glu Arg Tyr Gly Leu	
175 180 185	
TTG GTA GTG TTT ATT TTT TTG TTT ATC CCC CCT TTA TCG GAG TTT TTT	686
Leu Val Val Phe Ile Phe Leu Phe Ile Pro Pro Leu Ser Glu Phe Phe	
190 195 200	
ATC CAT GCG CCC ACA AGA TTT TTA TTT TCT TTA CTC CTC TCT TAATCTTTT	737
Ile His Ala Pro Thr Arg Phe Leu Phe Ser Leu Leu Leu Ser	
205 210 215	
ATCAAGGAGA GTTTATGAAT AAGCTCTTAA AGTTTTCTCA A	778

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

```

Met Phe Thr Gln Trp Phe Ile Leu Thr Ile Ala Ile Val Phe Ile Leu
 1             5             10             15
Tyr Met Gly Val Arg Thr Phe Phe Phe Lys Thr Val Ala Lys Arg Gln
      20             25             30
Glu Arg Thr Asn Ala Ser Met Lys Leu Thr Leu Gln Glu Ala Glu Ile
      35             40             45
Leu Ile Gln Lys His Gln Leu Gln Leu Gln Arg Ala Leu Gly Asn Ile
      50             55             60
Asp Ile Leu Thr Gln Glu Met Ser Ser Leu Lys Thr Glu Leu Lys Ala
      65             70             75             80
Leu Lys Gln Arg Asn Ser Glu Tyr Lys Gly Glu Ser Asp Lys Tyr Lys
      85             90             95
Asn Arg Ile Lys Glu Leu Glu Gln Lys Ile Glu Ala Leu Leu
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 78...728
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

```

AAAAAAGAAA ACGCAACGCA TTAAGGTTTT TTGTGCAATT TTTTGATTTC TCTTTAGAAA      60
GTTTTATTAC CACCTTA ATG AAA ATC CTA GCC CTT TTA ATC GCT ATC ATA      110
          Met Lys Ile Leu Ala Leu Leu Ile Ala Ile Ile
              1             5             10

GGG CAT GAG ATC ATG CAT GGC TTG AGC GCG TTT TTA TTT GGG GAT AGG      158
Gly His Glu Ile Met His Gly Leu Ser Ala Phe Leu Phe Gly Asp Arg
      15             20             25

```

Leu Glu Leu Glu 165 170 175
 180

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...357
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

```

TTTCGCTAAA AAGGATATTT TAACAGA ATG TTT ACC CAA TGG TTT ATT CTC ACT      54
      Met Phe Thr Gln Trp Phe Ile Leu Thr
                1                      5

ATC GCT ATT GTT TTT ATC CTT TAT ATG GGT GTG CGC ACT TTC TTT TTT      102
Ile Ala Ile Val Phe Ile Leu Tyr Met Gly Val Arg Thr Phe Phe Phe
10                15                      20                      25

AAA ACC GTG GCT AAA CGG CAA GAA CGC ACC AAC GCA TCC ATG AAG CTC      150
Lys Thr Val Ala Lys Arg Gln Glu Arg Thr Asn Ala Ser Met Lys Leu
                30                35                      40

ACC TTA CAA GAA GCT GAA ATT TTG ATC CAA AAA CAC CAG TTG CAA CTC      198
Thr Leu Gln Glu Ala Glu Ile Leu Ile Gln Lys His Gln Leu Gln Leu
                45                50                      55

CAA AGG GCT TTG GGC AAT ATT GAT ATT CTC ACC CAA GAA ATG AGC TCG      246
Gln Arg Ala Leu Gly Asn Ile Asp Ile Leu Thr Gln Glu Met Ser Ser
                60                65                      70

TTA AAA ACA GAA CTA AAA GCC CTT AAA CAG CGC AAC TCT GAA TAC AAA      294
Leu Lys Thr Glu Leu Lys Ala Leu Lys Gln Arg Asn Ser Glu Tyr Lys
                75                80                85

GGC GAA TCG GAT AAA TAT AAA AAT CGT ATT AAA GAA TTG GAG CAA AAA      342
Gly Glu Ser Asp Lys Tyr Lys Asn Arg Ile Lys Glu Leu Glu Gln Lys
90                95                100                105

ATA GAA GCT CTC CTT TAAAAACGCT ATAATAA      374
Ile Glu Ala Leu Leu
                110

```

```

GCT TTT AGG GGA ATT AAG GGG GTA AGG GTG GTG TTG ATT GAT GAT TTA      444
Ala Phe Arg Gly Ile Lys Gly Val Arg Val Val Leu Ile Asp Asp Leu
      115                      120                      125

TTA GCC ACT GGA GGC ACA GCT TTA GCG AGC CTT GAG CTT ATC AAA GCC      492
Leu Ala Thr Gly Gly Thr Ala Leu Ala Ser Leu Glu Leu Ile Lys Ala
      130                      135                      140

CTA CAA GCC GAA TGC ATA GAA GCA TGC TTT TTG ATA GGG TTA AAA GAA      540
Leu Gln Ala Glu Cys Ile Glu Ala Cys Phe Leu Ile Gly Leu Lys Glu
      145                      150                      155                      160

TTA CCG GGT ATC CAA CTT TTA GAA GAA CGC GTG AAA ACC TTT TGT TTG      588
Leu Pro Gly Ile Gln Leu Leu Glu Glu Arg Val Lys Thr Phe Cys Leu
      165                      170                      175

TTA GAG TTA GAA TAAGGGTGA      609
Leu Glu Leu Glu
      180

```

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

```

Met Asn Glu Thr Leu Lys Glu Glu Leu Leu Gln Ser Ile Arg Glu Val
 1           5           10           15
Lys Asp Tyr Pro Lys Lys Gly Ile Leu Phe Lys Asp Ile Thr Thr Leu
      20           25           30
Leu Asn Tyr Pro Lys Leu Phe Asn Lys Leu Ile Asp Thr Leu Lys Lys
      35           40           45
Arg Tyr Leu Ala Leu Asn Ile Asp Phe Ile Val Gly Ile Glu Ala Arg
      50           55           60
Gly Phe Ile Leu Gly Ser Ala Leu Ala Tyr Ala Leu Gly Val Gly Phe
      65           70           75           80
Val Pro Val Arg Lys Lys Gly Lys Leu Pro Ala His Thr Leu Ser Gln
      85           90           95
Ser Tyr Ser Leu Glu Tyr Gly Ser Asp Ser Ile Glu Ile His Ser Asp
      100          105          110
Ala Phe Arg Gly Ile Lys Gly Val Arg Val Val Leu Ile Asp Asp Leu
      115          120          125
Leu Ala Thr Gly Gly Thr Ala Leu Ala Ser Leu Glu Leu Ile Lys Ala
      130          135          140
Leu Gln Ala Glu Cys Ile Glu Ala Cys Phe Leu Ile Gly Leu Lys Glu
      145          150          155          160
Leu Pro Gly Ile Gln Leu Leu Glu Glu Arg Val Lys Thr Phe Cys Leu

```

```

His Ala Leu Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu
      115                      120                      125
Leu Val Ser Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser
      130                      135                      140
Lys Lys Asn Arg
145

```

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 61...600
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

```

TAAAAACGCT ATAATAAATC AAAATTCTAC AACCAATCCG TTATATTAAA GGAAATCAAA      60
ATG AAT GAA ACG CTC AAA GAA GAA CTT TTA CAA AGC ATC AGA GAA GTG      108
Met Asn Glu Thr Leu Lys Glu Glu Leu Leu Gln Ser Ile Arg Glu Val
  1             5             10             15

AAA GAC TAC CCT AAA AAA GGG ATT TTA TTC AAA GAC ATT ACC ACG CTA      156
Lys Asp Tyr Pro Lys Lys Gly Ile Leu Phe Lys Asp Ile Thr Thr Leu
      20             25             30

CTC AAC TAC CCT AAA CTC TTT AAC AAA CTC ATT GAC ACG CTC AAA AAA      204
Leu Asn Tyr Pro Lys Leu Phe Asn Lys Leu Ile Asp Thr Leu Lys Lys
      35             40             45

CGC TAT CTC GCT CTC AAT ATA GAC TTT ATC GTG GGC ATT GAA GCG AGA      252
Arg Tyr Leu Ala Leu Asn Ile Asp Phe Ile Val Gly Ile Glu Ala Arg
      50             55             60

GGG TTT ATT TTA GGC TCT GCT CTC GCT TAT GCG CTT GGG GTG GGT TTT      300
Gly Phe Ile Leu Gly Ser Ala Leu Ala Tyr Ala Leu Gly Val Gly Phe
      65             70             75             80

GTG CCT GTG AGG AAA AAG GGC AAA CTC CCC GCA CAC ACC CTA TCT CAA      348
Val Pro Val Arg Lys Lys Gly Lys Leu Pro Ala His Thr Leu Ser Gln
      85             90             95

AGC TAC AGC CTA GAA TAC GGG AGC GAC AGC ATA GAA ATC CAC TCC GAC      396
Ser Tyr Ser Leu Glu Tyr Gly Ser Asp Ser Ile Glu Ile His Ser Asp
      100             105             110

```

	55	60	65	
CGC ACC ATC ATT CCC ATT AGC ATA GGT CTC ACG CGT TAT AGC GCT TTA				297
Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr Ser Ala Leu				
	70	75	80	
AAA TTC GCT ATC ATC AAT CTC ATT AGC GCG ATG GTG TGG GCG AGC ATT				345
Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp Ala Ser Ile				
	85	90	95	
ACC ATT ATT CTA GCG TGG TAT TTA GGA GAA GAG TTA TTG CAT GCG TTA				393
Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Leu Leu His Ala Leu				
	100	105	110	115
GGG TGG CTT AAA AAA CAC CCT TAT GCG CTA ATA TTA CTA TTA GTA TCT				441
Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu Leu Val Ser				
	120	125	130	
TTC TTG GCG TTA GTG CTG TGG TAT TTC CAA TAC TAT AGT AAG AAA AAC				489
Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser Lys Lys Asn				
	135	140	145	
CGC TAGAGTGCAA TACAATTCTT GAAAGATATG AAATTAAAAA AGGAGACTTT ATGTTA				548
Arg				
AAAAATCAAAT TA				560

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

Met His Leu Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val				
1	5	10	15	
Gly Asp Gln Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile				
	20	25	30	
Gln Lys Lys Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu				
	35	40	45	
Leu Leu Gln Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met				
	50	55	60	
Tyr Gly Met Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr				
	65	70	75	80
Ser Ala Leu Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp				
	85	90	95	
Ala Ser Ile Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Glu Leu Leu				
	100	105	110	

```

      355              360              365
Thr Gly Ala Cys Val Val Gly Leu Gly Glu Phe Thr Ser Ala Ile Met
      370              375              380
Gly His Asn Glu Glu Leu Lys Asn Leu Phe Glu Thr Ser Gly Leu Glu
385              390              395              400
Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe Asn Arg His Leu Lys Lys
      405              410              415
Leu Ile Glu Ser Lys Ile Ala Asp Val Cys Asn Ile Ser Ser Ser Arg
      420              425              430
Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile Arg
      435              440              445
Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro Ala
      450              455              460
Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly Ala
465              470              475              480
Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys Ala
      485              490              495

```

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...492
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

```

GGCGAAATCG GGTTAATTTT AGCAGGGATT GCCAGCTATA CCGGTCAT ATG CAT TTA      57
                                   Met His Leu
                                   1

GGG TTA GCC ATT TTA GTC GCA GGG ATT GGG GGC TTT GTG GGG GAT CAG      105
Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val Gly Asp Gln
      5              10              15

ATC TAT TTT TAC ATC GGC CGC ACC AAT AAA GCT TAC ATC CAA AAA AAG      153
Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile Gln Lys Lys
      20              25              30              35

CTA GAA AAA CAA CGC CGA AAA CTA GCC CTA GCC CAT TTA TTG TTG CAA      201
Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu Leu Leu Gln
      40              45              50

AAA CAC GGC TGG TTT ATC ATT TTT ATC CAA CGC TAT ATG TAT GGC ATG      249
Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met Tyr Gly Met

```


(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

```

Met Leu Lys Ile Lys Leu Glu Lys Thr Thr Phe Glu Asn Ala Lys Ala
 1           5           10           15
Glu Cys Ser Leu Val Phe Ile Ile Asn Lys Asp Phe Ser His Ala Trp
          20           25           30
Val Lys Asn Lys Glu Leu Leu Glu Thr Phe Lys Tyr Glu Gly Glu Gly
          35           40           45
Val Phe Leu Asp Gln Glu Asn Lys Ile Leu Tyr Ala Gly Val Lys Glu
          50           55           60
Asp Asp Val His Leu Leu Arg Glu Ser Ala Cys Leu Ala Val Arg Thr
          65           70           75           80
Leu Lys Lys Leu Ala Phe Lys Ser Val Lys Val Gly Val Tyr Thr Cys
          85           90           95
Gly Ala His Ser Lys Asp Asn Ala Leu Leu Glu Asn Leu Lys Ala Leu
          100          105          110
Phe Leu Gly Leu Lys Leu Gly Leu Tyr Glu Tyr Asp Thr Phe Lys Ser
          115          120          125
Asn Lys Lys Glu Ser Val Leu Lys Glu Ala Ile Val Ala Leu Glu Leu
          130          135          140
His Lys Pro Cys Glu Lys Thr Cys Ala Asn Ser Leu Glu Lys Ser Ala
          145          150          155          160
Lys Glu Ala Leu Lys Tyr Ala Glu Ile Met Thr Glu Ser Leu Asn Ile
          165          170          175
Val Lys Asp Leu Val Asn Thr Pro Pro Met Ile Gly Thr Pro Val Tyr
          180          185          190
Met Ala Glu Val Ala Gln Lys Val Ala Lys Glu Asn His Leu Glu Ile
          195          200          205
His Val His Asp Glu Lys Phe Leu Glu Glu Lys Lys Met Asn Ala Phe
          210          215          220
Leu Ala Val Asn Lys Ala Ser Leu Ser Val Asn Pro Pro Arg Leu Ile
          225          230          235          240
His Leu Val Tyr Lys Pro Lys Lys Ala Lys Lys Lys Ile Ala Leu Val
          245          250          255
Gly Lys Gly Leu Thr Tyr Asp Cys Gly Gly Leu Ser Leu Lys Pro Ala
          260          265          270
Asp Tyr Met Val Thr Met Lys Ala Asp Lys Gly Gly Gly Ser Ala Val
          275          280          285
Ile Gly Leu Leu Asn Ala Leu Ala Lys Leu Gly Val Glu Ala Glu Val
          290          295          300
His Gly Ile Ile Gly Ala Thr Glu Asn Met Ile Gly Pro Ala Ala Tyr
          305          310          315          320
Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu Gly Lys Ser Ile Glu Val
          325          330          335
Arg Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Cys Leu Ser
          340          345          350
Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile Val Asp Phe Ala Thr Leu

```

GTG CAT GGC ATT ATT GGG GCT ACA GAA AAC ATG ATA GGC CCA GCC GCT	1020
Val His Gly Ile Ile Gly Ala Thr Glu Asn Met Ile Gly Pro Ala Ala	
305 310 315	
TAT AAA CCA GAT GAT ATT TTG ATC TCC AAA GAA GGC AAG AGC ATA GAG	1068
Tyr Lys Pro Asp Asp Ile Leu Ile Ser Lys Glu Gly Lys Ser Ile Glu	
320 325 330 335	
GTC CGT AAT ACC GAC GCT GAG GGG CGT TTG GTT TTA GCG GAT TGT TTG	1116
Val Arg Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala Asp Cys Leu	
340 345 350	
AGC TAC GCT CAA GAT TTA AAC CCT GAT GTG ATC GTG GAT TTT GCG ACC	1164
Ser Tyr Ala Gln Asp Leu Asn Pro Asp Val Ile Val Asp Phe Ala Thr	
355 360 365	
CTT ACT GGG GCA TGC GTT GTA GGC TTA GGC GAA TTC ACT TCA GCG ATC	1212
Leu Thr Gly Ala Cys Val Val Gly Leu Gly Glu Phe Thr Ser Ala Ile	
370 375 380	
ATG GGG CAT AAT GAA GAG TTA AAA AAC CTC TTT GAA ACT TCA GGG TTA	1260
Met Gly His Asn Glu Glu Leu Lys Asn Leu Phe Glu Thr Ser Gly Leu	
385 390 395	
GAA TCC GGC GAA TTA TTA GCC AAA CTC CCC TTT AAC CGC CAT TTA AAG	1308
Glu Ser Gly Glu Leu Leu Ala Lys Leu Pro Phe Asn Arg His Leu Lys	
400 405 410 415	
AAA TTG ATT GAA TCT AAA ATC GCT GAT GTG TGC AAT ATT TCT TCT TCA	1356
Lys Leu Ile Glu Ser Lys Ile Ala Asp Val Cys Asn Ile Ser Ser Ser	
420 425 430	
CGC TAT GGC GGT GCG ATC ACA GCG GGC TTG TTT TTA AAT GAA TTT ATT	1404
Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile	
435 440 445	
AGA GAT GAG TTT AAG GAT AAG TGG CTA CAC ATT GAC ATT GCA GGC CCT	1452
Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro	
450 455 460	
GCT TAT GTG GAA AAA GAA TGG GAT GTG AAT AGC TTT GGA GCG AGT GGG	1500
Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly	
465 470 475	
GCT GGC GTG AGA GCT TGC ACA GCT TTT GTG GAA GAG CTT TTG AAA AAG	1548
Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys	
480 485 490 495	
GCT TGAAATGGGC TTGTCTGTAG GCATTGTGGG TTTGCCTAAT GTGGGCAAAT CCAGCA	1607
Ala	
CCTTTA	1613

(2) INFORMATION FOR SEQ ID NO:736:

Thr	Leu	Lys	Lys	Leu	Ala	Phe	Lys	Ser	Val	Lys	Val	Gly	Val	Tyr	Thr	
80					85					90					95	
TGT	GGT	GCA	CAT	TCT	AAA	GAT	AAC	GCG	CTT	TTA	GAA	AAC	TTG	AAA	GCG	396
Cys	Gly	Ala	His	Ser	Lys	Asp	Asn	Ala	Leu	Leu	Glu	Asn	Leu	Lys	Ala	
				100					105					110		
CTG	TTT	TTG	GGC	TTG	AAA	TTA	GGT	TTG	TAT	GAA	TAC	GAC	ACT	TTT	AAA	444
Leu	Phe	Leu	Gly	Leu	Lys	Leu	Gly	Leu	Tyr	Glu	Tyr	Asp	Thr	Phe	Lys	
			115					120					125			
TCC	AAC	AAA	AAA	GAA	AGC	GTT	TTA	AAA	GAA	GCC	ATT	GTC	GCT	TTA	GAA	492
Ser	Asn	Lys	Lys	Glu	Ser	Val	Leu	Lys	Glu	Ala	Ile	Val	Ala	Leu	Glu	
		130					135					140				
TTG	CAC	AAA	CCT	TGC	GAA	AAA	ACT	TGC	GCA	AAT	TCT	TTA	GAA	AAG	AGT	540
Leu	His	Lys	Pro	Cys	Glu	Lys	Thr	Cys	Ala	Asn	Ser	Leu	Glu	Lys	Ser	
	145					150					155					
GCT	AAA	GAA	GCG	TTA	AAA	TAC	GCT	GAA	ATC	ATG	ACA	GAA	AGC	TTG	AAT	588
Ala	Lys	Glu	Ala	Leu	Lys	Tyr	Ala	Glu	Ile	Met	Thr	Glu	Ser	Leu	Asn	
160					165				170						175	
ATC	GTT	AAA	GAT	CTA	GTC	AAT	ACC	CCC	CCT	ATG	ATT	GGC	ACT	CCG	GTT	636
Ile	Val	Lys	Asp	Leu	Val	Asn	Thr	Pro	Pro	Met	Ile	Gly	Thr	Pro	Val	
				180					185					190		
TAT	ATG	GCT	GAA	GTG	GCG	CAA	AAA	GTG	GCT	AAA	GAA	AAC	CAT	TTA	GAA	684
Tyr	Met	Ala	Glu	Val	Ala	Gln	Lys	Val	Ala	Lys	Glu	Asn	His	Leu	Glu	
			195					200					205			
ATC	CAT	GTT	CAT	GAT	GAA	AAA	TTT	TTA	GAA	GAA	AAG	AAA	ATG	AAC	GCC	732
Ile	His	Val	His	Asp	Glu	Lys	Phe	Leu	Glu	Glu	Lys	Lys	Met	Asn	Ala	
		210					215					220				
TTT	TTA	GCG	GTC	AAT	AAA	GCC	TCT	CTT	AGC	GTC	AAT	CCT	CCT	CGC	TTG	780
Phe	Leu	Ala	Val	Asn	Lys	Ala	Ser	Leu	Ser	Val	Asn	Pro	Pro	Arg	Leu	
	225					230					235					
ATC	CAT	TTA	GTC	TAT	AAG	CCT	AAA	AAA	GCG	AAG	AAA	AAA	ATC	GCT	TTA	828
Ile	His	Leu	Val	Tyr	Lys	Pro	Lys	Lys	Ala	Lys	Lys	Lys	Ile	Ala	Leu	
240					245				250						255	
GTG	GGT	AAG	GGC	TTG	ACT	TAT	GAT	TGT	GGG	GGT	TTG	AGC	TTG	AAA	CCG	876
Val	Gly	Lys	Gly	Leu	Thr	Tyr	Asp	Cys	Gly	Gly	Leu	Ser	Leu	Lys	Pro	
				260					265					270		
GCC	GAT	TAC	ATG	GTT	ACT	ATG	AAA	GCG	GAT	AAA	GGC	GGT	GGC	TCT	GCG	924
Ala	Asp	Tyr	Met	Val	Thr	Met	Lys	Ala	Asp	Lys	Gly	Gly	Gly	Ser	Ala	
			275					280					285			
GTG	ATT	GGG	CTT	TTA	AAC	GCA	TTA	GCC	AAA	CTA	GGC	GTG	GAG	GCT	GAA	972
Val	Ile	Gly	Leu	Leu	Asn	Ala	Leu	Ala	Lys	Leu	Gly	Val	Glu	Ala	Glu	
		290					295					300				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

```

Met Pro Gly Ile Lys Val Arg Glu Gly Asp Ala Phe Asp Glu Ala Tyr
 1             5             10             15
Arg Arg Phe Lys Lys Gln Thr Asp Arg Asn Leu Val Val Thr Glu Cys
      20             25             30
Arg Ala Arg Arg Phe Phe Glu Ser Lys Thr Glu Lys Arg Lys Lys Gln
      35             40             45
Lys Ile Ser Ala Lys Lys Lys Val Leu Lys Arg Leu Tyr Met Leu Arg
 50             55             60
Arg Tyr Glu Ser Arg Leu
65             70

```

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 64...1551
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

```

TAAGAAAAAC CGCTAGAGTG CAATACAATT CTTGAAAGAT ATGAAATTAA AAAAGGAGAC      60
TTT ATG TTA AAA ATC AAA TTA GAA AAA ACC ACT TTT GAA AAC GCA AAA      108
    Met Leu Lys Ile Lys Leu Glu Lys Thr Thr Phe Glu Asn Ala Lys
      1             5             10             15

GCT GAA TGC AGT TTA GTT TTT ATT ATC AAT AAG GAT TTT AGC CAC GCT      156
Ala Glu Cys Ser Leu Val Phe Ile Ile Asn Lys Asp Phe Ser His Ala
      20             25             30

TGG GTC AAA AAT AAA GAG TTG CTA GAA ACC TTT AAA TAC GAA GGC GAA      204
Trp Val Lys Asn Lys Glu Leu Leu Glu Thr Phe Lys Tyr Glu Gly Glu
      35             40             45

GGC GTA TTT TTA GAC CAA GAA AAT AAA ATC CTG TAT GCG GGC GTT AAA      252
Gly Val Phe Leu Asp Gln Glu Asn Lys Ile Leu Tyr Ala Gly Val Lys
      50             55             60

GAA GAT GAT GTG CAT TTA TTG AGA GAG AGC GCG TGT TTA GCC GTT CGC      300
Glu Asp Asp Val His Leu Leu Arg Glu Ser Ala Cys Leu Ala Val Arg
      65             70             75

ACC CTT AAA AAA CTC GCT TTT AAA AGC GTT AAA GTG GGC GTT TAT ACT      348

```

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 103...312
- (D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

```

GAAAATTCTT GACACCCAGT TAATTCGTCT TATATAATAC TATTCATTT GTAGCCATTG      60
TTAAGCAATG ATTTTAAGCT ATGGAAAAGA GGTGATAGCA GT ATG CCA GGG ATT      114
                                     Met Pro Gly Ile
                                     1

AAG GTT AGA GAA GGC GAT GCG TTT GAT GAA GCT TAT AGG AGA TTC AAA      162
Lys Val Arg Glu Gly Asp Ala Phe Asp Glu Ala Tyr Arg Arg Phe Lys
  5                10                15                20

AAG CAA ACC GAT CGC AAT TTA GTG GTA ACA GAA TGC CGT GCT AGA AGG      210
Lys Gln Thr Asp Arg Asn Leu Val Val Thr Glu Cys Arg Ala Arg Arg
                25                30                35

TTC TTT GAG TCT AAG ACT GAA AAA CGC AAA AAA CAA AAA ATC AGC GCT      258
Phe Phe Glu Ser Lys Thr Glu Lys Arg Lys Lys Gln Lys Ile Ser Ala
                40                45                50

AAA AAG AAG GTT TTG AAG CGT CTT TAT ATG TTA AGG CGT TAT GAG TCA      306
Lys Lys Lys Val Leu Lys Arg Leu Tyr Met Leu Arg Arg Tyr Glu Ser
                55                60                65

AGA CTA TAATAGACTT TAAGAAAAAT TTAAAAATTA AGGATTATTG AATAATGCAA TT      364
Arg Leu
  70

CACAGGGGAA      373

```

- (2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

210

215

220

GTA GGN TTC TTT TGAGTGATCA CTCTAGTTAC ATCACTGGAG AGACTCTCAA AGTCA 789
 Val Xaa Phe Phe
 225

ATGGCGGGCT TTATA

804

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

Met Gln Phe Thr Gly Lys Asn Val Leu Ile Thr Gly Ala Ser Lys Gly
 1 5 10 15
 Ile Gly Ala Glu Ile Ala Lys Thr Leu Ala Ser Met Gly Leu Lys Val
 20 25 30
 Trp Ile Asn Tyr Arg Ser Asn Ala Glu Val Ala Asp Ala Leu Lys Asn
 35 40 45
 Glu Leu Glu Glu Lys Gly Tyr Lys Ala Ala Val Ile Lys Phe Asp Ala
 50 55 60
 Ala Ser Glu Ser Asp Phe Ile Glu Ala Ile Gln Thr Ile Val Gln Ser
 65 70 75 80
 Asp Gly Gly Leu Ser Tyr Leu Val Asn Asn Ala Gly Val Val Arg Asp
 85 90 95
 Lys Leu Ala Ile Lys Met Lys Thr Glu Asp Phe His His Val Ile Asp
 100 105 110
 Asn Asn Leu Thr Ser Ala Phe Ile Gly Cys Arg Glu Ala Leu Lys Val
 115 120 125
 Met Ser Lys Ser Arg Phe Gly Ser Val Val Asn Val Ala Ser Ile Ile
 130 135 140
 Gly Glu Arg Gly Asn Met Gly Gln Thr Asn Tyr Ser Ala Ser Lys Gly
 145 150 155 160
 Gly Met Ile Ala Met Ser Lys Ser Phe Ala Tyr Glu Gly Ala Leu Arg
 165 170 175
 Asn Ile Arg Phe Asn Ser Val Thr Pro Gly Phe Ile Glu Thr Asp Met
 180 185 190
 Asn Ala Asn Leu Lys Asp Glu Leu Lys Ala Asp Tyr Val Lys Asn Ile
 195 200 205
 Pro Leu Asn Arg Leu Gly Ser Ala Lys Glu Val Ala Glu Ala Val Xaa
 210 215 220
 Phe Phe
 225

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

AAGGCGTTAT GAGTCAAGAC TATAATAGAC TTTAAGAAAA ATTTAAAAAT TAAGGATTAT	60
TGAATA ATG CAA TTC ACA GGG AAA AAT GTT CTC ATT ACT GGG GCT TCT	108
Met Gln Phe Thr Gly Lys Asn Val Leu Ile Thr Gly Ala Ser	
1 5 10	
AAA GGC ATT GGG GCT GAA ATC GCC AAA ACT CTC GCT TCT ATG GGG CTG	156
Lys Gly Ile Gly Ala Glu Ile Ala Lys Thr Leu Ala Ser Met Gly Leu	
15 20 25 30	
AAA GTT TGG ATC AAT TAC CGC AGT AAT GCT GAA GTG GCT GAC GCT TTG	204
Lys Val Trp Ile Asn Tyr Arg Ser Asn Ala Glu Val Ala Asp Ala Leu	
35 40 45	
AAA AAT GAG CTT GAA GAA AAA GGC TAT AAG GCA GCT GTC ATT AAA TTT	252
Lys Asn Glu Leu Glu Glu Lys Gly Tyr Lys Ala Ala Val Ile Lys Phe	
50 55 60	
GAT GCG GCT TCT GAA AGC GAT TTT ATT GAA GCG ATA CAA ACC ATC GTC	300
Asp Ala Ala Ser Glu Ser Asp Phe Ile Glu Ala Ile Gln Thr Ile Val	
65 70 75	
CAA AGC GAT GGG GGG TTG TCT TAC TTG GTG AAT AAC GCC GGT GTG GTG	348
Gln Ser Asp Gly Gly Leu Ser Tyr Leu Val Asn Asn Ala Gly Val Val	
80 85 90	
CGC GAT AAA TTA GCG ATC AAA ATG AAA ACA GAA GAC TTT CAC CAT GTC	396
Arg Asp Lys Leu Ala Ile Lys Met Lys Thr Glu Asp Phe His His Val	
95 100 105 110	
ATA GAC AAT AAC CTC ACT TCA GCC TTT ATA GGT TGC CGA GAG GCT TTA	444
Ile Asp Asn Asn Leu Thr Ser Ala Phe Ile Gly Cys Arg Glu Ala Leu	
115 120 125	
AAG GTG ATG AGC AAG AGT CGT TTT GGG AGC GTG GTC AAT GTC GCT TCT	492
Lys Val Met Ser Lys Ser Arg Phe Gly Ser Val Val Asn Val Ala Ser	
130 135 140	
ATC ATT GGT GAA AGA GGC AAT ATG GGG CAG ACA AAC TAC TCA GCG AGT	540
Ile Ile Gly Glu Arg Gly Asn Met Gly Gln Thr Asn Tyr Ser Ala Ser	
145 150 155	
AAG GGG GGA ATG ATT GCA ATG AGC AAG TCC TTT GCT TAT GAG GGA GCT	588
Lys Gly Gly Met Ile Ala Met Ser Lys Ser Phe Ala Tyr Glu Gly Ala	
160 165 170	
TTA AGG AAT ATT CGT TTC AAC TCT GTA ACG CCC GGT TTT ATA GAA ACC	636
Leu Arg Asn Ile Arg Phe Asn Ser Val Thr Pro Gly Phe Ile Glu Thr	
175 180 185 190	
GAC ATG AAC GCC AAT TTG AAA GAC GAA CTC AAA GCG GAT TAT GTT AAA	684
Asp Met Asn Ala Asn Leu Lys Asp Glu Leu Lys Ala Asp Tyr Val Lys	
195 200 205	
AAC ATT CCT TTA AAC AGG CTA GGG TCT GCT AAG GAA GTG GCA GAA GCG	732
Asn Ile Pro Leu Asn Arg Leu Gly Ser Ala Lys Glu Val Ala Glu Ala	

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

Met	Ala	Val	Tyr	Leu	Asp	Phe	Glu	Asn	His	Ile	Lys	Glu	Ile	Gln	Asn
1				5					10					15	
Glu	Ile	Glu	Leu	Ala	Leu	Ile	Arg	Gly	Asp	Glu	Asp	Ala	Lys	Glu	Ile
			20					25					30		
Leu	Glu	Lys	Arg	Leu	Asp	Lys	Glu	Val	Lys	Ser	Ile	Tyr	Ser	Asn	Leu
		35					40					45			
Thr	Asp	Phe	Gln	Lys	Leu	Gln	Leu	Ala	Arg	His	Pro	Asp	Arg	Pro	Tyr
	50					55					60				
Ala	Met	Asp	Tyr	Ile	Asp	Leu	Ile	Leu	Lys	Asp	Lys	Tyr	Glu	Val	Phe
65					70					75					80
Gly	Asp	Arg	His	Tyr	Asn	Asp	Asp	Lys	Ala	Ile	Val	Cys	Phe	Val	Gly
			85						90					95	
Lys	Ile	Asp	Asn	Val	Pro	Val	Val	Val	Ile	Gly	Glu	Glu	Lys	Gly	Arg
			100					105					110		
Gly	Thr	Lys	Asn	Lys	Leu	Leu	Arg	Asn	Phe	Gly	Met	Pro	Asn	Pro	Cys
		115					120					125			
Gly	Tyr	Arg	Lys	Ala	Leu	Lys	Met	Ala	Lys	Phe	Ala	Glu	Lys	Phe	Asn
	130					135					140				
Leu	Pro	Ile	Leu	Met	Leu	Val	Asp	Thr	Ala	Gly	Ala	Tyr	Pro	Gly	Ile
145					150					155					160
Gly	Ala	Glu	Glu	Arg	Gly	Gln	Ser	Glu	Ala	Ile	Ala	Lys	Asn	Leu	Gln
				165					170					175	
Glu	Phe	Ala	Ser	Leu	Lys	Val	Pro	Thr	Ile	Ser	Val	Ile	Ile	Gly	Glu
			180					185					190		
Gly	Gly	Ser	Gly	Gly	Ala	Leu	Arg	Leu	Gln	Trp	Leu	Thr	Asn	Trp	Leu
		195					200						205		

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 67...744
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

35										40					45					
CTC	ACT	GAT	TTT	CAA	AAA	CTC	CAA	TTA	GCA	AGA	CAC	CCT	GAC	AGA	CCC	253				
Leu	Thr	Asp	Phe	Gln	Lys	Leu	Gln	Leu	Ala	Arg	His	Pro	Asp	Arg	Pro					
50					55					60										
TAC	GCT	ATG	GAT	TAC	ATT	GAT	CTC	ATC	TTA	AAA	GAT	AAA	TAT	GAA	GTC	301				
Tyr	Ala	Met	Asp	Tyr	Ile	Asp	Leu	Ile	Leu	Lys	Asp	Lys	Tyr	Glu	Val					
65					70					75										
TTT	GGG	GAT	AGG	CAT	TAT	AAC	GAT	GAT	AAA	GCG	ATC	GTG	TGC	TTT	GTA	349				
Phe	Gly	Asp	Arg	His	Tyr	Asn	Asp	Asp	Lys	Ala	Ile	Val	Cys	Phe	Val					
80					85					90					95					
GGG	AAA	ATT	GAT	AAT	GTC	CCA	GTT	GTG	GTG	ATC	GGA	GAA	GAA	AAG	GGC	397				
Gly	Lys	Ile	Asp	Asn	Val	Pro	Val	Val	Val	Ile	Gly	Glu	Glu	Lys	Gly					
100					105					110										
AGA	GGG	ACT	AAA	AAC	AAA	CTC	TTA	AGA	AAT	TTT	GGC	ATG	CCT	AAC	CCT	445				
Arg	Gly	Thr	Lys	Asn	Lys	Leu	Leu	Arg	Asn	Phe	Gly	Met	Pro	Asn	Pro					
115					120					125										
TGT	GGC	TAT	CGT	AAG	GCT	TTG	AAA	ATG	GCA	AAG	TTT	GCT	GAA	AAG	TTT	493				
Cys	Gly	Tyr	Arg	Lys	Ala	Leu	Lys	Met	Ala	Lys	Phe	Ala	Glu	Lys	Phe					
130					135					140										
AAT	TTG	CCT	ATT	TTA	ATG	CTT	GTG	GAT	ACA	GCC	GGG	GCG	TAT	CCG	GGG	541				
Asn	Leu	Pro	Ile	Leu	Met	Leu	Val	Asp	Thr	Ala	Gly	Ala	Tyr	Pro	Gly					
145					150					155										
ATT	GGT	GCA	GAA	GAA	AGG	GGG	CAA	AGT	GAA	GCG	ATC	GCT	AAA	AAT	CTC	589				
Ile	Gly	Ala	Glu	Glu	Arg	Gly	Gln	Ser	Glu	Ala	Ile	Ala	Lys	Asn	Leu					
160					165					170					175					
CAA	GAG	TTC	GCC	TCT	TTA	AAA	GTC	CCT	ACT	ATT	TCT	GTA	ATT	ATC	GGT	637				
Gln	Glu	Phe	Ala	Ser	Leu	Lys	Val	Pro	Thr	Ile	Ser	Val	Ile	Ile	Gly					
180					185					190										
GAG	GGG	GGC	AGT	GGT	GGT	GCG	CTA	CGA	TTG	CAG	TGG	CTG	ACA	AAT	TGG	685				
Glu	Gly	Gly	Ser	Gly	Gly	Ala	Leu	Arg	Leu	Gln	Trp	Leu	Thr	Asn	Trp					
195					200					205										
CTA TGATGGAATA TTCCATTTTT AGCGTTATAT CCCCAGAAGG TTGTGCGGCG ATTCTT																744				
Leu																				
TGGGATGACC CTAGCAAGAC TGAAGTGGCT ATTAAAGCGA TGAAAATCAC GCCTAGAGAC																804				
TTAAAGGAGG CGGGGCTTAT TGATGATATT ATCTTAGAGC CTAGCAAAGG GGCTCATAGA																864				
GACAAATTTT CAG																877				

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

```

        690                695                700
Pro Asp Gly Val Ile Ile Pro Leu Ala Asn Ala Gln Ala Ala Gly Met
705                710                715                720
Leu Gly Glu Ala Gly Val Asp Gly Tyr Val Asn Asn His Phe Met Lys
        725                730                735
Arg Ile Gly Phe Ala Val Ile Ala Ser Val Val Asn Ser Phe Leu Gln
        740                745                750
Thr Ala Pro Ile Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly Lys Gly
        755                760                765
Arg Ser Glu Arg Thr Pro Glu Phe Asn Tyr Ala Leu Gly Gln Ala Ile
        770                775                780
Asn Gly Ser Met Gln Ser Ser Ala Gln Met Ser Asn Gln Ile Leu Gly
785                790                795                800
Gln Leu Met Asn Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly Asp Ser
        805                810                815
Ile Lys Ile Leu Thr Met Asp Asp Ile Asp Phe Ser Gly Val Tyr Asp
        820                825                830
Val Lys Ile Thr Asn Lys Ser Val Val Asp Glu Ile Ile Lys Gln Ser
        835                840                845
Thr Lys Thr Leu Ser Arg Glu His Glu Glu Ile Thr Thr Ser Pro Lys
        850                855                860
Gly Gly Asn
865

```

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 65...688
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

```

TTTGGTGGCA CTAATGGTGT TGTGATTTTC AAAAAAGCCT AGTTTTACAA AGTTAGGATT      60
TTGA ATG GCC GTT TAT TTA GAT TTT GAA AAT CAT ATT AAA GAG ATT CAA      109
    Met Ala Val Tyr Leu Asp Phe Glu Asn His Ile Lys Glu Ile Gln
        1                5                10                15

AAT GAA ATT GAA TTA GCC CTT ATT AGA GGC GAT GAG GAC GCT AAA GAA      157
Asn Glu Ile Glu Leu Ala Leu Ile Arg Gly Asp Glu Asp Ala Lys Glu
        20                25                30

ATC TTA GAA AAA AGA TTG GAT AAG GAG GTT AAA AGC ATT TAT TCC AAT      205
Ile Leu Glu Lys Arg Leu Asp Lys Glu Val Lys Ser Ile Tyr Ser Asn

```

Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu Lys Leu
 260 265 270
 Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu Val Lys Lys Ser
 275 280 285
 Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu
 290 295 300
 Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Phe Leu
 305 310 315 320
 Ala Lys Glu Leu Gln Lys Asp Lys Ala Ile Lys Asp Cys Leu Lys
 325 330 335
 Asn Ala Asp Pro Asn Asp Arg Ala Ala Ile Met Lys Cys Leu Asp Gly
 340 345 350
 Leu Ser Asp Glu Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg Glu Lys
 355 360 365
 Ala Val Ala Asp Cys Leu Ala Met Ala Lys Thr Asp Glu Glu Lys Arg
 370 375 380
 Lys Cys Gln Asn Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln Asn Lys
 385 390 395 400
 Arg Thr Gln Asn Lys Gln Asn Gln Leu Ser Lys Thr Glu Arg Leu His
 405 410 415
 Gln Ala Ser Glu Cys Leu Asp Asn Leu Asp Asp Pro Thr Asp Gln Glu
 420 425 430
 Ala Ile Glu Gln Cys Leu Glu Gly Leu Ser Asp Ser Glu Arg Ala Leu
 435 440 445
 Ile Leu Gly Ile Lys Arg Gln Ala Asp Glu Val Asp Leu Ile Tyr Ser
 450 455 460
 Asp Leu Arg Asn Arg Lys Thr Phe Asp Asn Met Ala Ala Lys Gly Tyr
 465 470 475 480
 Pro Leu Leu Pro Met Asp Phe Lys Asn Gly Gly Asp Ile Ala Thr Ile
 485 490 495
 Asn Ala Thr Asn Val Asp Ala Asp Lys Ile Ala Ser Asp Asn Pro Ile
 500 505 510
 Tyr Ala Ser Ile Glu Pro Asp Ile Ala Lys Gln Tyr Glu Thr Glu Lys
 515 520 525
 Thr Ile Lys Asp Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala Leu Gly
 530 535 540
 Gly Asn Lys Lys Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser Thr Ala
 545 550 555 560
 Glu Ala Lys Ala Glu Asn Asn Lys Ile Asp Lys Asp Val Ala Glu Thr
 565 570 575
 Ala Lys Asn Ile Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu Lys Ser
 580 585 590
 Gly Glu Phe Val Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys Lys Lys
 595 600 605
 Ala Glu Lys Gln Asp Glu Thr Ser Pro Val Lys Gln Ala Phe Ile Gly
 610 615 620
 Lys Ser Asp Pro Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile Glu Ile
 625 630 635 640
 Thr Leu Thr Ser Lys Val Asp Ala Thr Leu Thr Gly Ile Val Ser Gly
 645 650 655
 Val Val Ala Lys Asp Val Trp Asn Met Asn Gly Thr Met Ile Leu Leu
 660 665 670
 Asp Lys Gly Thr Lys Val Tyr Gly Asn Tyr Gln Ser Val Lys Gly Gly
 675 680 685
 Thr Pro Ile Met Thr Arg Leu Met Ile Val Phe Thr Lys Ala Ile Thr

ACC AAA ACT TTG TCT AGA GAA CAT GAA GAA ATC ACC ACA AGC CCC AAA 2592
 Thr Lys Thr Leu Ser Arg Glu His Glu Glu Ile Thr Thr Ser Pro Lys
 850 855 860

GGT GGC AAT TAATTCAAGA GAAAGGATAA AATATATTCA TGTTACTAAA CTCGGTTCT 2650
 Gly Gly Asn
 865

TTACAAAATA AAAGACAAAA CCAACAACAG GCTCT 2685

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 867 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

Leu	Asp	Cys	Val	Ser	Gln	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Lys	Glu	Cys
1				5					10					15	
Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Ala	Lys
			20					25					30		
Glu	Ser	Val	Lys	Ala	Tyr	Lys	Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu
		35					40					45			
Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys
	50					55				60					
Leu	Leu	Glu	Gln	Gln	Val	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Glu
65					70					75					80
Ala	Asp	Lys	Lys	Arg	Cys	Val	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Lys
				85					90					95	
Lys	Val	Leu	Ala	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser
			100					105					110		
Arg	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr
		115				120					125				
Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Leu	Lys	Ala
	130					135					140				
Tyr	Lys	Asp	Cys	Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala
145					150					155					160
Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu
			165						170					175	
Val	Lys	Lys	Ser	Ile	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg
			180					185					190		
Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala
		195				200						205			
Arg	Lys	Phe	Leu	Ala	Lys	Gln	Val	Leu	Asn	Cys	Leu	Glu	Lys	Ala	Gly
	210					215					220				
Asn	Glu	Glu	Glu	Arg	Lys	Ala	Cys	Leu	Lys	Asn	Leu	Pro	Lys	Asp	Leu
225					230					235					240
Gln	Glu	Asn	Ile	Leu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys
				245					250					255	

AAG AGT GAT CCC ACA TTT GTT TTA GCG CAA TAC ACC CCC ATT GAA ATC	1920
Lys Ser Asp Pro Thr Phe Val Leu Ala Gln Tyr Thr Pro Ile Glu Ile	
625 630 635 640	
ACT CTG ACT TCT AAA GTA GAT GCC ACT CTC ACA GGT ATA GTG AGT GGG	1968
Thr Leu Thr Ser Lys Val Asp Ala Thr Leu Thr Gly Ile Val Ser Gly	
645 650 655	
GTT GTA GCC AAA GAT GTA TGG AAC ATG AAC GGC ACT ATG ATC TTA TTA	2016
Val Val Ala Lys Asp Val Trp Asn Met Asn Gly Thr Met Ile Leu Leu	
660 665 670	
GAC AAA GGC ACT AAG GTG TAT GGG AAT TAT CAA AGC GTG AAA GGT GGC	2064
Asp Lys Gly Thr Lys Val Tyr Gly Asn Tyr Gln Ser Val Lys Gly Gly	
675 680 685	
ACA CCC ATT ATG ACA CGC TTA ATG ATA GTC TTT ACT AAA GCC ATT ACG	2112
Thr Pro Ile Met Thr Arg Leu Met Ile Val Phe Thr Lys Ala Ile Thr	
690 695 700	
CCT GAT GGT GTG ATA ATA CCT CTA GCA AAC GCT CAA GCA GCA GGC ATG	2160
Pro Asp Gly Val Ile Ile Pro Leu Ala Asn Ala Gln Ala Ala Gly Met	
705 710 715 720	
TTG GGT GAA GCA GGG GTA GAT GGC TAT GTG AAT AAT CAC TTT ATG AAG	2208
Leu Gly Glu Ala Gly Val Asp Gly Tyr Val Asn Asn His Phe Met Lys	
725 730 735	
CGC ATA GGC TTT GCT GTG ATA GCA AGC GTG GTT AAT AGC TTC TTG CAA	2256
Arg Ile Gly Phe Ala Val Ile Ala Ser Val Val Asn Ser Phe Leu Gln	
740 745 750	
ACT GCG CCT ATC ATA GCT CTA GAT AAA CTC ATA GGC CTT GGC AAA GGT	2304
Thr Ala Pro Ile Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly Lys Gly	
755 760 765	
AGA AGT GAA AGG ACA CCT GAA TTT AAT TAC GCT TTG GGT CAA GCT ATC	2352
Arg Ser Glu Arg Thr Pro Glu Phe Asn Tyr Ala Leu Gly Gln Ala Ile	
770 775 780	
AAT GGT AGC ATG CAA AGT TCA GCT CAG ATG TCT AAT CAA ATT CTA GGG	2400
Asn Gly Ser Met Gln Ser Ser Ala Gln Met Ser Asn Gln Ile Leu Gly	
785 790 795 800	
CAA CTG ATG AAT ATC CCC CCA AGT TTT TAC AAA AAC GAG GGC GAT AGT	2448
Gln Leu Met Asn Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly Asp Ser	
805 810 815	
ATT AAG ATT CTC ACA ATG GAC GAT ATT GAT TTT AGC GGT GTG TAT GAT	2496
Ile Lys Ile Leu Thr Met Asp Asp Ile Asp Phe Ser Gly Val Tyr Asp	
820 825 830	
GTT AAA ATT ACT AAC AAA TCT GTG GTA GAT GAA ATT ATC AAA CAA AGC	2544
Val Lys Ile Thr Asn Lys Ser Val Val Asp Glu Ile Ile Lys Gln Ser	
835 840 845	

AGG ACA CAA AAC AAA CAA AAT CAA TTG AGT AAA ACA GAA AGG TTG CAT	1248
Arg Thr Gln Asn Lys Gln Asn Gln Leu Ser Lys Thr Glu Arg Leu His	
405 410 415	
CAA GCA AGC GAG TGC TTG GAT AAC TTA GAT GAC CCT ACT GAT CAA GAG	1296
Gln Ala Ser Glu Cys Leu Asp Asn Leu Asp Asp Pro Thr Asp Gln Glu	
420 425 430	
GCC ATA GAG CAA TGT TTA GAG GGC TTG AGC GAT AGT GAA AGG GCG CTA	1344
Ala Ile Glu Gln Cys Leu Glu Gly Leu Ser Asp Ser Glu Arg Ala Leu	
435 440 445	
ATT CTA GGA ATT AAA CGA CAA GCT GAT GAA GTG GAT CTG ATT TAT AGC	1392
Ile Leu Gly Ile Lys Arg Gln Ala Asp Glu Val Asp Leu Ile Tyr Ser	
450 455 460	
GAT CTA AGA AAC CGT AAA ACC TTT GAT AAC ATG GCG GCT AAA GGT TAT	1440
Asp Leu Arg Asn Arg Lys Thr Phe Asp Asn Met Ala Ala Lys Gly Tyr	
465 470 475 480	
CCA TTG TTA CCA ATG GAT TTC AAA AAT GGC GGC GAT ATT GCC ACT ATT	1488
Pro Leu Leu Pro Met Asp Phe Lys Asn Gly Gly Asp Ile Ala Thr Ile	
485 490 495	
AAC GCC ACT AAT GTT GAT GCG GAC AAA ATA GCT AGC GAT AAT CCT ATT	1536
Asn Ala Thr Asn Val Asp Ala Asp Lys Ile Ala Ser Asp Asn Pro Ile	
500 505 510	
TAT GCT TCC ATA GAG CCT GAT ATT GCC AAG CAA TAC GAA ACA GAA AAA	1584
Tyr Ala Ser Ile Glu Pro Asp Ile Ala Lys Gln Tyr Glu Thr Glu Lys	
515 520 525	
ACC ATT AAG GAT AAG AAT TTA GAA GCT AAA TTA GCT AAG GCT TTA GGT	1632
Thr Ile Lys Asp Lys Asn Leu Glu Ala Lys Leu Ala Lys Ala Leu Gly	
530 535 540	
GGC AAT AAA AAA GAT GAC GAT AAA GAA AAA AGT AAA AAA TCC ACA GCA	1680
Gly Asn Lys Lys Asp Asp Asp Lys Glu Lys Ser Lys Lys Ser Thr Ala	
545 550 555 560	
GAA GCT AAA GCA GAA AAC AAT AAG ATA GAC AAA GAT GTC GCA GAA ACT	1728
Glu Ala Lys Ala Glu Asn Asn Lys Ile Asp Lys Asp Val Ala Glu Thr	
565 570 575	
GCC AAG AAT ATC AGT GAA ATC GCT CTT AAG AAC AAA AAA GAA AAG AGT	1776
Ala Lys Asn Ile Ser Glu Ile Ala Leu Lys Asn Lys Lys Glu Lys Ser	
580 585 590	
GGG GAA TTT GTA GAT GAA AAT GGT AAT CCC ATT GAT GAC AAA AAG AAA	1824
Gly Glu Phe Val Asp Glu Asn Gly Asn Pro Ile Asp Asp Lys Lys Lys	
595 600 605	
GCA GAA AAA CAA GAT GAA ACA AGC CCT GTC AAA CAG GCC TTT ATA GGC	1872
Ala Glu Lys Gln Asp Glu Thr Ser Pro Val Lys Gln Ala Phe Ile Gly	
610 615 620	

GTT AAG AAA AGC ATT AAG GCT TAT TTG GAC TGC GTA TCA AGA GCT AGG	576
Val Lys Lys Ser Ile Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg	
180 185 190	
AAT GAA AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT GAA GCG	624
Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala	
195 200 205	
AGA AAA TTT TTA GCG AAG CAA GTG CTA AAT TGT TTG GAA AAA GCT GGA	672
Arg Lys Phe Leu Ala Lys Gln Val Leu Asn Cys Leu Glu Lys Ala Gly	
210 215 220	
AAT GAA GAA GAA AGA AAA GCA TGT CTT AAA AAT CTC CCT AAA GAC TTA	720
Asn Glu Glu Glu Arg Lys Ala Cys Leu Lys Asn Leu Pro Lys Asp Leu	
225 230 235 240	
CAG GAA AAT ATT TTA GCT AAA GAG AGT CTT AAA GCT TAT AAA GAC TGC	768
Gln Glu Asn Ile Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys Asp Cys	
245 250 255	
CTC TCT CAA GCT AGA AAT GAA GAA GAA AGG AGA GCT TGC GAG AAA CTA	816
Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu Lys Leu	
260 265 270	
CTC ACG CCT GAA GCG AGA AAA CTC TTA GAG CAA GAA GTT AAG AAA AGC	864
Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu Val Lys Lys Ser	
275 280 285	
GTT AAG GCT TAT TTG GAC TGC GTA TCA AGA GCT AGG AAT GAA AAA GAG	912
Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu Lys Glu	
290 295 300	
AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT GAA GCG AGA AAA TTT TTA	960
Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Phe Leu	
305 310 315 320	
GCG AAA GAA CTC CAA CAA AAA GAT AAA GCG ATC AAA GAT TGC TTG AAA	1008
Ala Lys Glu Leu Gln Gln Lys Asp Lys Ala Ile Lys Asp Cys Leu Lys	
325 330 335	
AAC GCC GAT CCT AAC GAC AGA GCG GCT ATC ATG AAG TGT TTG GAT GGT	1056
Asn Ala Asp Pro Asn Asp Arg Ala Ala Ile Met Lys Cys Leu Asp Gly	
340 345 350	
TTG AGC GAT GAA GAG AAG CTC AAA TAC CTG CAA GAA GCT AGA GAA AAG	1104
Leu Ser Asp Glu Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg Glu Lys	
355 360 365	
GCT GTT GCG GAT TGT TTG GCT ATG GCT AAA ACC GAT GAA GAA AAA AGG	1152
Ala Val Ala Asp Cys Leu Ala Met Ala Lys Thr Asp Glu Glu Lys Arg	
370 375 380	
AAA TGC CAA AAC CTT TAT AGC GAT TTG ATC CAA GAA ATC CAA AAT AAA	1200
Lys Cys Gln Asn Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln Asn Lys	
385 390 395 400	

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2601

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

TTG GAT TGC GTA TCT CAA GCC AAA ACT GAA GCT GAG AAA AAA GAA TGC	48
Leu Asp Cys Val Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys Glu Cys	
1 5 10 15	
GAG AAA TTA CTC ACC CCT GAA GCG AGA AAA CTC TTA GAA GAA GCT AAA	96
Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu Ala Lys	
20 25 30	
GAG AGC GTT AAA GCT TAT AAA GAC TGC GTA TCA AAA GCT AGG AAT GAA	144
Glu Ser Val Lys Ala Tyr Lys Asp Cys Val Ser Lys Ala Arg Asn Glu	
35 40 45	
AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT GAA GCG AAA AAA	192
Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Lys Lys	
50 55 60	
CTT TTA GAG CAA CAA GTG CTA GAT TGT TTG AAA AAC GCT AAA ACC GAA	240
Leu Leu Glu Gln Gln Val Leu Asp Cys Leu Lys Asn Ala Lys Thr Glu	
65 70 75 80	
GCT GAT AAA AAA AGG TGT GTC AAA GAT CTC CCT AAA GAC TTG CAG AAA	288
Ala Asp Lys Lys Arg Cys Val Lys Asp Leu Pro Lys Asp Leu Gln Lys	
85 90 95	
AAG GTT TTA GCT AAA GAG AGC GTT AAG GCT TAT TTG GAC TGC GTA TCA	336
Lys Val Leu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys Val Ser	
100 105 110	
AGA GCT AGG AAT GAA AAA GAG AAA AAA GAA TGC GAG AAA TTG CTC ACC	384
Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr	
115 120 125	
CCT GAA GCG AAA AAA CTT TTA GAA GAA GCC AAA GAG AGT CTT AAA GCT	432
Pro Glu Ala Lys Lys Leu Leu Glu Glu Ala Lys Glu Ser Leu Lys Ala	
130 135 140	
TAT AAA GAC TGC CTC TCT CAA GCT AGA AAT GAA GAA GAA AGG AGA GCT	480
Tyr Lys Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala	
145 150 155 160	
TGC GAG AAA CTA CTC ACG CCT GAA GCG AGA AAA CTC TTA GAG CAA GAA	528
Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu	
165 170 175	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

```

Met Phe Lys Asp Phe Tyr Arg Thr Thr Leu Ser Phe Leu Lys Pro Leu
 1           5           10           15
Leu Leu Leu Leu Val Leu Leu Leu Pro Phe Ser Leu Cys Ile Ala Asp
      20           25           30
Glu Tyr Ile Ser Ile Ser Asp Asp Trp Asp Glu Ile Val Arg Asn His
      35           40           45
Lys Thr Tyr Tyr Phe Glu Asn Gly Leu Asp His Phe Asn Gln Gly Gln
      50           55           60
Tyr Gln Gln Ala Phe Lys Asp Phe Arg Leu Ala Gln Glu Tyr Ser Ile
      65           70           75           80
Gly Leu Gly Ser Val Tyr Leu Ala Lys Met Tyr Leu Glu Gly Lys Gly
      85           90           95
Val Lys Val Asp Tyr Lys Lys Ala Gln Phe Tyr Ala Glu Asn Ala Ile
      100          105          110
Lys Gly Tyr Gly Ser Gly Leu Leu Gly Gly Ala Leu Ile Leu Gly Arg
      115          120          125
Met Gln Ala Glu Gly Leu Gly Met Lys Lys Asp Leu Lys Gln Ala Leu
      130          135          140
Lys Thr Tyr Arg His Val Val Arg Met Phe Ser Asn Lys Ser Thr Asn
      145          150          155          160
Phe Ala Asn Asn Phe Arg Leu Pro Asn Leu Ala Glu Phe Thr Ser Met
      165          170          175
Leu Ile Gly Ser Arg Phe Ile Asp Leu Ser Gly Leu Ser Ala Asn Pro
      180          185          190
Ile Lys Phe Gly Lys Lys Phe Gly Ile Leu Val Lys Lys Ser Thr Gln
      195          200          205
Ile Lys Asp Lys Thr Leu Leu Trp Glu Asp Ile Ala Glu Ile Ser Ser
      210          215          220
Asn Ile Thr Leu Leu Lys Gln Gln Met Gly Glu Ile Leu Tyr Arg Ile
      225          230          235          240
Gly Ile Ala Tyr Lys Glu Gly Leu Gly Thr Arg Lys Lys Lys Asp Arg
      245          250          255
Ala Lys Lys Phe Leu Gln Lys Ser Ala Glu Phe Gly Tyr Glu Lys Ala
      260          265          270
Met Glu Ala Leu
      275

```

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

70	75	80	
GTT TAT TTA GCC AAA ATG TAT TTG GAG GGA AAG GGC GTG AAA GTG GAT			342
Val Tyr Leu Ala Lys Met Tyr Leu Glu Gly Lys Gly Val Lys Val Asp			
85	90	95	100
TAC AAA AAA GCA CAA TTT TAT GCA GAA AAC GCT ATC AAA GGG TAT GGG			390
Tyr Lys Lys Ala Gln Phe Tyr Ala Glu Asn Ala Ile Lys Gly Tyr Gly			
	105	110	115
AGC GGA TTG TTA GGG GGT GCT CTT ATT TTA GGA CGC ATG CAA GCA GAA			438
Ser Gly Leu Leu Gly Gly Ala Leu Ile Leu Gly Arg Met Gln Ala Glu			
	120	125	130
GGC TTA GGG ATG AAA AAG GAT TTG AAA CAA GCG CTC AAG ACT TAT AGG			486
Gly Leu Gly Met Lys Lys Asp Leu Lys Gln Ala Leu Lys Thr Tyr Arg			
	135	140	145
CAT GTG GTT CGC ATG TTT TCT AAT AAA AGC ACA AAT TTT GCT AAC AAT			534
His Val Val Arg Met Phe Ser Asn Lys Ser Thr Asn Phe Ala Asn Asn			
	150	155	160
TTT AGA TTA CCA AAC CTT GCG GAA TTT ACT AGT ATG CTT ATT GGA TCG			582
Phe Arg Leu Pro Asn Leu Ala Glu Phe Thr Ser Met Leu Ile Gly Ser			
	165	170	180
CGA TTC ATT GAT CTT TCA GGT TTG AGC GCG AAT CCT ATA AAA TTT GGA			630
Arg Phe Ile Asp Leu Ser Gly Leu Ser Ala Asn Pro Ile Lys Phe Gly			
	185	190	195
AAG AAA TTT GGA ATA CTT GTT AAG AAA TCC ACT CAA ATC AAA GAT AAG			678
Lys Lys Phe Gly Ile Leu Val Lys Lys Ser Thr Gln Ile Lys Asp Lys			
	200	205	210
ACA CTT CTT TGG GAA GAT ATT GCT GAA ATT TCA AGC AAT ATT ACT TTA			726
Thr Leu Leu Trp Glu Asp Ile Ala Glu Ile Ser Ser Asn Ile Thr Leu			
	215	220	225
CTC AAA CAA CAA ATG GGG GAG ATC CTT TAT AGG ATT GGG ATC GCT TAT			774
Leu Lys Gln Gln Met Gly Glu Ile Leu Tyr Arg Ile Gly Ile Ala Tyr			
	230	235	240
AAA GAA GGG CTT GGC ACT AGA AAG AAA AAG GAC AGG GCT AAA AAA TTC			822
Lys Glu Gly Leu Gly Thr Arg Lys Lys Lys Asp Arg Ala Lys Lys Phe			
	245	250	255
CTG CAA AAA TCC GCA GAA TTT GGC TAT GAA AAA GCC ATG GAA GCT CTG T			871
Leu Gln Lys Ser Ala Glu Phe Gly Tyr Glu Lys Ala Met Glu Ala Leu			
	265	270	275
AGTTTTTTTAA TCAAACCTTGT ATCAAGCTTG ACTGAATGGG TTAGAAAAAT CCGCTTAGAT			931
TATCCTAATT AAAACAAAGC CCTATTTTTC TTATTTTTC ATTATAATAG ACACTTGAT			990

(2) INFORMATION FOR SEQ ID NO:726:

```

Met Lys Phe Asn Ala Phe Lys Glu Tyr Lys Lys Arg Val Phe Ala Lys
225                               230                               235                               240
Asn Glu Lys Lys Asn Ile Ala Phe Ser Ser Ile Asn Val Ile Pro Tyr
                               245                               250                               255
Pro Asn Ser Gln Asn Lys Arg Leu Phe Tyr Val Val Phe Asp Gln Asp
                               260                               265                               270
Tyr Lys Ala Tyr Gln His Asn Lys Leu Ser Tyr Ser Ser Asn Ser Gln
                               275                               280                               285
Lys Glu Leu Tyr Ile Glu Ile Glu Asn Asn Gln Val Ser Ile Ile Met
                               290                               295                               300
Glu Lys
305

```

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 43...870
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

```

AAAACAAGCT AAAGAATGGC TCAAATTGTA AAAGGATCTG AC ATG TTT AAA GAT      54
                               Met Phe Lys Asp
                               1

TTT TAT CGC ACC ACC CTC TCT TTT TTA AAG CCT TTA TTG CTT TTA CTA      102
Phe Tyr Arg Thr Thr Leu Ser Phe Leu Lys Pro Leu Leu Leu Leu Leu
5                               10                               15                               20

GTT TTA TTA TTG CCG TTT TCA CTT TGT ATA GCT GAT GAA TAT ATT AGC      150
Val Leu Leu Leu Pro Phe Ser Leu Cys Ile Ala Asp Glu Tyr Ile Ser
                               25                               30                               35

ATA AGT GAT GAT TGG GAT GAA ATT GTG CGA AAT CAT AAG ACA TAT TAT      198
Ile Ser Asp Asp Trp Asp Glu Ile Val Arg Asn His Lys Thr Tyr Tyr
                               40                               45                               50

TTT GAA AAT GGT TTA GAC CAT TTT AAT CAA GGC CAA TAC CAG CAA GCC      246
Phe Glu Asn Gly Leu Asp His Phe Asn Gln Gly Gln Tyr Gln Gln Ala
55                               60                               65

TTT AAA GAT TTT AGA TTG GCG CAA GAA TAC AGC ATC GGG CTT GGC AGT      294
Phe Lys Asp Phe Arg Leu Ala Gln Glu Tyr Ser Ile Gly Leu Gly Ser

```

```

TCT CAG AAC AAA CGC TTG TTT TAT GTG GTG TTT GAC CAA GAT TAT AAA      872
Ser Gln Asn Lys Arg Leu Phe Tyr Val Val Phe Asp Gln Asp Tyr Lys
    260                      265                      270

GCC TAC CAG CAT AAC AAG CTC TCT TAT AGC TCC AAT TCT CAA AAA GAA      920
Ala Tyr Gln His Asn Lys Leu Ser Tyr Ser Ser Asn Ser Gln Lys Glu
    275                      280                      285                      290

CTC TAT ATA GAG ATT GAA AAC AAT CAA GTG TCT ATT ATA ATG GAA AAA T      969
Leu Tyr Ile Glu Ile Glu Asn Asn Gln Val Ser Ile Ile Met Glu Lys
    295                      300                      305

AAGAAAAATA GGGCTTTGTT TTAATTAGGA TAATCTAAGC GGATTTTTTCT AA      1021

```

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

```

Met Arg Leu Tyr Gln Lys Gln Gly Leu Glu Met Val Gly Gln Lys Leu
 1              5              10              15
Asp Ser Tyr Leu Ala Asp Lys Ser Phe Trp Ala Glu Glu Leu Gln Asn
    20              25              30
Lys Asp Thr Asp Phe Gly Tyr Tyr Gln Asn Lys Gln Phe Leu Phe Val
    35              40              45
Ala Asn Lys Ser Lys Pro Ser Leu Glu Phe Tyr Glu Ile Glu Asn Asn
    50              55              60
Met Leu Lys Lys Ile Asn Ser Ser Lys Ala Leu Val Gly Ser Lys Lys
    65              70              75              80
Gly Asp Lys Thr Leu Glu Gly Asp Leu Ala Thr Pro Ile Gly Val Tyr
    85              90              95
Arg Ile Thr Gln Lys Leu Glu Arg Leu Asp Gln Tyr Tyr Gly Val Leu
    100             105             110
Ala Phe Val Thr Asn Tyr Pro Asn Leu Tyr Asp Thr Leu Lys Lys Arg
    115             120             125
Thr Gly His Gly Ile Trp Val His Gly Met Pro Leu Asn Gly Asp Arg
    130             135             140
Asn Glu Leu Asn Thr Lys Gly Cys Ile Ala Ile Glu Asn Pro Leu Leu
    145             150             155             160
Ser Ser Tyr Asp Lys Val Leu Lys Gly Glu Lys Ala Phe Leu Ile Thr
    165             170             175
Tyr Glu Asp Lys Phe Phe Pro Ser Thr Lys Glu Glu Leu Ser Met Ile
    180             185             190
Leu Ser Ser Leu Phe Gln Trp Lys Glu Ala Trp Ala Arg Gly Asp Phe
    195             200             205
Glu Arg Tyr Met Arg Phe Tyr Asn Pro Asn Phe Thr Arg Tyr Asp Gly
    210             215             220

```

Thr 35	Asp	Phe	Gly	Tyr	Tyr 40	Gln	Asn	Lys	Gln	Phe 45	Leu	Phe	Val	Ala	Asn 50		
AAA	TCC	AAG	CCC	AGT	TTG	GAG	TTT	TAT	GAG	ATA	GAA	AAT	AAC	ATG	CTT	248	
Lys	Ser	Lys	Pro	Ser 55	Leu	Glu	Phe	Tyr	Glu 60	Ile	Glu	Asn	Asn	Met	Leu		
AAA	AAA	ATC	AAC	AGC	TCT	AAA	GCT	CTT	GTA	GGC	TCT	AAA	AAG	GGC	GAT	296	
Lys	Lys	Ile	Asn 70	Ser	Ser	Lys	Ala	Leu 75	Val	Gly	Ser	Lys	Lys	Gly	Asp		
AAG	ACT	TTA	GAG	GGC	GAT	TTG	GCC	ACG	CCT	ATT	GGA	GTG	TAT	CGT	ATC	344	
Lys	Thr	Leu	Glu	Gly	Asp	Leu	Ala	Thr 90	Pro	Ile	Gly	Val	Tyr	Arg	Ile		
ACG	CAG	AAA	TTA	GAG	CGC	TTG	GAT	CAA	TAT	TAT	GGC	GTT	TTG	GCT	TTT	392	
Thr	Gln	Lys	Leu	Glu	Arg	Leu	Asp	Gln 105	Tyr	Tyr	Gly	Val	Leu	Ala	Phe		
GTA	ACG	AAT	TAC	CCT	AAT	TTG	TAT	GAT	ACC	TTG	AAA	AAA	CGC	ACC	GGG	440	
Val	Thr	Asn	Tyr	Pro	Asn 120	Leu	Tyr	Asp	Thr	Leu 125	Lys	Lys	Arg	Thr	Gly		
CAT	GGC	ATT	TGG	GTG	CAT	GGA	ATG	CCT	TTA	AAT	GGC	GAT	CGG	AAT	GAA	488	
His	Gly	Ile	Trp	Val 135	His	Gly	Met	Pro	Leu 140	Asn	Gly	Asp	Arg	Asn	Glu		
TTG	AAC	ACC	AAG	GGC	TGT	ATT	GCG	ATT	GAA	AAC	CCG	CTT	TTA	AGC	TCT	536	
Leu	Asn	Thr	Lys 150	Gly	Cys	Ile	Ala	Ile 155	Glu	Asn	Pro	Leu	Leu	Ser	Ser		
TAT	GAC	AAA	GTG	TTA	AAA	GGC	GAA	AAA	GCG	TTC	CTC	ATC	ACC	TAT	GAA	584	
Tyr	Asp	Lys	Val	Leu	Lys	Gly	Glu	Lys 170	Ala	Phe	Leu	Ile	Thr	Tyr	Glu		
GAC	AAG	TTT	TTC	CCA	AGC	ACC	AAA	GAA	GAA	TTG	AGC	ATG	ATT	TTA	AGC	632	
Asp	Lys	Phe	Phe	Pro	Ser	Thr	Lys	Glu 185	Glu	Glu	Leu	Ser	Met	Ile	Leu	Ser	
TCC	CTT	TTT	CAA	TGG	AAA	GAA	GCC	TGG	GCT	AGG	GGC	GAT	TTT	GAA	CGC	680	
Ser	Leu	Phe	Gln	Trp	Lys 200	Glu	Ala	Trp	Ala	Arg	Gly	Asp	Phe	Glu	Arg		
TAC	ATG	CGT	TTT	TAT	AAC	CCC	AAT	TTC	ACT	CGC	TAT	GAC	GGC	ATG	AAA	728	
Tyr	Met	Arg	Phe	Tyr 215	Asn	Pro	Asn	Phe	Thr 220	Arg	Tyr	Asp	Gly	Met	Lys		
TTT	AAC	GCT	TTT	AAA	GAG	TAT	AAA	AAA	AGG	GTG	TTT	GCA	AAA	AAC	GAA	776	
Phe	Asn	Ala	Phe 230	Lys	Glu	Tyr	Lys	Lys 235	Arg	Val	Phe	Ala	Lys	Asn	Glu		
AAA	AAG	AAT	ATC	GCT	TTT	TCC	TCT	ATC	AAT	GTG	ATC	CCT	TAC	CCC	AAC	824	
Lys	Lys	Asn	Ile 245	Ala	Phe	Ser	Ser	Ile 250	Asn	Val	Ile	Pro	Tyr	Pro	Asn		

AATGCGAACA ATTATGGGAT GATATTATAA AAATTGGTGG GAATGATAAG AT

376

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

Met	His	Ala	Val	Lys	Ser	Ala	Lys	Ser	Arg	Ser	Val	Ile	Met	Glu	Ala
1				5				10					15		
Asp	Ala	Thr	Thr	Leu	Leu	Gly	Phe	Phe	Glu	Glu	Asn	Gln	Asn	Asn	Gln
			20				25					30			
Phe	Val	Ile	Pro	Ile	Tyr	Gln	Arg	Leu	Tyr	Ser	Trp	Lys	Lys	Glu	
		35				40					45				

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...968
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

TATTAATGGG	GTTTGTGGGA	TTGAATGCTA	GTGATCGTTT	GTTAGAAATC	ATG CGC	56
					Met Arg	
					1	
CTT TAT CAA AAA CAA GGC TTG GAA ATG GTG GGT CAA AAG TTG GAT TCT						104
Leu Tyr Gln Lys Gln Gly Leu Glu Met Val Gly Gln Lys Leu Asp Ser						
	5		10		15	
TAT TTA GCG GAT AAA TCT TTT TGG GCA GAA GAA CTT CAA AAC AAG GAC						152
Tyr Leu Ala Asp Lys Ser Phe Trp Ala Glu Glu Leu Gln Asn Lys Asp						
	20		25		30	
ACG GAT TTT GGC TAT TAT CAA AAC AAG CAG TTT TTA TTT GTG GCT AAT						200

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```

Met Phe Lys Gly Ile Tyr Pro Met Arg Asn Phe Pro Ile His His Asn
 1             5             10             15
Gly Phe Lys His Glu Val Leu Ala His Met Leu Lys Arg His Lys Glu
             20             25             30
Pro Phe Ile Leu Ser Tyr Asn Asp Cys Glu Phe Val Arg Asn Ala Tyr
             35             40             45
Lys Asp Phe Lys Ile Leu Glu Pro Ser Trp Gln Tyr Thr Met Gly Gln
             50             55             60
Gly Glu Ile Arg Met Gly Lys Asn Arg Leu Glu Arg Gly Asp Asn Asn
65             70             75             80
His Val Lys Gln Ser His Glu Leu Leu Ile Ile Lys Glu
             85             90

```

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 183...323
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

```

ATCCACAAAT TCCACTTCAT TTTCTTTGCA AAATTCAAAA AATTCTTTGA TCTTGCTTTC      60
ACTATTTTGA GTTCTTACTA TCATTAACCA CCTTTAATTG TTATGAATTG AGTTTGATTG      120
ATAGGGGTGA TTATAGCATT TATGGGGCAA AAAAAGTAGA ATCTGTATCA AGTTTTATTA      180
AG ATG CAT GCG GTA AAA TCC GCT AAA TCA AGG AGT GTT ATT ATG GAA      227
  Met His Ala Val Lys Ser Ala Lys Ser Arg Ser Val Ile Met Glu
    1             5             10             15

GCA GAC GCA ACC ACA CTA TTA GGA TTT TTT GAA GAA AAT CAA AAC AAT      275
Ala Asp Ala Thr Thr Leu Leu Gly Phe Phe Glu Glu Asn Gln Asn Asn
             20             25             30

CAA TTT GTC ATT CCT ATC TAT CAG AGG TTG TAT AGT TGG AAA AAG GAA T      324
Gln Phe Val Ile Pro Ile Tyr Gln Arg Leu Tyr Ser Trp Lys Lys Glu
             35             40             45

```

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...329
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

CCTAATGATT TTTTCTATCT TGCCCCCCTT ATGTGTTAGA AAATTCTAAA	ATG TTT	56
	Met Phe	
	1	
AAG GGG ATT TAT CCT ATG CGT AAT TTT CCT ATC CAC CAT AAT GGT TTT		104
Lys Gly Ile Tyr Pro Met Arg Asn Phe Pro Ile His His Asn Gly Phe		
5 10 15		
AAA CAT GAA GTG TTA GCT CAC ATG CTA AAA AGG CAT AAA GAG CCA TTT		152
Lys His Glu Val Leu Ala His Met Leu Lys Arg His Lys Glu Pro Phe		
20 25 30		
ATT TTA AGC TAT AAT GAC TGC GAA TTT GTA AGG AAT GCT TAT AAA GAT		200
Ile Leu Ser Tyr Asn Asp Cys Glu Phe Val Arg Asn Ala Tyr Lys Asp		
35 40 45 50		
TTT AAA ATT TTA GAA CCA TCT TGG CAA TAC ACT ATG GGA CAA GGC GAG		248
Phe Lys Ile Leu Glu Pro Ser Trp Gln Tyr Thr Met Gly Gln Gly Glu		
55 60 65		
ATC AGA ATG GGT AAA AAT CGC TTA GAA AGA GGC GAT AAT AAC CAT GTC		296
Ile Arg Met Gly Lys Asn Arg Leu Glu Arg Gly Asp Asn Asn His Val		
70 75 80		
AAA CAA TCT CAT GAG TTA TTG ATT ATC AAG GAG TAAAAATGCA TATTAGCGAA		349
Lys Gln Ser His Glu Leu Leu Ile Ile Lys Glu		
85 90		
GTCAAAACTG CCTTTAAAAT CGCTGATGTA GAA		382

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid

			20				25				30				
Ala	Asn	Gln	Gly	Lys	Phe	Phe	Leu	Arg	Ile	Glu	Asp	Thr	Asp	Leu	Ser
			35				40				45				
Arg	Asn	Ser	Ile	Glu	Ala	Ala	Asn	Ala	Ile	Ile	Glu	Ala	Phe	Lys	Trp
			50				55				60				
Val	Gly	Leu	Glu	Tyr	Asp	Gly	Glu	Ile	Leu	Tyr	Gln	Ser	Lys	Arg	Phe
65							70				75				
Glu	Ile	Tyr	Lys	Glu	Tyr	Ile	Gln	Lys	Leu	Leu	Asp	Glu	Asp	Lys	Ala
						85				90					
Tyr	Tyr	Cys	Tyr	Met	Ser	Lys	Glu	Glu	Leu	Asp	Ala	Leu	Arg	Glu	Glu
						100				105					
Gln	Lys	Ala	Arg	Lys	Glu	Thr	Pro	Arg	Tyr	Asp	Asn	Arg	Tyr	Arg	Asp
						115				120					
Phe	Lys	Gly	Thr	Pro	Pro	Lys	Gly	Ile	Glu	Pro	Val	Val	Arg	Ile	Lys
						130				135					
Val	Pro	Gln	Asn	Glu	Val	Ile	Gly	Phe	Asn	Asp	Gly	Val	Lys	Gly	Glu
145							150				155				
Val	Lys	Val	Asn	Thr	Asn	Glu	Leu	Asp	Asp	Phe	Ile	Ile	Ala	Arg	Ser
						165				170					
Asp	Gly	Thr	Pro	Thr	Tyr	Asn	Phe	Val	Val	Thr	Ile	Asp	Asp	Ala	Leu
						180				185					
Met	Gly	Ile	Thr	Asp	Val	Ile	Arg	Gly	Asp	Asp	His	Leu	Ser	Asn	Thr
						195				200					
Pro	Lys	Gln	Ile	Val	Leu	Tyr	Lys	Ala	Leu	Asn	Phe	Lys	Ile	Pro	Asn
						210				215					
Phe	Phe	His	Val	Pro	Met	Ile	Leu	Asn	Glu	Glu	Gly	Gln	Lys	Leu	Ser
225							230				235				
Lys	Arg	His	Gly	Ala	Thr	Asn	Val	Met	Asp	Tyr	Gln	Glu	Met	Gly	Tyr
						245				250					
Leu	Lys	Glu	Ala	Leu	Val	Asn	Phe	Leu	Ala	Arg	Leu	Gly	Trp	Ser	Tyr
						260				265					
Gln	Asp	Lys	Glu	Val	Phe	Ser	Met	Gln	Glu	Leu	Leu	Glu	Leu	Phe	Asp
						275				280					
Pro	Lys	Asp	Leu	Asn	Ser	Ser	Pro	Ser	Cys	Phe	Ser	Trp	His	Lys	Leu
						290				295					
Asn	Trp	Leu	Asn	Ala	His	Tyr	Leu	Lys	Asn	Gln	Ser	Val	Gln	Glu	Leu
305							310				315				
Leu	Lys	Leu	Leu	Lys	Pro	Phe	Ser	Phe	Ser	Asp	Leu	Ser	His	Leu	Asn
						325				330					
Pro	Thr	Gln	Leu	Asp	Arg	Leu	Leu	Asp	Ala	Leu	Lys	Glu	Arg	Ser	Gln
						340				345					
Thr	Leu	Lys	Glu	Leu	Ala	Leu	Lys	Ile	Asp	Glu	Val	Leu	Ile	Ala	Pro
						355				360					
Val	Glu	Tyr	Glu	Glu	Lys	Val	Phe	Lys	Lys	Leu	Asn	Gln	Ala	Leu	Val
						370				375					
Met	Pro	Leu	Leu	Glu	Lys	Phe	Lys	Leu	Glu	Leu	Asn	Lys	Ala	Asn	Phe
385							390				395				
Asn	Asp	Glu	Ser	Ala	Leu	Glu	Asn	Ala	Met	Arg	Gln	Ile	Ile	Glu	Glu
						405				410					
Glu	Lys	Ile	Lys	Ala	Gly	Ser	Phe	Met	Gln	Pro	Leu	Arg	Leu	Ala	Leu
						420				425					
Leu	Gly	Lys	Gly	Gly	Gly	Ile	Gly	Leu	Lys	Glu	Ala	Leu	Phe	Ile	Leu
						435				440					
Gly	Lys	Thr	Glu												

CTT TTA AAG CCT TTT AGT TTT AGC GAT CTC TCG CAT TTA AAC CCC ACT	1065
Leu Leu Lys Pro Phe Ser Phe Ser Asp Leu Ser His Leu Asn Pro Thr	
325 330 335	
CAA TTG GAT CGC TTG TTA GAC GCT CTC AAA GAA AGA TCT CAA ACA CTA	1113
Gln Leu Asp Arg Leu Leu Asp Ala Leu Lys Glu Arg Ser Gln Thr Leu	
340 345 350	
AAA GAA TTA GCC CTT AAA ATA GAT GAG GTT TTA ATC GCC CCT GTG GAG	1161
Lys Glu Leu Ala Leu Lys Ile Asp Glu Val Leu Ile Ala Pro Val Glu	
355 360 365 370	
TAT GAA GAA AAG GTT TTT AAA AAA CTC AAT CAA GCG CTC GTT ATG CCC	1209
Tyr Glu Glu Lys Val Phe Lys Lys Leu Asn Gln Ala Leu Val Met Pro	
375 380 385	
TTG TTA GAA AAG TTT AAG CTA GAA TTA AAC AAA GCC AAT TTC AAC GAT	1257
Leu Leu Glu Lys Phe Lys Leu Glu Leu Asn Lys Ala Asn Phe Asn Asp	
390 395 400	
GAA AGC GCG CTA GAA AAC GCC ATG CGC CAA ATC ATT GAA GAA GAA AAG	1305
Glu Ser Ala Leu Glu Asn Ala Met Arg Gln Ile Ile Glu Glu Glu Lys	
405 410 415	
ATT AAA GCG GGT AGT TTT ATG CAG CCT TTA AGA TTG GCC CTT TTG GGT	1353
Ile Lys Ala Gly Ser Phe Met Gln Pro Leu Arg Leu Ala Leu Leu Gly	
420 425 430	
AAG GGA GGC GGG ATA GGC CTT AAA GAA GCG CTT TTT ATT TTA GGC AAA	1401
Lys Gly Gly Gly Ile Gly Leu Lys Glu Ala Leu Phe Ile Leu Gly Lys	
435 440 445 450	
ACA GAG AGC GTC AAA AGA ATA GAG GAT TTT TTG AAA AAC TAAAAAATTG GC	1452
Thr Glu Ser Val Lys Arg Ile Glu Asp Phe Leu Lys Asn	
455 460	
TCTGTTTTC TTTGGGTATTA AAATAAAAGA GTTTGATTTT AGCGGTTGTT AAGCAACTCC	1512
TTTTGAAAAA TAAGAGGG	1530

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

Met Ser Leu Ile Val Thr Arg Phe Ala Pro Ser Pro Thr Gly Tyr Leu
1 5 10 15
His Ile Gly Gly Leu Arg Thr Ala Ile Phe Asn Tyr Leu Phe Ala Arg

TGT TAC ATG AGC AAA GAA GAG TTG GAC GCT TTG AGA GAA GAG CAA AAA	393
Cys Tyr Met Ser Lys Glu Glu Leu Asp Ala Leu Arg Glu Glu Gln Lys	
100 105 110	
GCC AGG AAA GAA ACC CCA CGC TAT GAC AAT CGC TAT CGT GAT TTT AAA	441
Ala Arg Lys Glu Thr Pro Arg Tyr Asp Asn Arg Tyr Arg Asp Phe Lys	
115 120 125 130	
GGC ACG CCT CCT AAA GGC ATA GAG CCT GTG GTA AGG ATT AAA GTC CCC	489
Gly Thr Pro Pro Lys Gly Ile Glu Pro Val Val Arg Ile Lys Val Pro	
135 140 145	
CAA AAT GAG GTG ATT GGT TTT AAT GAC GGG GTT AAA GGC GAA GTG AAA	537
Gln Asn Glu Val Ile Gly Phe Asn Asp Gly Val Lys Gly Glu Val Lys	
150 155 160	
GTG AAT ACT AAC GAA TTA GAC GAT TTT ATT ATC GCC AGG AGC GAT GGG	585
Val Asn Thr Asn Glu Leu Asp Asp Phe Ile Ile Ala Arg Ser Asp Gly	
165 170 175	
ACA CCC ACT TAT AAC TTT GTG GTT ACT ATT GAT GAC GCT TTA ATG GGG	633
Thr Pro Thr Tyr Asn Phe Val Val Thr Ile Asp Asp Ala Leu Met Gly	
180 185 190	
ATT ACT GAT GTG ATT AGA GGC GAT GAT CAC CTT TCT AAC ACC CCT AAA	681
Ile Thr Asp Val Ile Arg Gly Asp Asp His Leu Ser Asn Thr Pro Lys	
195 200 205 210	
CAA ATC GTT CTT TAT AAG GCT TTG AAT TTT AAA ATC CCT AAT TTT TTC	729
Gln Ile Val Leu Tyr Lys Ala Leu Asn Phe Lys Ile Pro Asn Phe Phe	
215 220 225	
CAT GTG CCG ATG ATT TTG AAT GAA GAA GGG CAA AAA TTA AGC AAA CGC	777
His Val Pro Met Ile Leu Asn Glu Glu Gly Gln Lys Leu Ser Lys Arg	
230 235 240	
CAT GGG GCC ACT AAT GTG ATG GAC TAT CAA GAA ATG GGC TAT CTT AAG	825
His Gly Ala Thr Asn Val Met Asp Tyr Gln Glu Met Gly Tyr Leu Lys	
245 250 255	
GAA GCT TTA GTG AAT TTT TTA GCG CGT TTG GGG TGG AGC TAT CAG GAT	873
Glu Ala Leu Val Asn Phe Leu Ala Arg Leu Gly Trp Ser Tyr Gln Asp	
260 265 270	
AAA GAG GTT TTT AGC ATG CAA GAA TTG CTA GAA TTA TTT GAT CCT AAA	921
Lys Glu Val Phe Ser Met Gln Glu Leu Leu Glu Leu Phe Asp Pro Lys	
275 280 285 290	
GAT TTG AAT TCT TCG CCC AGT TGC TTC AGC TGG CAC AAG CTT AAT TGG	969
Asp Leu Asn Ser Ser Pro Ser Cys Phe Ser Trp His Lys Leu Asn Trp	
295 300 305	
CTC AAC GCT CAT TAT TTA AAA AAC CAA AGT GTG CAA GAA TTG TTA AAA	1017
Leu Asn Ala His Tyr Leu Lys Asn Gln Ser Val Gln Glu Leu Leu Lys	
310 315 320	

```

Asp Glu Asn Tyr Cys His Tyr Glu Val Ile Ser Gln Thr Ile Ser Leu
      115                      120                      125
Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys Leu Asp Phe Asn Gln Asn
      130                      135                      140
Lys Lys Phe
145

```

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1440
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```

TTAAGCCATT TTTGAATACA ATAAGAGTAT TTTATTTTTA AGGTTAGAAC A ATG AGT      57
                                     Met Ser
                                     1

TTG ATC GTT ACG CGC TTC GCT CCA TCG CCC ACT GGC TAC CTC CAC ATA      105
Leu Ile Val Thr Arg Phe Ala Pro Ser Pro Thr Gly Tyr Leu His Ile
      5                      10                      15

GGA GGC TTA AGA ACA GCC ATT TTC AAT TAT CTT TTT GCA CGA GCC AAT      153
Gly Gly Leu Arg Thr Ala Ile Phe Asn Tyr Leu Phe Ala Arg Ala Asn
      20                      25                      30

CAA GGA AAA TTT TTT TTA CGC ATT GAA GAC ACG GAT TTG AGC CGT AAC      201
Gln Gly Lys Phe Phe Leu Arg Ile Glu Asp Thr Asp Leu Ser Arg Asn
      35                      40                      45                      50

TCT ATA GAA GCG GCT AAC GCC ATT ATA GAA GCT TTC AAA TGG GTA GGG      249
Ser Ile Glu Ala Ala Asn Ala Ile Ile Glu Ala Phe Lys Trp Val Gly
                        55                      60                      65

CTA GAA TAC GAT GGC GAA ATC CTC TAC CAA TCC AAA CGC TTT GAG ATT      297
Leu Glu Tyr Asp Gly Glu Ile Leu Tyr Gln Ser Lys Arg Phe Glu Ile
                        70                      75                      80

TAT AAA GAA TAC ATT CAA AAA CTC TTA GAT GAA GAC AAA GCC TAT TAT      345
Tyr Lys Glu Tyr Ile Gln Lys Leu Leu Asp Glu Asp Lys Ala Tyr Tyr
      85                      90                      95

```

	55	60	65	
GTG TTA TTG GTA AGC CAT AAC CCC AAT GAA ATC ACC AAG CTC GCG CAA				296
Val Leu Leu Val Ser His Asn Pro Asn Glu Ile Thr Lys Leu Ala Gln				
	70	75	80	
ACT TTC CTC TTT TTA AAC AAT GGC GTT ATT GAT CCT AAT CAA GAA AAT				344
Thr Phe Leu Phe Leu Asn Asn Gly Val Ile Asp Pro Asn Gln Glu Asn				
	85	90	95	
CGG CTT TTT TCA AAC CGC TTA TTA ATA AAA CCT CTC TTT GAA GAT GAA				392
Arg Leu Phe Ser Asn Arg Leu Leu Ile Lys Pro Leu Phe Glu Asp Glu				
	100	105	110	
AAT TAT TGC CAT TAT GAG GTC ATT TCT CAA ACG ATT AGT TTG CCC AAA				440
Asn Tyr Cys His Tyr Glu Val Ile Ser Gln Thr Ile Ser Leu Pro Lys				
	115	120	125	130
GAT TGT CTG AAC CCA ACT TTT AAG CTT GAT TTC AAT CAA AAC AAA AAA				488
Asp Cys Leu Asn Pro Thr Phe Lys Leu Asp Phe Asn Gln Asn Lys Lys				
	135	140	145	
TTT TAGAAATATT TTTTCATTTT CCTCTTAAAA CCCTCTTATT TTTCAAAAGG AGTTGC				547
Phe				
TTAACAACCG CTAAATCAA ACTCTTTTAT TTTAATACCC AATGAAAACA GAGC				601

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

Met	Arg	Leu	Glu	Asn	Leu	Ser	Gln	Gln	Lys	Ile	Leu	Gln	Leu	Ser	Gly
1				5				10					15		
Gly	Gln	Ala	Gln	Arg	Val	Ala	Leu	Ala	Arg	Ala	Leu	Ile	Ala	Ala	Lys
		20					25					30			
Asn	Leu	Leu	Leu	Leu	Asp	Glu	Pro	Leu	Asn	Ala	Leu	Asp	Asn	Ala	Leu
		35				40					45				
Lys	Asn	Glu	Val	Gln	Gln	Gly	Leu	Leu	Asp	Phe	Ile	Lys	Arg	Glu	Asn
	50				55				60						
Leu	Ser	Val	Leu	Leu	Val	Ser	His	Asn	Pro	Asn	Glu	Ile	Thr	Lys	Leu
65				70				75						80	
Ala	Gln	Thr	Phe	Leu	Phe	Leu	Asn	Asn	Gly	Val	Ile	Asp	Pro	Asn	Gln
			85				90							95	
Glu	Asn	Arg	Leu	Phe	Ser	Asn	Arg	Leu	Leu	Ile	Lys	Pro	Leu	Phe	Glu
		100					105						110		

```

Ile Lys Ile Pro Thr Ala Leu Phe Pro Met Gly Val Leu Ser Cys Leu
      100                      105                      110
Glu Ser Ser Lys Asn Phe Ser Thr Ile Ala Val Glu Glu Ser Glu Ser
      115                      120                      125
Pro Met Pro Lys Thr Arg Glu Lys Met Gly Glu Arg Pro Lys Thr Lys
      130                      135                      140
Tyr Pro Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser
      145                      150                      155                      160
Pro Lys Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu
      165                      170                      175
Asn Ser Met Pro Ile Ile Asn Ile Lys Lys Thr Ile Pro Asn Ser Pro
      180                      185                      190
Ile Ser Asp Asn Lys Ser Lys Ser Leu Ile Leu Lys Lys Ala Ala Lys
      195                      200                      205
Thr Val Pro Val Gln Met
      210

```

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...491
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

```

GCCTTTGCTC ACCCTAAAGA TAAAAATAAA ATTCACGAAG GTTACGCTTA  ATG CGT      56
                                     Met Arg
                                     1

TTA GAA AAT CTA AGC CAG CAA AAA ATT CTT CAA CTC TCT GGC GGG CAA      104
Leu Glu Asn Leu Ser Gln Gln Lys Ile Leu Gln Leu Ser Gly Gly Gln
      5                      10                      15

GCC CAA CGA GTC GCT TTA GCA AGA GCT TTA ATC GCA GCC AAG AAT CTA      152
Ala Gln Arg Val Ala Leu Ala Arg Ala Leu Ile Ala Ala Lys Asn Leu
      20                      25                      30

TTG CTT TTA GAT GAG CCT TTA AAC GCC TTA GAT AAC GCC TTA AAA AAC      200
Leu Leu Leu Asp Glu Pro Leu Asn Ala Leu Asp Asn Ala Leu Lys Asn
      35                      40                      45                      50

GAA GTG CAA CAA GGT TTG CTT GAT TTT ATC AAG CGT GAA AAT TTA AGC      248
Glu Val Gln Gln Gly Leu Leu Asp Phe Ile Lys Arg Glu Asn Leu Ser

```

```

TCA AAG AAT TTC AGC ACA ATA GCG GTT GAA GAG AGC GAA AGC CCC ATG      440
Ser Lys Asn Phe Ser Thr Ile Ala Val Glu Glu Ser Glu Ser Pro Met
115                               120                               125                               130

CCT AAA ACA AGG GAA AAA ATG GGT GAA AGA CCC AAA ACA AAA TAC CCC      488
Pro Lys Thr Arg Glu Lys Met Gly Glu Arg Pro Lys Thr Lys Tyr Pro
                               135                               140                               145

AAT AAA AAA GCG ATT AAA GCG CAT AAA ACC ACT TGT AAA AGC CCA AAA      536
Asn Lys Lys Ala Ile Lys Ala His Lys Thr Thr Cys Lys Ser Pro Lys
                               150                               155                               160

ACC AGC ACT TCT TGT TTG ATG GAT TTG AGC TTG TCA AAA TTA AAC TCA      584
Thr Ser Thr Ser Cys Leu Met Asp Leu Ser Leu Ser Lys Leu Asn Ser
                               165                               170                               175

ATG CCT ATC ATA AAC ATT AAA AAG ACG ATA CCA AAT TCG CCA ATA TCA      632
Met Pro Ile Ile Asn Ile Lys Lys Thr Ile Pro Asn Ser Pro Ile Ser
                               180                               185                               190

GAC AAC AAA TCA AAA TCA TTA ATT TTA AAA AAA GCC GCT AAG ACC GTT      680
Asp Asn Lys Ser Lys Ser Leu Ile Leu Lys Lys Ala Ala Lys Thr Val
195                               200                               205                               210

CCT GTG CAA ATG TAACCAATGA TAACAGGCAT GTCTAATTTC TTAAAAAAGA TTCCA      737
Pro Val Gln Met

AAGCCCAC                                                                745

```

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

```

Met Pro Thr Met Asn Ala Pro Lys Asp Ile Glu Asn Pro Lys Lys Trp
 1           5           10           15
Leu Asn Pro Ala Leu Gln Thr Ile Thr Lys Ile Val Pro Ile Lys
 20           25           30
Ile Ser Gly Arg Arg Val Ser Phe Ala Cys Ser Lys Met Arg Leu Ala
 35           40           45
Pro Phe Phe Pro Gly Asn Asn Lys Arg Thr Lys Ile Ile Pro Ala Glu
 50           55           60
Ile Lys Val Leu Arg Met Ser Lys Leu Thr Leu Glu Ser Leu Leu Pro
 65           70           75           80
Arg Ile Val Arg Ile Lys Ser Met Gly Met Ala Ala Ile Ser Trp Lys
 85           90           95

```

	35		40		45
Phe	Asp	Pro	Ser	Ala	Leu
				Ala	Leu
				Glu	Pro
				Lys	Phe
50			55		60

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...692
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

GCGCGAATTC TTCTTGGACA TTGATTTTAT AGCGCGATTT AGAAATGGCC	ATG CCC	56
	Met Pro	
	1	
ACA ATG AAC GCT CCT AAA GAC ATA GAA AAC CCA AAA AAA TGG CTC AAC		104
Thr Met Asn Ala Pro Lys Asp Ile Glu Asn Pro Lys Lys Trp Leu Asn		
5 10 15		
CCT GCT GCG CTG CAA ACA ATC ACT AAA ATC GTG CCT ATA AAA ATT TCA		152
Pro Ala Ala Leu Gln Thr Ile Thr Lys Ile Val Pro Ile Lys Ile Ser		
20 25 30		
GGC AGG CGC GTG TCT TTT GCT TGC TCT AAG ATG AGA TTA GCC CCT TTT		200
Gly Arg Arg Val Ser Phe Ala Cys Ser Lys Met Arg Leu Ala Pro Phe		
35 40 45 50		
TTT CCA GGC AAT AAT AAA AGA ACT AAA ATA ATC CCT GCT GAA ATA AAG		248
Phe Pro Gly Asn Asn Lys Arg Thr Lys Ile Ile Pro Ala Glu Ile Lys		
55 60 65		
GTT TTA AGA ATG AGT AAA TTA ACA TTA GAA TCT TTA CTA CCT AGA ATA		296
Val Leu Arg Met Ser Lys Leu Thr Leu Glu Ser Leu Leu Pro Arg Ile		
70 75 80		
GTG AGG ATT AAA AGC ATG GGA ATG GCT GCA ATA TCT TGG AAA ATC AAA		344
Val Arg Ile Lys Ser Met Gly Met Ala Ala Ile Ser Trp Lys Ile Lys		
85 90 95		
ATC CCC ACC GCG CTC TTT CCC ATG GGC GTG CTA AGC TGT TTG GAA TCT		392
Ile Pro Thr Ala Leu Phe Pro Met Gly Val Leu Ser Cys Leu Glu Ser		
100 105 110		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...180
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

AAC AAA ACT TTT TTA AGG GGT AAA AAC CCT TTA GTT ACA AGA AAG AGA	48
Asn Lys Thr Phe Leu Arg Gly Lys Asn Pro Leu Val Thr Arg Lys Arg	
1 5 10 15	
AGT TTT GTC ATC AAA ATG AAG TTT TTT AAA GAA AAA GAA AAA GAA GTT	96
Ser Phe Val Ile Lys Met Lys Phe Phe Lys Glu Lys Glu Lys Glu Val	
20 25 30	
TCA AAA ATT AAA AGT TTG AGA AAG TTT GAG TCA AAT CCG CTA GTA AGA	144
Ser Lys Ile Lys Ser Leu Arg Lys Phe Glu Ser Asn Pro Leu Val Arg	
35 40 45	
TTT GAC CCT AGC GCT CTT GCG CTA GAG CCA AAA TTT TAGTATAATG GCGTTG	196
Phe Asp Pro Ser Ala Leu Ala Leu Glu Pro Lys Phe	
50 55 60	
CGGATACCAT TAAAACTATG ATTACTAATC TCATGTTAGG TTATCTCCTT TTCTGAGGTA	256
ACCACCCACT ATTACCCCCA ACCCT	281

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

Asn Lys Thr Phe Leu Arg Gly Lys Asn Pro Leu Val Thr Arg Lys Arg
1 5 10 15
Ser Phe Val Ile Lys Met Lys Phe Phe Lys Glu Lys Glu Lys Glu Val
20 25 30
Ser Lys Ile Lys Ser Leu Arg Lys Phe Glu Ser Asn Pro Leu Val Arg

595	600	605
Val Met Glu Trp Gln Arg	Ile Asp Arg Val Glu Leu	Pro Thr Pro Asp
610	615	620
Ser Ile Lys Lys Pro Ser	Ile Asp Glu Leu Lys	Asn Asp Phe Asn Pro
625	630	635
Lys Arg Gly Lys Ser Ser	Asp Leu Phe Glu Trp	Ala Leu Glu Gln Leu
645	650	655
Glu Thr Leu Lys Asp Leu	Asn Ser Pro Arg Phe	Val Leu Glu Lys
660	665	670
Lys Leu Glu Cys Gly Gly	Ile Ser Ile Ile Gly	Glu Asp Arg Asn Asn
675	680	685
Glu Leu Phe Tyr Ile Met	Glu Thr Asn Gly Lys	Lys Val Phe Cys His
690	695	700
Ser Arg Gln Cys Lys Gly	Ser Val Asn Lys Asp	Glu Leu Ser Leu Gly
705	710	715
Ala Arg Val Cys Leu Glu	Val Gly Pro Asp Lys	Asn Asp His Gly Lys
725	730	735
Tyr Arg Gly Lys Ile Tyr	Gly Leu Glu Lys Asn	Arg Glu Ile Val Leu
740	745	750
Leu Asn Thr Ala Lys Asn	Ser Tyr Gln Arg Lys	Pro Leu Asp Glu Lys
755	760	765
Ile Lys His Arg Ile Glu	Ala Leu Lys Arg Ile	Lys Tyr Pro Cys Leu
770	775	780
Lys Ile Phe Ser His Tyr	Met Leu Glu Glu Leu	Glu Thr Leu Asn Pro
785	790	795
Glu Phe Ala Thr Pro Phe	Lys Glu Tyr Leu Lys	Arg Leu Glu Glu Tyr
805	810	815
Tyr Phe Asp Pro Gln Thr	Asp Arg Asp Phe Lys	Lys Gly Leu Leu Asp
820	825	830
Phe Phe Ser Arg Leu Asn	Asp Ser Ile Pro Ala	Lys Leu Gln Gln Glu
835	840	845
Phe Ile Asn Leu Pro Ser	Thr Asp Phe Leu Ser	Arg Cys Leu Gly Ser
850	855	860
Leu Glu Lys Asp Phe Gln	Lys Thr Ile Phe Lys	Lys Leu Lys Val Thr
865	870	875
Asn Leu Lys Thr Leu Ser	Ile Val Ala Arg Ala	Ser Trp Asn Asn Glu
885	890	895
Lys Phe Leu Glu Asn Leu	Met Ala Gln Thr Ser	Leu Glu Gln Gln Lys
900	905	910
Asp Phe Leu Lys Arg Ile	Glu Glu Cys Leu Lys	Asn Pro Glu Ser Phe
915	920	925
Tyr Phe Ser Ser Ala Cys	Glu Leu Leu Leu Ala	Phe Leu Ser Tyr Arg
930	935	940
Asn Ala Lys Arg Glu Leu	Glu Leu Ile Pro Glu	Ser Glu Lys Thr Met
945	950	955
Arg Leu Leu Asp Ser Ile	Asp Lys Ala Ile Glu	Lys Glu Thr Glu Ile
965	970	975
Lys Ser Phe Val Lys Leu	Glu Leu Lys Asn Gln	Ser Phe Asn Asn Ile
980	985	990
Pro Pro Leu Leu Ser Ala	Leu Arg Leu Tyr Leu	Arg Gly Asp Leu Glu
995	1000	1005
Gly Val Gly Ile Glu Ile	Asn Gly Thr Glu Glu	Asp Glu
1010	1015	1020

(2) INFORMATION FOR SEQ ID NO:711:

Phe Glu Glu Leu Ile Phe Ser Ile Thr Ser Phe Leu Lys Asn Gly Val
 165 170 175
 Ala Gln Gln Ile Asp Glu Lys Gln Ala Ile Ile Pro Asn Asn Leu Leu
 180 185 190
 His Phe Asp Lys His Tyr Lys Arg Ile Phe Lys Ala His Asp Trp Leu
 195 200 205
 Tyr Asp Gly Val Gly Ser Leu Met Asn Leu Asp Gln Ile Phe Tyr Leu
 210 215 220
 Glu Cys Leu Tyr Gln Ala Gln Phe Tyr Thr Ser Lys Asn Ile Glu Pro
 225 230 235 240
 Thr Leu Ile Arg Asn Glu Gln Asp Leu Tyr Ala Leu Ile Lys Asn Ser
 245 250 255
 Phe Pro Ile Lys Asp Leu Ser Phe Glu Lys Met Arg Leu Lys Ala Lys
 260 265 270
 Glu Phe Phe Glu Asn Glu Leu Arg Gln Pro Ile Asn Leu Asp Gln Glu
 275 280 285
 Ile Pro Gln Leu Glu Leu Cys Lys Gly Val Tyr Lys Glu Met Tyr Ile
 290 295 300
 Asp Met Phe Ser Pro Glu Pro Phe Ala Leu Leu Val Gly Asn Gly Asn
 305 310 315 320
 Glu Glu Lys Ile Leu Lys Leu Pro Leu Leu Val Lys Lys Gln Glu Asn
 325 330 335
 Asn Thr Tyr Ile Asn Ala Asn Gly Ala Lys Gly Lys Ile Asp Glu Lys
 340 345 350
 Gly Tyr Leu Ala Asn Ala Leu Lys Asn Tyr Asp Glu Thr Leu Val Glu
 355 360 365
 Ala Phe Met Arg Asp Phe Lys Glu Arg Tyr Lys Ile Glu Lys Leu Tyr
 370 375 380
 Tyr Leu Leu Asp Asp Asn Ile Lys Asn Phe Glu Phe Ala Lys Ile Lys
 385 390 395 400
 His Lys Ile Ser Leu Tyr Phe Lys Asp Ala Lys Phe Tyr Pro Lys Ser
 405 410 415
 Val Ala Leu Gly Phe Ser Ser Leu Phe Glu Asn Lys Leu Lys Lys Asn
 420 425 430
 Glu Arg Leu Arg Tyr Asn Ser Val Asp Leu Val Val Lys Glu Asn His
 435 440 445
 Lys Ser Lys Thr Phe Asn Asp Cys Gly Leu Val Leu Glu Arg Gln Lys
 450 455 460
 Ser Asp Asp Ser Lys Glu Phe Leu Ile Leu Gln Asp Ser Phe Ile Lys
 465 470 475 480
 Lys Ala Leu Lys Asn Phe Lys Arg Ala Leu Gly Leu Glu Lys Glu Gly
 485 490 495
 Phe Ile Leu Tyr Lys Glu Cys Leu Pro Lys Leu Ser Met Glu Val Val
 500 505 510
 Lys Asp Gly Arg Phe Lys Asn Phe Glu Ile Ile Lys Asp Lys Thr Ile
 515 520 525
 Leu Gly Asp Lys Glu Thr Leu Glu Ile Glu Thr Pro Phe Ile Ile Pro
 530 535 540
 Lys Gly Arg Glu Ser Phe Ala Leu Pro Leu Ile Leu Asn Glu Glu Lys
 545 550 555 560
 Ile Ala Tyr Gln Gly Lys Ile Thr Ser Lys Asp Phe Pro Leu Glu Asn
 565 570 575
 Asp Glu Glu Tyr Lys Leu Thr Leu Thr Tyr Asp Ile Gly Thr Glu Phe
 580 585 590
 Asn Tyr Val Leu Glu Phe Lys Pro Val Asn Asn Asp Leu Lys Pro Ile

```

AAA AGA GAG TTG GAA TTG ATC CCT GAA AGC GAA AAA ACC ATG CGT TTA      2936
Lys Arg Glu Leu Glu Leu Ile Pro Glu Ser Glu Lys Thr Met Arg Leu
          950                      955                      960

TTG GAC AGC ATA GAT AAA GCG ATA GAA AAA GAG ACT GAA ATT AAA AGC      2984
Leu Asp Ser Ile Asp Lys Ala Ile Glu Lys Glu Thr Glu Ile Lys Ser
          965                      970                      975

TTT GTA AAA TTA GAG CTA AAA AAT CAA AGC TTC AAC AAT ATC CCA CCT      3032
Phe Val Lys Leu Glu Leu Lys Asn Gln Ser Phe Asn Asn Ile Pro Pro
          980                      985                      990

TTG TTG TCG GCG TTA CGC TTG TAT TTA AGG GGG GAT TTG GAA GGT GTT      3080
Leu Leu Ser Ala Leu Arg Leu Tyr Leu Arg Gly Asp Leu Glu Gly Val
          995                      1000                      1005                      1010

GGA ATT GAA ATT AAT GGG ACA GAA GAG GAT GAA TAAATCAAAC AAATTAGTCA      3133
Gly Ile Glu Ile Asn Gly Thr Glu Glu Asp Glu
          1015                      1020

TTATCAATCG CGCCATTCCA GGTGGGGGCA AGA      3166

```

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

```

Met Asp Leu Glu Glu Leu Tyr Ala Pro Asn His Ile Glu Arg Leu Lys
 1          5          10          15
Ala Arg Ser Phe Leu Arg Ser Ile Ala Phe Phe Asp Asp Phe Ser Ala
          20          25          30
Ser Phe Glu Tyr Arg Asp Leu Phe Ser Val Leu Glu Asn Ile Val Gln
          35          40          45
Phe Asp Tyr Glu Lys Lys Pro Tyr Lys Asp Asp Leu Tyr Phe Leu Cys
          50          55          60
Lys Phe Val Glu Pro Ala Leu Lys Ala Ile Phe Ser Asn Leu Asn Thr
          65          70          75          80
Asn Ile Tyr Arg Lys His Leu Lys Met Pro Leu Glu Lys Ala Arg Glu
          85          90          95
Phe Asp Ala Lys Cys Ala Leu Asp Leu Ala Lys Arg Pro Gly Arg Ser
          100          105          110
Leu Lys Glu Lys Leu Cys Asp Asn Lys Val Leu Ser Val Lys Arg Tyr
          115          120          125
Val Asn Ala Asn Thr His Glu Asn Arg Phe Leu Lys Arg Phe Ile Lys
          130          135          140
Glu Leu Leu Arg Ile Ile His Trp Arg Glu Ile Glu Phe Gln Gln Val
          145          150          155          160

```

GTG	TGT	TTG	GAA	GTG	GGG	CCA	GAT	AAG	AAC	GAC	CAT	GGT	AAA	TAT	CGA	2264
Val	Cys	Leu	Glu	Val	Gly	Pro	Asp	Lys	Asn	Asp	His	Gly	Lys	Tyr	Arg	
		725					730					735				
GGT	AAA	ATT	TAT	GGT	TTG	GAA	AAA	AAT	AGA	GAA	ATT	GTT	TTA	TTA	AAT	2312
Gly	Lys	Ile	Tyr	Gly	Leu	Glu	Lys	Asn	Arg	Glu	Ile	Val	Leu	Leu	Asn	
	740					745					750					
ACA	GCT	AAA	AAT	TCT	TAT	CAA	AGA	AAA	CCT	CTA	GAT	GAG	AAA	ATT	AAA	2360
Thr	Ala	Lys	Asn	Ser	Tyr	Gln	Arg	Lys	Pro	Leu	Asp	Glu	Lys	Ile	Lys	
755					760					765					770	
CAC	AGA	ATA	GAA	GCG	CTC	AAA	AGA	ATC	AAG	TAT	CCT	TGT	TTA	AAA	ATT	2408
His	Arg	Ile	Glu	Ala	Leu	Lys	Arg	Ile	Lys	Tyr	Pro	Cys	Leu	Lys	Ile	
			775						780					785		
TTT	TCA	CAT	TAC	ATG	CTT	GAA	GAG	TTA	GAA	ACC	TTA	AAT	CCT	GAA	TTT	2456
Phe	Ser	His	Tyr	Met	Leu	Glu	Glu	Leu	Glu	Thr	Leu	Asn	Pro	Glu	Phe	
			790					795					800			
GCT	ACT	CCC	TTT	AAA	GAA	TAT	TTG	AAG	CGG	TTA	GAA	GAA	TAT	TAT	TTT	2504
Ala	Thr	Pro	Phe	Lys	Glu	Tyr	Leu	Lys	Arg	Leu	Glu	Glu	Tyr	Tyr	Phe	
		805					810					815				
GAC	CCA	CAA	ACA	GAC	AGA	GAT	TTT	AAA	AAA	GGA	CTC	TTG	GAT	TTC	TTT	2552
Asp	Pro	Gln	Thr	Asp	Arg	Asp	Phe	Lys	Lys	Gly	Leu	Leu	Asp	Phe	Phe	
	820					825					830					
AGC	CGC	TTG	AAT	GAT	AGT	ATT	CCC	GCA	AAA	TTA	CAA	CAA	GAA	TTT	ATT	2600
Ser	Arg	Leu	Asn	Asp	Ser	Ile	Pro	Ala	Lys	Leu	Gln	Gln	Glu	Phe	Ile	
835					840					845					850	
AAT	TTA	CCT	TCT	ACG	GAT	TTT	TTA	AGC	AGA	TGT	TTA	GGC	TCT	CTT	GAA	2648
Asn	Leu	Pro	Ser	Thr	Asp	Phe	Leu	Ser	Arg	Cys	Leu	Gly	Ser	Leu	Glu	
				855					860					865		
AAA	GAC	TTT	CAA	AAA	ACG	ATT	TTT	AAG	AAG	CTT	AAA	GTT	ACT	AAC	CTA	2696
Lys	Asp	Phe	Gln	Lys	Thr	Ile	Phe	Lys	Lys	Leu	Lys	Val	Thr	Asn	Leu	
		870						875				880				
AAG	ACT	TTA	AGT	ATT	GTG	GCT	AGG	GCT	AGT	TGG	AAT	AAT	GAG	AAA	TTT	2744
Lys	Thr	Leu	Ser	Ile	Val	Ala	Arg	Ala	Ser	Trp	Asn	Asn	Glu	Lys	Phe	
		885					890					895				
TTA	GAG	AAC	TTG	ATG	GCT	CAA	ACC	AGC	TTG	GAG	CAG	CAA	AAA	GAC	TTT	2792
Leu	Glu	Asn	Leu	Met	Ala	Gln	Thr	Ser	Leu	Glu	Gln	Gln	Lys	Asp	Phe	
	900					905					910					
TTG	AAG	CGT	ATA	GAA	GAG	TGT	TTG	AAA	AAT	CCT	GAG	TCA	TTT	TAT	TTC	2840
Leu	Lys	Arg	Ile	Glu	Glu	Cys	Leu	Lys	Asn	Pro	Glu	Ser	Phe	Tyr	Phe	
915					920					925					930	
AGT	AGC	GCA	TGC	GAA	TTG	CTG	TTA	GCG	TTT	TTG	TCT	TAT	CGC	AAC	GCT	2888
Ser	Ser	Ala	Cys	Glu	Leu	Leu	Leu	Ala	Phe	Leu	Ser	Tyr	Arg	Asn	Ala	
				935					940					945		

CTG TAT AAA GAA TGC TTG CCT AAG CTC TCT ATG GAA GTG GTT AAA GAC	1592
Leu Tyr Lys Glu Cys Leu Pro Lys Leu Ser Met Glu Val Val Lys Asp	
500 505 510	
GGG CGG TTT AAA AAT TTT GAG ATC ATT AAA GAT AAA ACC ATT TTA GGA	1640
Gly Arg Phe Lys Asn Phe Glu Ile Ile Lys Asp Lys Thr Ile Leu Gly	
515 520 525 530	
GAT AAA GAA ACC CTA GAG ATT GAA ACG CCT TTT ATT ATC CCT AAA GGG	1688
Asp Lys Glu Thr Leu Glu Ile Glu Thr Pro Phe Ile Ile Pro Lys Gly	
535 540 545	
CGA GAA AGT TTT GCT TTG CCC TTG ATC CTA AAT GAA GAA AAA ATC GCC	1736
Arg Glu Ser Phe Ala Leu Pro Leu Ile Leu Asn Glu Glu Lys Ile Ala	
550 555 560	
TAT CAA GGT AAA ATC ACC TCT AAA GAT TTT CCC CTA GAA AAT GAC GAA	1784
Tyr Gln Gly Lys Ile Thr Ser Lys Asp Phe Pro Leu Glu Asn Asp Glu	
565 570 575	
GAA TAC AAA CTC ACG CTC ACT TAT GAC ATT GGC ACC GAG TTT AAC TAT	1832
Glu Tyr Lys Leu Thr Leu Thr Tyr Asp Ile Gly Thr Glu Phe Asn Tyr	
580 585 590	
GTG TTA GAG TTT AAA CCT GTC AAT AAT GAT TTA AAG CCC ATT GTC ATG	1880
Val Leu Glu Phe Lys Pro Val Asn Asn Asp Leu Lys Pro Ile Val Met	
595 600 605 610	
GAA TGG CAG CGT ATT GAT AGG GTT GAA CTC CCT ACG CCC GAT TCC ATC	1928
Glu Trp Gln Arg Ile Asp Arg Val Glu Leu Pro Thr Pro Asp Ser Ile	
615 620 625	
AAA AAA CCA AGT ATT GAT GAA CTA AAA AAT GAC TTT AAT CCT AAA AGG	1976
Lys Lys Pro Ser Ile Asp Glu Leu Lys Asn Asp Phe Asn Pro Lys Arg	
630 635 640	
GGC AAA AGT TCT GAT TTG TTT GAG TGG GCG CTA GAG CAA TTA GAG ACA	2024
Gly Lys Ser Ser Asp Leu Phe Glu Trp Ala Leu Glu Gln Leu Glu Thr	
645 650 655	
TTG AAA GAT TTA AAT AGT CCA CCC AGA TTT GTT TTA GAG AAA AAA CTA	2072
Leu Lys Asp Leu Asn Ser Pro Pro Arg Phe Val Leu Glu Lys Lys Leu	
660 665 670	
GAA TGC GGT GGA ATC TCA ATA ATA GGG GAA GAT AGA AAC AAT GAA CTT	2120
Glu Cys Gly Gly Ile Ser Ile Ile Gly Glu Asp Arg Asn Asn Glu Leu	
675 680 685 690	
TTT TAC ATA ATG GAA ACA AAT GGT AAA AAA GTT TTT TGT CAT AGC CGT	2168
Phe Tyr Ile Met Glu Thr Asn Gly Lys Lys Val Phe Cys His Ser Arg	
695 700 705	
CAA TGC AAA GGG AGC GTG AAC AAA GAT GAG CTT TCA TTA GGC GCG CGA	2216
Gln Cys Lys Gly Ser Val Asn Lys Asp Glu Leu Ser Leu Gly Ala Arg	
710 715 720	

Phe Glu Asn Glu Leu Arg Gln Pro Ile Asn Leu Asp Gln Glu Ile Pro	
275 280 285 290	
CAA TTG GAA TTG TGT AAG GGA GTT TAT AAA GAA ATG TAT ATT GAT ATG	968
Gln Leu Glu Leu Cys Lys Gly Val Tyr Lys Glu Met Tyr Ile Asp Met	
295 300 305	
TTT AGC CCT GAA CCT TTC GCT TTG TTA GTG GGT AAT GGC AAT GAA GAA	1016
Phe Ser Pro Glu Pro Phe Ala Leu Leu Val Gly Asn Gly Asn Glu Glu	
310 315 320	
AAG ATT TTA AAG CTC CCC CTT TTA GTC AAA AAG CAG GAG AAT AAT ACT	1064
Lys Ile Leu Lys Leu Pro Leu Leu Val Lys Lys Gln Glu Asn Asn Thr	
325 330 335	
TAT ATC AAC GCT AAT GGC GCT AAG GGT AAG ATA GAT GAA AAA GGT TAT	1112
Tyr Ile Asn Ala Asn Gly Ala Lys Gly Lys Ile Asp Glu Lys Gly Tyr	
340 345 350	
TTG GCC AAC GCT CTC AAA AAC TAT GAT GAG ACT CTT GTG GAA GCT TTT	1160
Leu Ala Asn Ala Leu Lys Asn Tyr Asp Glu Thr Leu Val Glu Ala Phe	
355 360 365 370	
ATG AGA GAT TTC AAG GAA CGC TAT AAG ATA GAA AAA CTA TAT TAT TTA	1208
Met Arg Asp Phe Lys Glu Arg Tyr Lys Ile Glu Lys Leu Tyr Tyr Leu	
375 380 385	
TTA GAT GAT AAT ATT AAA AAT TTT GAA TTT GCT AAG ATC AAG CAT AAA	1256
Leu Asp Asp Asn Ile Lys Asn Phe Glu Phe Ala Lys Ile Lys His Lys	
390 395 400	
ATA AGC TTG TAT TTT AAA GAC GCA AAA TTC TAT CCT AAA AGC GTT GCT	1304
Ile Ser Leu Tyr Phe Lys Asp Ala Lys Phe Tyr Pro Lys Ser Val Ala	
405 410 415	
TTA GGA TTT AGT TCT TTG TTT GAA AAT AAA TTA AAG AAA AAT GAG CGT	1352
Leu Gly Phe Ser Ser Leu Phe Glu Asn Lys Leu Lys Lys Asn Glu Arg	
420 425 430	
TTG CGT TAT AAC AGC GTG GAT TTG GTC GTT AAA GAA AAC CAT AAA AGT	1400
Leu Arg Tyr Asn Ser Val Asp Leu Val Val Lys Glu Asn His Lys Ser	
435 440 445 450	
AAG ACC TTT AAT GAT TGT GGC TTG GTT TTG GAG AGG CAA AAA AGC GAT	1448
Lys Thr Phe Asn Asp Cys Gly Leu Val Leu Glu Arg Gln Lys Ser Asp	
455 460 465	
GAT TCA AAA GAG TTC CTT ATT CTA CAA GAT TCT TTT ATC AAA AAA GCT	1496
Asp Ser Lys Glu Phe Leu Ile Leu Gln Asp Ser Phe Ile Lys Lys Ala	
470 475 480	
TTA AAA AAT TTT AAA AGA GCC TTA GGA TTA GAA AAA GAA GGC TTT ATT	1544
Leu Lys Asn Phe Lys Arg Ala Leu Gly Leu Glu Lys Glu Gly Phe Ile	
485 490 495	

55							60					65					
GTG	GAG	CCA	GCC	CTA	AAG	GCT	ATC	TTT	AGC	AAT	CTA	AAT	ACC	AAT	ATC	296	
Val	Glu	Pro	Ala	Leu	Lys	Ala	Ile	Phe	Ser	Asn	Leu	Asn	Thr	Asn	Ile		
			70					75					80				
TAC	CGA	AAA	CAT	TTA	AAA	ATG	CCT	TTA	GAA	AAG	GCT	AGG	GAA	TTT	GAC	344	
Tyr	Arg	Lys	His	Leu	Lys	Met	Pro	Leu	Glu	Lys	Ala	Arg	Glu	Phe	Asp		
		85					90					95					
GCT	AAA	TGC	GCG	TTG	GAT	TTA	GCC	AAG	CGA	CCA	GGT	CGT	AGT	TTG	AAA	392	
Ala	Lys	Cys	Ala	Leu	Asp	Leu	Ala	Lys	Arg	Pro	Gly	Arg	Ser	Leu	Lys		
	100					105					110						
GAA	AAG	TTG	TGC	GAC	AAT	AAA	GTA	TTG	AGC	GTC	AAG	CGT	TAT	GTG	AAT	440	
Glu	Lys	Leu	Cys	Asp	Asn	Lys	Val	Leu	Ser	Val	Lys	Arg	Tyr	Val	Asn		
115					120					125					130		
GCC	AAT	ACG	CAT	GAA	AAC	AGG	TTT	CTC	AAG	CGT	TTC	ATT	AAA	GAA	CTT	488	
Ala	Asn	Thr	His	Glu	Asn	Arg	Phe	Leu	Lys	Arg	Phe	Ile	Lys	Glu	Leu		
			135					140						145			
TTA	AGA	ATA	ATT	CAT	TGG	CGC	GAG	ATA	GAA	TTC	CAA	CAG	GTT	TTT	GAA	536	
Leu	Arg	Ile	Ile	His	Trp	Arg	Glu	Ile	Glu	Phe	Gln	Gln	Val	Phe	Glu		
			150					155					160				
GAG	TTA	ATT	TTC	AGC	ATA	ACA	AGT	TTT	TTA	AAG	AAT	GGA	GTA	GCC	CAA	584	
Glu	Leu	Ile	Phe	Ser	Ile	Thr	Ser	Phe	Leu	Lys	Asn	Gly	Val	Ala	Gln		
		165					170					175					
CAA	ATT	GAT	GAA	AAA	CAA	GCC	ATC	ATT	CCT	AAT	AAC	TTG	TTG	CAT	TTT	632	
Gln	Ile	Asp	Glu	Lys	Gln	Ala	Ile	Ile	Pro	Asn	Asn	Leu	Leu	His	Phe		
	180					185					190						
GAT	AAG	CAC	TAC	AAA	CGC	ATT	TTT	AAA	GCC	CAT	GAT	TGG	CTT	TAT	GAT	680	
Asp	Lys	His	Tyr	Lys	Arg	Ile	Phe	Lys	Ala	His	Asp	Trp	Leu	Tyr	Asp		
195					200					205					210		
GGT	GTG	GGG	TCA	TTG	ATG	AAT	TTG	GAT	CAA	ATT	TTC	TAT	TTG	GAG	TGT	728	
Gly	Val	Gly	Ser	Leu	Met	Asn	Leu	Asp	Gln	Ile	Phe	Tyr	Leu	Glu	Cys		
			215					220					225				
TTA	TAC	CAA	GCC	CAA	TTT	TAT	ACT	TCT	AAA	AAC	ATT	GAA	CCC	ACG	CTA	776	
Leu	Tyr	Gln	Ala	Gln	Phe	Tyr	Thr	Ser	Lys	Asn	Ile	Glu	Pro	Thr	Leu		
			230					235					240				
ATT	AGA	AAT	GAA	CAA	GAT	TTA	TAC	GCG	CTA	ATT	AAA	AAT	AGT	TTT	CCA	824	
Ile	Arg	Asn	Glu	Gln	Asp	Leu	Tyr	Ala	Leu	Ile	Lys	Asn	Ser	Phe	Pro		
		245					250					255					
ATA	AAA	GAT	TTA	TCG	TTT	GAA	AAG	ATG	CGT	TTA	AAA	GCG	AAA	GAG	TTT	872	
Ile	Lys	Asp	Leu	Ser	Phe	Glu	Lys	Met	Arg	Leu	Lys	Ala	Lys	Glu	Phe		
	260					265					270						
TTT	GAA	AAT	GAA	TTA	AGA	CAG	CCT	ATA	AAT	TTA	GAT	CAA	GAA	ATT	CCG	920	

Gly	Leu	Asn	Gly	Glu	Ser	Asn	Leu	Pro	Asn	Ser	Phe	Phe	Leu	Gly	Ile
145					150				155					160	
Cys	Gly	Tyr	Leu	Lys	Lys	Leu	Phe	Lys	Lys	Leu	Lys	Asp	Arg	Ala	Phe
			165					170						175	
Arg	Leu	Ala	Asn	Lys	His	Gly	Val	Phe	Phe	Leu	Lys	Ile	Pro	Lys	His
			180					185					190		
Phe	Gln	Met	Gln	Asn	Phe	Asn	Asn	Ile	Phe	Leu	Glu	Phe	Val	Ser	Val
		195				200						205			
Asn	Asn	Pro	Cys	Phe	Ser	Tyr	Arg	Leu	Thr	Tyr	Asp	Gln	Leu	Val	Gly
	210					215					220				
Lys	Lys	Ile	Pro	Asn	Ile	Lys	Cys	Ser	Tyr	Gln	Gln	Ala	Ile	Val	Lys
225				230						235				240	
Lys	Asn	Ile	His	Arg	Ala	Leu	Asp	Glu	Leu	Ser	Ile	Asp	Lys	Glu	Ile
			245					250						255	
Leu	Ala	Ser													

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...3113
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

ACTATTTGAA	TAATGTCGAA	TATGAAAAAC	TTCTTAAAAA	GTAGCATGCA	ATG	GAT	56
					Met	Asp	
					1		
CTA GAA GAA CTC	TAT GCG CCT	AAT CAC ATA	GAG CGT	TTG AAA GCG	CGG		104
Leu Glu Glu Leu	Tyr Ala Pro	Asn His Ile	Glu Arg Leu	Lys Ala Arg			
5		10		15			
AGT TTT TTA	AGA TCG ATT	GCT TTT TTT	GAT GAT	TTT AGC GCT	TCT TTT		152
Ser Phe Leu	Arg Ser Ile	Ala Phe Phe	Asp Asp	Phe Ser Ala	Ser Phe		
20		25		30			
GAA TAC AGA	GAT CTA TTT	AGC GTT TTG	GAA AAT ATC	GTG CAA TTT	GAT		200
Glu Tyr Arg	Asp Leu Phe	Ser Val Leu	Glu Asn Ile	Val Gln Phe	Asp		
35		40		45		50	
TAT GAA AAA	AAG CCG TAT	AAA GAT GAT	TTG TAT TTT	TTG TGC AAA	TTT		248
Tyr Glu Lys	Lys Pro Tyr	Lys Asp Asp	Leu Tyr Phe	Leu Cys Lys	Phe		

170	175	180	185	
TTT TTG AAA ATT CCT AAG CAT TTT CAA ATG CAA AAC TTT AAC AAT ATT				688
Phe Leu Lys Ile Pro Lys His Phe Gln Met Gln Asn Phe Asn Asn Ile				
	190	195	200	
TTT TTG GAG TTT GTG TCG GTT AAT AAT CCT TGT TTT TCT TAT AGA TTG				736
Phe Leu Glu Phe Val Ser Val Asn Asn Pro Cys Phe Ser Tyr Arg Leu				
	205	210	215	
ACT TAT GAT CAA CTT GTT GGT AAA AAA ATT CCA AAT ATC AAG TGC TCT				784
Thr Tyr Asp Gln Leu Val Gly Lys Lys Ile Pro Asn Ile Lys Cys Ser				
	220	225	230	
TAC CAA CAA GCA ATT GTA AAA AAG AAT ATC CAT AGA GCA TTA GAT GAA				832
Tyr Gln Gln Ala Ile Val Lys Lys Asn Ile His Arg Ala Leu Asp Glu				
	235	240	245	
CTA TCT ATA GAT AAG GAA ATT TTA GCA TCA TAAAGAAGAC AAAGGATAAA AAT				885
Leu Ser Ile Asp Lys Glu Ile Leu Ala Ser				
	250	255		
GCAATTCCCA CTCAAAAAAG ATTTAAGA				913

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

Met	Gln	Glu	Arg	Val	Phe	Lys	Arg	Lys	Val	Leu	Asp	Ala	Asn	Ile	Leu
1				5					10					15	
Lys	Glu	Met	His	Ala	Asn	Asn	Val	Cys	Tyr	Ser	Lys	His	Ser	Lys	Asp
			20					25					30		
Arg	Phe	Ile	Pro	Phe	Lys	Phe	Asp	Lys	Phe	Gly	Tyr	Val	Gly	Cys	Lys
		35					40					45			
Leu	Phe	Lys	Lys	Ile	Leu	Asn	Phe	Pro	Ser	Asn	Thr	Thr	Phe	Phe	Gly
	50					55					60				
Gly	Thr	Gly	Cys	Lys	Lys	Leu	Met	Glu	Leu	Leu	Ser	Glu	Ile	Val	Ile
65					70					75				80	
Asp	Ser	Arg	Ser	Ser	Lys	Ile	Ala	Leu	Asn	Arg	His	Tyr	Ala	Leu	Thr
				85					90					95	
Arg	Leu	Gln	Trp	Cys	Asp	Arg	Thr	Leu	Arg	His	Asn	Leu	Gln	Ile	Leu
			100					105					110		
Glu	Arg	Ile	Gly	Phe	Leu	Thr	Ala	Phe	Lys	Asn	Lys	Lys	Gly	Tyr	Ile
		115					120					125			
Phe	Leu	Ser	Met	His	Asp	Phe	Thr	Lys	Ile	Glu	Asn	Tyr	Glu	His	Ser
	130						135					140			

(B) LOCATION: 86...862

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

ATTTCATATT TTCTTTTAGG GGCATTCTTT AGAGAATGCA ATTATTTTCT AATCTCTAAG	60
AAATCAATAT CTAGGAATTA GGACC ATG CAA GAA AGA GTT TTT AAA AGA AAA	112
Met Gln Glu Arg Val Phe Lys Arg Lys	
1 5	
GTT TTA GAT GCG AAT ATC TTA AAA GAA ATG CAT GCG AAC AAT GTC TGT	160
Val Leu Asp Ala Asn Ile Leu Lys Glu Met His Ala Asn Asn Val Cys	
10 15 20 25	
TAT TCC AAG CAT TCA AAA GAT AGG TTT ATT CCT TTC AAA TTT GAT AAA	208
Tyr Ser Lys His Ser Lys Asp Arg Phe Ile Pro Phe Lys Phe Asp Lys	
30 35 40	
TTT GGT TAT GTT GGA TGT AAA CTT TTT AAA AAG ATA TTA AAC TTT CCT	256
Phe Gly Tyr Val Gly Cys Lys Leu Phe Lys Lys Ile Leu Asn Phe Pro	
45 50 55	
AGC AAT ACA ACT TTC TTT GGT GGC ACA GGT TGT AAG AAA CTC ATG GAA	304
Ser Asn Thr Thr Phe Phe Gly Gly Thr Gly Cys Lys Lys Leu Met Glu	
60 65 70	
CTT TTA AGT GAA ATC GTT ATA GAT TCT AGA AGT TCT AAA ATT GCG TTA	352
Leu Leu Ser Glu Ile Val Ile Asp Ser Arg Ser Ser Lys Ile Ala Leu	
75 80 85	
AAC CGC CAT TAT GCC TTA ACT CGC TTG CAA TGG TGC GAT AGA ACC TTA	400
Asn Arg His Tyr Ala Leu Thr Arg Leu Gln Trp Cys Asp Arg Thr Leu	
90 95 100 105	
AGA CAT AAT CTC CAA ATT TTA GAG AGA ATA GGA TTT CTA ACT GCT TTT	448
Arg His Asn Leu Gln Ile Leu Glu Arg Ile Gly Phe Leu Thr Ala Phe	
110 115 120	
AAG AAC AAA AAA GGT TAT ATT TTT TTG TCT ATG CAT GAC TTC ACT AAA	496
Lys Asn Lys Lys Gly Tyr Ile Phe Leu Ser Met His Asp Phe Thr Lys	
125 130 135	
ATA GAA AAC TAC GAA CAT TCA GGT TTG AAT GGG GAG AGC AAT TTA CCT	544
Ile Glu Asn Tyr Glu His Ser Gly Leu Asn Gly Glu Ser Asn Leu Pro	
140 145 150	
AAT AGC TTC TTT TTA GGA ATT TGT GGG TAT TTG AAA AAA CTC TTC AAG	592
Asn Ser Phe Phe Leu Gly Ile Cys Gly Tyr Leu Lys Lys Leu Phe Lys	
155 160 165	
AAA TTA AAA GAT AGA GCA TTC AGG CTC GCA AAC AAG CAC GGT GTA TTC	640
Lys Leu Lys Asp Arg Ala Phe Arg Leu Ala Asn Lys His Gly Val Phe	

Glu Phe Leu Lys Glu Ile Glu Lys Asn Glu Ser Phe Phe
 180 185 190

GCGTGAAAAG CTAAGCCAAT TAAAAGCAAG GCAGCAAAAA C

676

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

Met	Asp	Glu	Val	Leu	Lys	Glu	Ile	Leu	Ser	Ser	Tyr	Gln	Lys	Arg	Ala	1	5	10	15
Leu	Lys	Leu	Thr	Lys	Arg	Val	Arg	Lys	Lys	Ile	Phe	Lys	Asn	Asp	Pro	20	25	30	
Thr	Glu	Asn	Gln	Lys	Lys	Ala	Ile	Lys	Ile	Ala	Leu	Asn	Thr	Pro	Asp	35	40	45	
Ile	Ala	Ile	Ile	Gln	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Thr	Val	Ile	50	55	60	
Asn	Ala	Ile	Cys	Glu	Arg	Leu	Phe	Glu	Glu	Tyr	Pro	Lys	Asp	Lys	Asn	65	70	75	80
Ile	Lys	Gly	Gln	Ile	Leu	Leu	Cys	Ala	Gln	Gly	His	Asp	Ala	Thr	Asn	85	90	95	
Asn	Ala	Arg	Glu	Arg	Ile	Lys	Val	Gly	Gly	Leu	Pro	Thr	Phe	Lys	Phe	100	105	110	
Gly	Ala	Lys	Lys	Asn	Ala	Lys	Glu	Glu	Gln	Tyr	Lys	Gln	Asp	Glu	Arg	115	120	125	
Leu	Asn	Glu	Arg	Leu	Arg	Glu	Phe	Ala	Glu	Thr	Leu	Ile	Glu	Ser	Val	130	135	140	
Arg	Lys	Lys	Leu	Gln	Lys	Leu	Gly	Asp	Tyr	Glu	Asn	Ile	Glu	Lys	Ile	145	150	155	160
Leu	Asp	Leu	Glu	Glu	Ala	Leu	Arg	Arg	Tyr	Tyr	Ser	Ser	Pro	Ile	Ser	165	170	175	
Glu	Leu	Glu	Phe	Leu	Lys	Glu	Ile	Glu	Lys	Asn	Glu	Ser	Phe	Phe		180	185	190	

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

TTAAAGAGGA TAAAGAGAAT AGTGATAGCG ATAATGATAC TGCAGACACG	ATG GAT	56
	Met Asp	
	1	
GAA GTC TTA AAA GAG ATT TTA TCA AGT TAT CAA AAA AGA GCT TTA AAA		104
Glu Val Leu Lys Glu Ile Leu Ser Ser Tyr Gln Lys Arg Ala Leu Lys		
5 10 15		
TTA ACC AAA AGA GTT AGA AAG AAG ATT TTT AAG AAT GAT CCC ACA GAA		152
Leu Thr Lys Arg Val Arg Lys Lys Ile Phe Lys Asn Asp Pro Thr Glu		
20 25 30		
AAT CAA AAA AAA GCC ATA AAG ATC GCT CTA AAT ACC CCT GAT ATT GCT		200
Asn Gln Lys Lys Ala Ile Lys Ile Ala Leu Asn Thr Pro Asp Ile Ala		
35 40 45 50		
ATT ATC CAA GGG CCT CCT GGA ACG GGC AAA ACC ACT GTG ATC AAT GCC		248
Ile Ile Gln Gly Pro Pro Gly Thr Gly Lys Thr Thr Val Ile Asn Ala		
55 60 65		
ATT TGT GAG AGA TTG TTT GAA GAA TAC CCT AAG GAT AAA AAT ATC AAG		296
Ile Cys Glu Arg Leu Phe Glu Glu Tyr Pro Lys Asp Lys Asn Ile Lys		
70 75 80		
GGG CAA ATT TTA CTG TGC GCT CAA GGG CAT GAT GCG ACT AAC AAT GCG		344
Gly Gln Ile Leu Leu Cys Ala Gln Gly His Asp Ala Thr Asn Asn Ala		
85 90 95		
CGT GAG CGC ATC AAA GTA GGG GGA TTG CCC ACT TTT AAA TTT GGT GCT		392
Arg Glu Arg Ile Lys Val Gly Gly Leu Pro Thr Phe Lys Phe Gly Ala		
100 105 110		
AAA AAA AAT GCT AAA GAA GAA CAA TAC AAG CAA GAT GAA AGA TTG AAT		440
Lys Lys Asn Ala Lys Glu Glu Gln Tyr Lys Gln Asp Glu Arg Leu Asn		
115 120 125 130		
GAG CGA TTG AGA GAG TTT GCT GAA ACG CTC ATA GAA AGC GTG AGA AAA		488
Glu Arg Leu Arg Glu Phe Ala Glu Thr Leu Ile Glu Ser Val Arg Lys		
135 140 145		
AAA CTG CAA AAA TTA GGG GAT TAT GAA AAT ATA GAA AAA ATT TTG GAT		536
Lys Leu Gln Lys Leu Gly Asp Tyr Glu Asn Ile Glu Lys Ile Leu Asp		
150 155 160		
TTA GAA GAA GCC CTT AGA CGC TAC TAT AGT TCG CCT ATC AGT GAA TTG		584
Leu Glu Glu Ala Leu Arg Arg Tyr Tyr Ser Ser Pro Ile Ser Glu Leu		
165 170 175		
GAA TTT TTA AAA GAA ATA GAA AAA AAT GAG AGC TTT TTT TAATTCCTCT AT		635

```

Asn Leu Tyr Ala Glu Leu Arg Lys Met Gly Ala Lys Asn Leu Asn Ser
    260                      265                      270
Val Asn Ile Gly Gly Gly Leu Ala Val Glu Tyr Thr Gln His Lys His
    275                      280                      285
His Gln Asp Lys Asn Tyr Thr Leu Glu Glu Phe Ser Ala Asp Val Val
    290                      295                      300
Phe Leu Leu Arg Glu Ile Val Lys Asn Lys Gln Glu Ile Glu Pro Asp
    305                      310                      315                      320
Ile Phe Ile Glu Ser Gly Arg Tyr Ile Ser Ala Asn His Ala Val Leu
    325                      330                      335
Val Ala Pro Val Leu Glu Leu Phe Ser His Glu Tyr Asn Glu Lys Ser
    340                      345                      350
Leu Lys Ile Lys Glu Asn Asn Asn Pro Pro Leu Ile Asp Glu Met Leu
    355                      360                      365
Asp Leu Leu Ala Asn Ile Asn Glu Lys Asn Ala Ile Glu Tyr Leu His
    370                      375                      380
Asp Ser Phe Asp His Thr Glu Ser Leu Phe Thr Leu Phe Asp Leu Gly
    385                      390                      395                      400
Tyr Ile Asp Leu Ile Asp Arg Ser Asn Thr Glu Val Leu Ala His Leu
    405                      410                      415
Ile Val Lys Lys Ala Val Gln Leu Leu Tyr Val Lys Asp His Asn Asp
    420                      425                      430
Ile Leu Arg Ile Gln Glu Gln Val Gln Glu Arg Tyr Leu Leu Asn Cys
    435                      440                      445
Ser Phe Phe Gln Ser Leu Pro Asp Tyr Trp Gly Leu Arg Gln Asn Phe
    450                      455                      460
Pro Val Met Pro Leu Asn Lys Leu Asp Glu Lys Pro Thr Arg Ser Ala
    465                      470                      475                      480
Ser Leu Trp Asp Ile Thr Cys Asp Ser Asp Gly Glu Ile Ala Phe Asp
    485                      490                      495
Ser Thr Lys Pro Leu Phe Leu His Asp Ile Asp Ile Asp Glu Glu Glu
    500                      505                      510
Tyr Phe Leu Ala Phe Phe Leu Val Gly Ala Tyr Gln Glu Val Leu Gly
    515                      520                      525
Met Lys His Asn Leu Phe Thr His Leu Arg Asn Leu Ala Trp Phe Leu
    530                      535                      540
Met Lys Lys Ala Ile Met Lys Trp Lys Ile Phe Val Lys Pro Lys Arg
    545                      550                      555                      560
Phe

```

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...623
- (D) OTHER INFORMATION:

CAC AAT TTA TTC ACG CAC CTA CGG AAT TTA GCG TGG TTT TTG ATG AAA 1688
 His Asn Leu Phe Thr His Leu Arg Asn Leu Ala Trp Phe Leu Met Lys
 535 540 545

AAG GCG ATT ATG AAG TGG AAG ATA TTT GTG AAG CCC AAA CGA TTT TAGAT 1738
 Lys Ala Ile Met Lys Trp Lys Ile Phe Val Lys Pro Lys Arg Phe
 550 555 560

GTGCTAGACG ATTTAGACTA TGACACTAAA GAGATCGAGC GCCTTTTA 1786

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

Met	Gln	Glu	Val	His	Asp	Tyr	Gly	Ile	Lys	Phe	Trp	Ser	Asn	Asn	Glu	1	5	10	15
Phe	Lys	Ile	Glu	Lys	Gly	Leu	Val	Lys	Val	Cys	His	Gly	Lys	Asn	Pro	20	25	30	
Ser	Leu	Leu	Glu	Ile	Val	Gln	Ser	Val	Arg	Asp	Lys	Gly	Tyr	Arg	Gly	35	40	45	
Pro	Leu	Leu	Val	Arg	Phe	Pro	His	Leu	Val	Gln	Lys	Gln	Ile	Lys	Ser	50	55	60	
Leu	Phe	Asp	Ala	Phe	Ser	Ser	Ala	Ile	Lys	Glu	Tyr	Gln	Tyr	Ser	Gly	65	70	75	80
Ala	Phe	Lys	Ala	Val	Phe	Pro	Leu	Lys	Val	Asn	Gln	Met	Pro	Ser	Phe	85	90	95	
Val	Phe	Pro	Leu	Val	Gln	Gly	Ala	Lys	Gly	Leu	Asn	Tyr	Gly	Leu	Glu	100	105	110	
Ala	Gly	Ser	Lys	Ser	Glu	Leu	Ile	Ile	Ala	Met	Ser	Tyr	Thr	Asn	Pro	115	120	125	
Lys	Ala	Pro	Ile	Thr	Val	Asn	Gly	Phe	Lys	Asp	Lys	Glu	Met	Ile	Glu	130	135	140	
Leu	Gly	Phe	Ile	Ala	Lys	Ser	Met	Gln	His	Glu	Ile	Thr	Leu	Thr	Ile	145	150	155	160
Glu	Gly	Leu	Asn	Glu	Leu	Lys	Thr	Ile	Ile	Ala	Val	Ala	Lys	Gln	Asn	165	170	175	
Glu	Phe	Leu	Ala	Cys	Pro	Lys	Ile	Gly	Ile	Arg	Ile	Arg	Leu	His	Ser	180	185	190	
Thr	Gly	Thr	Gly	Val	Trp	Ala	Lys	Ser	Gly	Gly	Ile	Asn	Ser	Lys	Phe	195	200	205	
Gly	Leu	Ser	Ser	Thr	Glu	Val	Leu	Glu	Ala	Met	Arg	Leu	Leu	Glu	Glu	210	215	220	
Asn	Asp	Leu	Leu	Glu	His	Phe	His	Met	Ile	His	Phe	His	Ile	Gly	Ser	225	230	235	240
Gln	Ile	Ser	Asp	Ile	Ser	Pro	Leu	Lys	Lys	Ala	Leu	Arg	Glu	Ala	Gly	245	250	255	

TTG AGA GAA ATT GTG AAA AAT AAG CAG GAA ATC GAG CCG GAC ATT TTC	1016
Leu Arg Glu Ile Val Lys Asn Lys Gln Glu Ile Glu Pro Asp Ile Phe	
310 315 320	
ATT GAA TCA GGC CGT TAT ATT TCC GCT AAC CAT GCC GTT TTA GTG GCC	1064
Ile Glu Ser Gly Arg Tyr Ile Ser Ala Asn His Ala Val Leu Val Ala	
325 330 335	
CCG GTG TTA GAA TTG TTT TCG CAT GAA TAC AAT GAA AAA TCC CTA AAA	1112
Pro Val Leu Glu Leu Phe Ser His Glu Tyr Asn Glu Lys Ser Leu Lys	
340 345 350	
ATC AAA GAA AAT AAT AAC CCC CCT TTG ATT GAT GAA ATG CTA GAC TTG	1160
Ile Lys Glu Asn Asn Asn Pro Pro Leu Ile Asp Glu Met Leu Asp Leu	
355 360 365 370	
CTC GCT AAT ATC AAT GAA AAA AAC GCC ATT GAA TAC TTG CAT GAT AGT	1208
Leu Ala Asn Ile Asn Glu Lys Asn Ala Ile Glu Tyr Leu His Asp Ser	
375 380 385	
TTT GAT CAC ACC GAG TCG CTA TTC ACG CTT TTT GAT CTG GGC TAT ATT	1256
Phe Asp His Thr Glu Ser Leu Phe Thr Leu Phe Asp Leu Gly Tyr Ile	
390 395 400	
GAT TTG ATT GAC AGG AGC AAC ACT GAA GTT TTA GCC CAT TTG ATC GTC	1304
Asp Leu Ile Asp Arg Ser Asn Thr Glu Val Leu Ala His Leu Ile Val	
405 410 415	
AAA AAA GCG GTG CAA TTG CTT TAT GTT AAG GAT CAT AAC GAT ATT TTA	1352
Lys Lys Ala Val Gln Leu Leu Tyr Val Lys Asp His Asn Asp Ile Leu	
420 425 430	
CGC ATT CAA GAG CAG GTC CAA GAG CGC TAT TTA TTG AAT TGC TCG TTT	1400
Arg Ile Gln Glu Gln Val Gln Glu Arg Tyr Leu Leu Asn Cys Ser Phe	
435 440 445 450	
TTC CAA AGC TTG CCG GAT TAT TGG GGC TTG AGA CAG AAT TTC CCG GTC	1448
Phe Gln Ser Leu Pro Asp Tyr Trp Gly Leu Arg Gln Asn Phe Pro Val	
455 460 465	
ATG CCC TTG AAT AAA TTA GAT GAA AAG CCC ACC AGG AGT GCG AGC TTG	1496
Met Pro Leu Asn Lys Leu Asp Glu Lys Pro Thr Arg Ser Ala Ser Leu	
470 475 480	
TGG GAT ATT ACT TGC GAT AGC GAT GGG GAA ATC GCT TTT GAT TCC ACG	1544
Trp Asp Ile Thr Cys Asp Ser Asp Gly Glu Ile Ala Phe Asp Ser Thr	
485 490 495	
AAG CCC TTG TTT TTG CAC GAT ATA GAT ATA GAT GAA GAA GAA TAC TTT	1592
Lys Pro Leu Phe Leu His Asp Ile Asp Ile Asp Glu Glu Glu Tyr Phe	
500 505 510	
TTA GCG TTC TTT TTA GTG GGA GCG TAT CAA GAA GTT TTA GGC ATG AAA	1640
Leu Ala Phe Phe Leu Val Gly Ala Tyr Gln Glu Val Leu Gly Met Lys	
515 520 525 530	

AAG GCG GTT TTC CCT TTA AAA GTC AAT CAA ATG CCC TCG TTT GTT TTC	344
Lys Ala Val Phe Pro Leu Lys Val Asn Gln Met Pro Ser Phe Val Phe	
85 90 95	
CCT TTA GTG CAG GGG GCT AAG GGT TTG AAT TAC GGA TTA GAG GCT GGG	392
Pro Leu Val Gln Gly Ala Lys Gly Leu Asn Tyr Gly Leu Glu Ala Gly	
100 105 110	
AGC AAG TCT GAA CTC ATC ATC GCA ATG AGT TAC ACT AAC CCT AAA GCC	440
Ser Lys Ser Glu Leu Ile Ile Ala Met Ser Tyr Thr Asn Pro Lys Ala	
115 120 125 130	
CCT ATC ACC GTG AAT GGC TTT AAA GAC AAA GAA ATG ATT GAG CTT GGC	488
Pro Ile Thr Val Asn Gly Phe Lys Asp Lys Glu Met Ile Glu Leu Gly	
135 140 145	
TTT ATC GCT AAA AGC ATG CAG CAT GAG ATC ACT TTA ACG ATT GAG GGT	536
Phe Ile Ala Lys Ser Met Gln His Glu Ile Thr Leu Thr Ile Glu Gly	
150 155 160	
TTG AAT GAA TTG AAA ACC ATT ATC GCC GTG GCT AAA CAA AAC GAG TTT	584
Leu Asn Glu Leu Lys Thr Ile Ile Ala Val Ala Lys Gln Asn Glu Phe	
165 170 175	
TTA GCC TGC CCT AAA ATT GGC ATC CGC ATC CGT TTG CAC AGC ACT GGC	632
Leu Ala Cys Pro Lys Ile Gly Ile Arg Ile Arg Leu His Ser Thr Gly	
180 185 190	
ACT GGC GTT TGG GCA AAG AGT GGG GGG ATC AAT TCT AAA TTT GGT CTT	680
Thr Gly Val Trp Ala Lys Ser Gly Gly Ile Asn Ser Lys Phe Gly Leu	
195 200 205 210	
AGC AGC ACT GAA GTT TTA GAG GCG ATG CGC CTT TTA GAA GAA AAC GAC	728
Ser Ser Thr Glu Val Leu Glu Ala Met Arg Leu Leu Glu Glu Asn Asp	
215 220 225	
TTG TTA GAG CAT TTC CAC ATG ATA CAT TTC CAT ATA GGC TCT CAA ATC	776
Leu Leu Glu His Phe His Met Ile His Phe His Ile Gly Ser Gln Ile	
230 235 240	
AGC GAT ATT TCG CCC TTA AAA AAG GCT TTA AGA GAA GCG GGT AAC TTG	824
Ser Asp Ile Ser Pro Leu Lys Lys Ala Leu Arg Glu Ala Gly Asn Leu	
245 250 255	
TAT GCA GAA TTG CGT AAA ATG GGC GCT AAA AAT CTT AAT AGC GTG AAT	872
Tyr Ala Glu Leu Arg Lys Met Gly Ala Lys Asn Leu Asn Ser Val Asn	
260 265 270	
ATT GGA GGG GGG TTA GCC GTA GAA TAC ACC CAA CAC AAG CAC CAA	920
Ile Gly Gly Gly Leu Ala Val Glu Tyr Thr Gln His Lys His His Gln	
275 280 285 290	
GAC AAA AAC TAC ACT TTA GAG GAA TTC AGC GCT GAT GTG GTG TTT TTA	968
Asp Lys Asn Tyr Thr Leu Glu Glu Phe Ser Ala Asp Val Val Phe Leu	
295 300 305	

```

Val His Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu
65              70              75              80
Val Asn Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His
              85              90              95
Phe Lys Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro
              100             105             110
Ser Tyr Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys
              115             120             125
Gln Tyr Ile Gln Asp Gln Glu Thr Pro His
              130             135

```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1733
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

```

AAAAATAACC CCCATCTCTT TAAAACCTTA TCATAATGAA AGGATAAAAA  ATG CAA      56
                                     Met Gln
                                     1

GAA GTC CAT GAT TAT GGG ATT AAA TTT TGG AGC AAT AAC GAA TTT AAG      104
Glu Val His Asp Tyr Gly Ile Lys Phe Trp Ser Asn Asn Glu Phe Lys
              5              10              15

ATA GAA AAA GGC TTG GTT AAA GTC TGT CAT GGT AAA AAC CCC TCG CTT      152
Ile Glu Lys Gly Leu Val Lys Val Cys His Gly Lys Asn Pro Ser Leu
              20              25              30

TTA GAA ATC GTT CAA AGC GTG CGC GAT AAG GGC TAT AGA GGA CCT TTG      200
Leu Glu Ile Val Gln Ser Val Arg Asp Lys Gly Tyr Arg Gly Pro Leu
              35              40              45              50

TTG GTG CGA TTC CCC CAT TTG GTG CAA AAA CAA ATC AAA AGC CTG TTT      248
Leu Val Arg Phe Pro His Leu Val Gln Lys Gln Ile Lys Ser Leu Phe
              55              60              65

GAT GCG TTT TCT TCA GCG ATT AAA GAG TAT CAA TAC AGC GGG GCT TTT      296
Asp Ala Phe Ser Ser Ala Ile Lys Glu Tyr Gln Tyr Ser Gly Ala Phe
              70              75              80

```

GTG CAT TTT GTA TTT GTT ACT AAA TAC AGG CGT TCA GCA TTC AAT AAG	152
Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe Asn Lys	
20 25 30	
GAA GTG ATA GAT TTT TTA GGA TCG GTG TTT GCC AAA GTG TGT AAG GAC	200
Glu Val Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys Lys Asp	
35 40 45 50	
TTT GAG AGC GAA TTG GTA GAA TTT GAT GGG GAG AGC GAT CAT GTG CAT	248
Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His Val His	
55 60 65	
TTG CTT ATC AAC TAC CCT CCA AAA GTG AGC GTG AGT AAG TTA GTT AAT	296
Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu Val Asn	
70 75 80	
TCT TTA AAA GGC GTT AGC AGT CGT TTG ACT AGA CAA CAC CAT TTC AAA	344
Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His Phe Lys	
85 90 95	
AGC GTT GAA GCT AGT TTG TGG GGG AAG CAT TTA TGG TCG CCT AGT TAT	392
Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro Ser Tyr	
100 105 110	
TTC GCT GGG AGT TGT GGG GAC GCG CCT TTA GAG ATG ATT AAG CAA TAC	440
Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys Gln Tyr	
115 120 125 130	
ATA CAA GAT CAA GAA ACA CCG CAT TAAATTAGCT AACTTTGATT TTTAAGTAGA	494
Ile Gln Asp Gln Glu Thr Pro His	
135	
ACGCGCTAAA AAGCGAATGG ATC	517

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

Met Lys Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu	
1 5 10 15	
Met His Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe	
20 25 30	
Asn Lys Glu Val Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys	
35 40 45	
Lys Asp Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His	
50 55 60	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

```

Met Gln Asp Thr Phe Tyr Phe Lys Asp His Lys Leu Leu Arg Thr His
 1           5           10           15
Thr Ser Pro Val Gln Ile His Thr Met Gln Glu Gln Thr Pro Pro Ile
           20           25           30
Lys Met Ile Cys Leu Gly Glu Thr Phe Arg Arg Asp Tyr Asp Leu Thr
           35           40           45
His Thr Pro Met Phe His Gln Ile Glu Gly Leu Val Val Asp Gln Lys
           50           55           60
Gly Asn Ile Arg Phe Thr His Leu Lys Gly Val Ile Glu Asp Phe Leu
65           70           75           80
His Tyr Phe Phe Gly Gly Val Lys Leu Arg Trp Arg Ser Ser Phe Phe
           85           90           95
Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Ile Ser Cys Val Phe Cys
           100          105          110
Lys Gln Glu Gly Cys Arg Val Cys Ser His Thr Gly Trp Leu Glu Val
           115          120          125
Leu Gly Cys Gly Met Val Asn Asn Ala Val Phe Glu Ala Ile Gly Tyr
           130          135          140
Glu Asn Val Ser Gly Phe Ala Phe Gly Met Gly Ile Glu Arg Leu Ala
145           150          155          160
Met Leu Thr Cys Gln Ile Asn Asp Leu Arg Ser Phe Phe Glu Thr Asp
           165          170          175
Leu Arg Val Leu Glu Ser Phe
           180

```

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...464
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

```

TATTGACTTT CATAGAAAGT ATTTTAACCT CTTTTTGTTA AAATAGGTCT ATG AAA      56
                               Met Lys
                               1

AAA ATT GAT GAT ATG AGA CAC GGA AGA CAT TGT GTT TTT TTA ATG CAT      104
Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu Met His
      5              10              15

```

Arg	Thr	His	Thr	Ser	Pro	Val	Gln	Ile	His	Thr	Met	Gln	Glu	Gln	Thr	
15						20					25					
CCA	CCC	ATT	AAG	ATG	ATT	TGT	TTA	GGC	GAA	ACC	TTT	AGG	CGC	GAT	TAT	626
Pro	Pro	Ile	Lys	Met	Ile	Cys	Leu	Gly	Glu	Thr	Phe	Arg	Arg	Asp	Tyr	
30					35					40					45	
GAT	TTG	ACC	CAC	ACG	CCC	ATG	TTC	CAC	CAA	ATT	GAA	GGG	CTT	GTC	GTG	674
Asp	Leu	Thr	His	Thr	Pro	Met	Phe	His	Gln	Ile	Glu	Gly	Leu	Val	Val	
				50					55					60		
GAT	CAA	AAA	GGG	AAT	ATC	CGT	TTC	ACA	CAT	TTA	AAA	GGT	GTG	ATC	GAA	722
Asp	Gln	Lys	Gly	Asn	Ile	Arg	Phe	Thr	His	Leu	Lys	Gly	Val	Ile	Glu	
			65					70					75			
GAC	TTT	TTG	CAT	TAT	TTC	TTT	GGG	GGC	GTG	AAG	TTA	AGG	TGG	CGC	TCT	770
Asp	Phe	Leu	His	Tyr	Phe	Phe	Gly	Gly	Val	Lys	Leu	Arg	Trp	Arg	Ser	
		80					85					90				
AGC	TTT	TTC	CCT	TTC	ACA	GAG	CCA	AGC	GCT	GAA	GTG	GAT	ATT	AGT	TGC	818
Ser	Phe	Phe	Pro	Phe	Thr	Glu	Pro	Ser	Ala	Glu	Val	Asp	Ile	Ser	Cys	
		95				100					105					
GTG	TTT	TGC	AAG	CAA	GAA	GGC	TGT	AGG	GTT	TGC	TCG	CAC	ACA	GGC	TGG	866
Val	Phe	Cys	Lys	Gln	Glu	Gly	Cys	Arg	Val	Cys	Ser	His	Thr	Gly	Trp	
110					115					120				125		
TTA	GAA	GTG	TTG	GGC	TGT	GGC	ATG	GTC	AAT	AAT	GCG	GTG	TTT	GAA	GCC	914
Leu	Glu	Val	Leu	Gly	Cys	Gly	Met	Val	Asn	Asn	Ala	Val	Phe	Glu	Ala	
				130					135					140		
ATA	GGG	TAT	GAG	AAT	GTG	AGC	GGG	TTT	GCT	TTT	GGC	ATG	GGG	ATT	GAA	962
Ile	Gly	Tyr	Glu	Asn	Val	Ser	Gly	Phe	Ala	Phe	Gly	Met	Gly	Ile	Glu	
			145					150					155			
AGA	TTA	GCC	ATG	CTG	ACT	TGC	CAG	ATC	AAT	GAT	TTG	CGC	AGT	TTC	TTT	1010
Arg	Leu	Ala	Met	Leu	Thr	Cys	Gln	Ile	Asn	Asp	Leu	Arg	Ser	Phe	Phe	
		160					165					170				
GAA	ACT	GAT	TTG	AGA	GTG	TTG	GAG	AGC	TTT	TAATGAAACT	GAGCATTAAAT	GAT				1063
Glu	Thr	Asp	Leu	Arg	Val	Leu	Glu	Ser	Phe							
		175				180										
TTGAATGTTT	TTGTCAATAC	GCCTAAAGAT	ATAG													1097

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(2) INFORMATION FOR SEO ID NO:699:

(A) LENGTH: 1097 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 492...1040
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:699:

- 1069 -

```

Ser Leu Thr Pro Asn Arg Gly Asp Cys Leu Ser Val Leu Gly Ile Ala
165 170 175
Arg Glu Ile Ser Ala Phe Tyr His Thr Pro Leu Lys Pro Ile Lys Ala
180 185 190
Leu Asn Phe Thr Pro Lys Ser Gly Leu Ile Thr Leu Ser Ala Gly Glu
195 200 205
Asn Ile Glu Ser His Leu Ala Tyr Tyr Leu Ile Cys Asn His Ser Leu
210 215 220
Lys Thr Pro Leu Asn Ile Lys Leu Ser Leu Ala His Asn Asn Ala Leu
225 230 235 240
Ser Glu Asn Asp Leu Asn Asn Phe Ile Glu Phe Ser Thr His Phe Ser
245 250 255
Gly Val Ile Met Asn Ala Tyr Ser Leu Asn Thr Thr Pro Met Asp Leu
260 265 270
Ser Val Lys Asn Asp Glu Asn Asn Leu Glu Ser Val Tyr Ile Asn His
275 280 285
Gln Lys Arg Ser Thr Ile Ala Ile Lys His Gln Val Gln Lys Asp Leu
290 295 300
Ser Glu Cys Leu Leu Leu Glu Ala Ser Tyr Thr Asp Pro Ile Ser Leu
305 310 315 320
Ser Leu Lys Leu His Ala Leu Lys Asp Lys Thr Leu Gln Lys Asp Asn
325 330 335
Ala Leu Ile Tyr Arg Ser Ala Arg Gly Ser Asn Pro Asn Leu Ser Asp
340 345 350
Gly Leu Asn Phe Leu Ser Ala His Leu Lys Ala Thr Ile Leu Glu Ser
355 360 365
Lys Gln Thr Glu His Ser Leu Lys Asp Arg Thr Leu Thr Phe Gln Leu
370 375 380
Glu Asp Ile Thr Glu Ile Leu Gly Leu Ala Val Glu Lys Glu Lys Ile
385 390 395 400
Gln Gly Ile Leu Lys Asn Leu Gly Phe Lys Val Ser Val Lys Glu Pro
405 410 415
Asn Ser Lys Pro Gln Ile Leu Glu Val Ile Ala Pro Asn Phe Arg His
420 425 430
Asp Ile Lys Thr Ile Gln Asp Ile Ala Glu Glu Ile Leu Arg Phe Val
435 440 445
Gly Ile Asp Asn Leu Val Ser Lys Pro Leu His Cys Val Ser Ser Lys
450 455 460
Asn Ser Asn Pro Asn Tyr Asp Thr His Arg Phe Phe Glu Asn Leu Lys
465 470 475 480
His Lys Ala Leu Ala Cys Gly Phe Lys Glu Val Ile His Tyr Val Phe
485 490 495
Tyr Ser Lys Glu Lys Gln Gln Lys Leu Gly Phe Glu Val Leu Glu Asp
500 505 510
Pro Leu Glu Leu Gln Asn Pro Ile Thr Thr Glu Leu Asn Thr Leu Arg
515 520 525
Thr Ser Leu Val Cys Gly Leu Leu Asp Ala Ser Leu Arg Asn Lys Asn
530 535 540
Leu Gly Phe Lys Ser Ile Ala Leu Tyr Glu Lys Gly Ser Val Tyr Asn
545 550 555 560
Ser Lys Arg Glu Glu Ile Gln Lys Leu Gly Phe Leu Ile Ser Gly Leu
565 570 575
Gln Lys Lys Glu Ser Tyr Pro Asp Thr Lys Gly Lys Ala Trp Asp Phe
580 585 590
Tyr Ser Phe Ala Glu Cys Val Ser Lys Val Ile Gly Asp Phe Ser Leu

```

CTA AAG GAC GCT CAA ATC CCT AAT TTA AGC GAG ATT CTA CCC CTT GAT 2223
 Leu Lys Asp Ala Gln Ile Pro Asn Leu Ser Glu Ile Leu Pro Leu Asp
 700 705 710

ATT TTT AAA GAA AGT AAT AAT TCC ATA GCC TTA AGC GTG CGT TGC GTG 2271
 Ile Phe Lys Glu Ser Asn Asn Ser Ile Ala Leu Ser Val Arg Cys Val
 715 720 725 730

ATC CAT TCT TTA GAA AAA ACC CTG AAT GAT GAA GAG GTC AAT TCA GCC 2319
 Ile His Ser Leu Glu Lys Thr Leu Asn Asp Glu Glu Val Asn Ser Ala
 735 740 745

GTG CAA AAA GCA CTT GAA ATT TTA GAA AAA GAA TTT AAC GCC CGC CTT 2367
 Val Gln Lys Ala Leu Glu Ile Leu Glu Lys Glu Phe Asn Ala Arg Leu
 750 755 760

AAA GGA TAATATAAAG GATAATATGT GATAGAGCTT GACATTAACG CTAGCGATAA AT 2425
 Lys Gly

CGCTCTCACA CAG 2438

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

Met Lys Leu Ser Ile Asn Asp Leu Asn Val Phe Val Asn Thr Pro Lys
 1 5 10 15
 Asp Ile Ala Lys Leu Cys Glu Asp Leu Ser Arg Leu Gly Leu Glu Val
 20 25 30
 Glu Ser Cys Ile Pro Cys Ile Ala Pro Lys Asn Val Val Val Gly Lys
 35 40 45
 Ile Leu Glu Lys Ala Pro His Lys Asn Ala Glu Lys Leu Ser Val Cys
 50 55 60
 Gln Val Asp Val Gly Lys Glu Val Leu Gln Ile Val Cys Gly Ala Lys
 65 70 75 80
 Asn Val Ala Pro Asn Gln Phe Val Pro Val Ala Leu Asn Gly Ala Leu
 85 90 95
 Ile Gly Ser Thr Thr Ile Ala Lys Thr Glu Leu Arg Gly Val Glu Ser
 100 105 110
 His Gly Met Ile Cys Ser Ser Ile Glu Leu Gly Phe Pro Lys Ile Asn
 115 120 125
 Asp Gly Ile Leu Glu Leu Asp Glu Ser Val Gly Glu Leu Val Leu Gly
 130 135 140
 Lys Glu Leu Asn Glu Tyr Ala Pro Phe Asn Thr His Val Leu Glu Ile
 145 150 155 160

TTT TTT GAA AAC CTT AAA CAC AAG GCT CTC GCT TGC GGT TTT AAA GAA	1551
Phe Phe Glu Asn Leu Lys His Lys Ala Leu Ala Cys Gly Phe Lys Glu	
475 480 485 490	
GTC ATT CAT TAC GTG TTT TAC TCT AAA GAA AAA CAG CAA AAA TTA GGC	1599
Val Ile His Tyr Val Phe Tyr Ser Lys Glu Lys Gln Gln Lys Leu Gly	
495 500 505	
TTT GAA GTT TTA GAA GAT CCC CTA GAA TTG CAA AAC CCT ATC ACA ACG	1647
Phe Glu Val Leu Glu Asp Pro Leu Glu Leu Gln Asn Pro Ile Thr Thr	
510 515 520	
GAG TTA AAC ACC CTA AGG ACG AGT CTT GTT TGC GGG CTT TTA GAC GCC	1695
Glu Leu Asn Thr Leu Arg Thr Ser Leu Val Cys Gly Leu Leu Asp Ala	
525 530 535	
AGT TTA AGG AAT AAA AAT TTA GGG TTT AAA AGC ATA GCC CTT TAT GAA	1743
Ser Leu Arg Asn Lys Asn Leu Gly Phe Lys Ser Ile Ala Leu Tyr Glu	
540 545 550	
AAG GGG AGC GTG TAT AAC TCT AAA AGA GAA GAA ATC CAA AAA CTA GGC	1791
Lys Gly Ser Val Tyr Asn Ser Lys Arg Glu Glu Ile Gln Lys Leu Gly	
555 560 565 570	
TTT TTA ATA AGC GGC TTG CAA AAA AAA GAA AGC TAC CCT GAT ACT AAG	1839
Phe Leu Ile Ser Gly Leu Gln Lys Lys Glu Ser Tyr Pro Asp Thr Lys	
575 580 585	
GGC AAG GCT TGG GAT TTT TAC TCT TTT GCC GAA TGC GTT TCA AAA GTT	1887
Gly Lys Ala Trp Asp Phe Tyr Ser Phe Ala Glu Cys Val Ser Lys Val	
590 595 600	
ATA GGG GAT TTC AGC TTG GAA AAA CTA ACC ACT CAA ACC CCC ATT AAC	1935
Ile Gly Asp Phe Ser Leu Glu Lys Leu Thr Thr Gln Thr Pro Ile Asn	
605 610 615	
CAC CCC TAC CAG AGC GCT AAA ATC ATT CAA AAT CAT GAA ATC ATA GGC	1983
His Pro Tyr Gln Ser Ala Lys Ile Ile Gln Asn His Glu Ile Ile Gly	
620 625 630	
GTG ATC GCT AAA ATC CAC CCT AAA GTG ATC CAG GAA TTG GAT TTG TTT	2031
Val Ile Ala Lys Ile His Pro Lys Val Ile Gln Glu Leu Asp Leu Phe	
635 640 645 650	
GAA AGC TAT TAC GCT GAG ATA GAC GCT TTT AAA CTC AAA CGC CCT GCT	2079
Glu Ser Tyr Tyr Ala Glu Ile Asp Ala Phe Lys Leu Lys Arg Pro Ala	
655 660 665	
ATG CTA TTA AAA CCC TTT AGC ATT TAT CCT AGC AGT GTT AGG GAT TTG	2127
Met Leu Leu Lys Pro Phe Ser Ile Tyr Pro Ser Ser Val Arg Asp Leu	
670 675 680	
ACT CTC ATC ATT GAT GAG AAT ACC GCT TTT AGT GGG ATT AAA AAA GCC	2175
Thr Leu Ile Ile Asp Glu Asn Thr Ala Phe Ser Gly Ile Lys Lys Ala	
685 690 695	

Phe Ser Thr His	Phe Ser Gly Val Ile Met Asn Ala Tyr Ser Leu Asn	
	255 260 265	
ACA ACC CCT ATG GAT TTG AGC GTG AAA AAC GAT GAA AAC AAC CTT GAA		927
Thr Thr Pro Met Asp Leu Ser Val Lys Asn Asp Glu Asn Asn Leu Glu	270 275 280	
AGC GTT TAT ATC AAC CAT CAA AAA CGC TCC ACG ATC GCT ATC AAG CAT		975
Ser Val Tyr Ile Asn His Gln Lys Arg Ser Thr Ile Ala Ile Lys His	285 290 295	
CAA GTT CAA AAA GAT TTG AGC GAG TGT TTG CTT TTA GAG GCA AGT TAC		1023
Gln Val Gln Lys Asp Leu Ser Glu Cys Leu Leu Leu Glu Ala Ser Tyr	300 305 310	
ACC GAT CCG ATA AGC CTG TCT TTA AAA TTA CAC GCC CTA AAA GAT AAA		1071
Thr Asp Pro Ile Ser Leu Ser Leu Lys Leu His Ala Leu Lys Asp Lys	315 320 325 330	
ACG CTT CAA AAA GAC AAC GCC CTT ATT TAT AGA AGC GCT AGG GGG AGT		1119
Thr Leu Gln Lys Asp Asn Ala Leu Ile Tyr Arg Ser Ala Arg Gly Ser	335 340 345	
AAC CCT AAT TTA TCA GAC GGC TTG AAT TTT TTA AGC GCT CAT TTG AAA		1167
Asn Pro Asn Leu Ser Asp Gly Leu Asn Phe Leu Ser Ala His Leu Lys	350 355 360	
GCC ACG ATT TTA GAA AGC AAA CAA ACT GAG CAT TCT TTA AAA GAT CGC		1215
Ala Thr Ile Leu Glu Ser Lys Gln Thr Glu His Ser Leu Lys Asp Arg	365 370 375	
ACC CTT ACA TTC CAG CTT GAA GAC ATT ACT GAA ATT TTG GGG CTT GCT		1263
Thr Leu Thr Phe Gln Leu Glu Asp Ile Thr Glu Ile Leu Gly Leu Ala	380 385 390	
GTA GAG AAA GAA AAA ATT CAA GGC ATT TTA AAA AAT TTA GGC TTT AAA		1311
Val Glu Lys Glu Lys Ile Gln Gly Ile Leu Lys Asn Leu Gly Phe Lys	395 400 405 410	
GTC AGC GTA AAA GAG CCA AAC TCA AAA CCC CAA ATT TTA GAG GTT ATT		1359
Val Ser Val Lys Glu Pro Asn Ser Lys Pro Gln Ile Leu Glu Val Ile	415 420 425	
GCG CCA AAT TTC AGG CAT GAC ATT AAA ACG ATC CAA GAT ATT GCT GAA		1407
Ala Pro Asn Phe Arg His Asp Ile Lys Thr Ile Gln Asp Ile Ala Glu	430 435 440	
GAA ATT TTG CGC TTT GTA GGG ATT GAT AAT CTA GTC TCA AAG CCC CTT		1455
Glu Ile Leu Arg Phe Val Gly Ile Asp Asn Leu Val Ser Lys Pro Leu	445 450 455	
CAT TGT GTC AGT AGC AAA AAT TCA AAC CCC AAT TAC GAC ACG CAC CGC		1503
His Cys Val Ser Ser Lys Asn Ser Asn Pro Asn Tyr Asp Thr His Arg	460 465 470	

30					35					40						
AAT	GTG	GTT	GTG	GGT	AAA	ATT	TTA	GAA	AAA	GCC	CCC	CAT	AAA	AAC	GCT	255
Asn	Val	Val	Val	Gly	Lys	Ile	Leu	Glu	Lys	Ala	Pro	His	Lys	Asn	Ala	
45					50					55						
GAA	AAA	CTC	AGC	GTG	TGT	CAA	GTG	GAT	GTG	GGT	AAA	GAA	GTG	TTG	CAA	303
Glu	Lys	Leu	Ser	Val	Cys	Gln	Val	Asp	Val	Gly	Lys	Glu	Val	Leu	Gln	
60					65					70						
ATC	GTG	TGT	GGG	GCT	AAA	AAT	GTC	GCG	CCA	AAC	CAA	TTC	GTG	CCA	GTC	351
Ile	Val	Cys	Gly	Ala	Lys	Asn	Val	Ala	Pro	Asn	Gln	Phe	Val	Pro	Val	
75					80					85					90	
GCT	TTA	AAC	GGG	GCG	CTA	ATC	GGC	TCA	ACC	ACC	ATC	GCT	AAA	ACG	GAG	399
Ala	Leu	Asn	Gly	Ala	Leu	Ile	Gly	Ser	Thr	Thr	Ile	Ala	Lys	Thr	Glu	
95					100					105						
CTT	AGG	GGG	GTT	GAA	AGC	CAT	GGC	ATG	ATT	TGC	TCT	AGC	ATT	GAA	TTA	447
Leu	Arg	Gly	Val	Glu	Ser	His	Gly	Met	Ile	Cys	Ser	Ser	Ile	Glu	Leu	
110					115					120						
GGC	TTC	CCT	AAA	ATC	AAT	GAT	GGC	ATC	TTG	GAA	TTA	GAT	GAG	AGC	GTT	495
Gly	Phe	Pro	Lys	Ile	Asn	Asp	Gly	Ile	Leu	Glu	Leu	Asp	Glu	Ser	Val	
125					130					135						
GGG	GAG	TTG	GTT	TTA	GGG	AAA	GAA	TTA	AAC	GAA	TAC	GCC	CCT	TTC	AAC	543
Gly	Glu	Leu	Val	Leu	Gly	Lys	Glu	Leu	Asn	Glu	Tyr	Ala	Pro	Phe	Asn	
140					145					150						
ACG	CAT	GTT	TTA	GAA	ATT	TCA	TTG	ACT	CCC	AAT	CGT	GGG	GAT	TGC	TTG	591
Thr	His	Val	Leu	Glu	Ile	Ser	Leu	Thr	Pro	Asn	Arg	Gly	Asp	Cys	Leu	
155					160					165					170	
AGC	GTT	TTA	GGT	ATT	GCC	AGA	GAA	ATT	AGC	GCC	TTT	TAT	CAC	ACG	CCC	639
Ser	Val	Leu	Gly	Ile	Ala	Arg	Glu	Ile	Ser	Ala	Phe	Tyr	His	Thr	Pro	
175					180					185						
CTA	AAG	CCT	ATT	AAG	GCT	TTA	AAT	TTT	ACG	CCC	AAA	AGC	GGT	TTG	ATC	687
Leu	Lys	Pro	Ile	Lys	Ala	Leu	Asn	Phe	Thr	Pro	Lys	Ser	Gly	Leu	Ile	
190					195					200						
ACG	CTT	AGT	GCG	GGT	GAA	AAT	ATT	GAA	TCG	CAT	CTG	GCT	TAT	TAT	TTG	735
Thr	Leu	Ser	Ala	Gly	Glu	Asn	Ile	Glu	Ser	His	Leu	Ala	Tyr	Tyr	Leu	
205					210					215						
ATT	TGC	AAC	CAT	TCA	TTA	AAA	ACC	CCT	TTA	AAT	ATC	AAA	CTT	TCG	CTC	783
Ile	Cys	Asn	His	Ser	Leu	Lys	Thr	Pro	Leu	Asn	Ile	Lys	Leu	Ser	Leu	
220					225					230						
GCT	CAT	AAT	AAT	GCC	TTG	AGT	GAG	AAC	GAT	CTG	AAC	AAT	TTC	ATA	GAA	831
Ala	His	Asn	Asn	Ala	Leu	Ser	Glu	Asn	Asp	Leu	Asn	Asn	Phe	Ile	Glu	
235					240					245					250	
TTT	AGC	ACG	CAT	TTT	AGT	GGG	GTA	ATA	ATG	AAC	GCT	TAT	AGC	CTA	AAT	879

```

      435              440              445
Ala Lys Val Ser Leu Ala Val Val Leu Gly Ile Asp Asn Ile Ile Lys
      450              455              460
Ser Asn Ser Tyr Arg Ala Leu Glu Glu Gly Val Ser Leu Leu Tyr Gln
465              470              475              480
Ile Ala Gly Arg Ser Ala Arg Gln Ile Ser Gly Gln Val Phe Ile Gln
      485              490              495
Ser Thr Glu Thr Asp Leu Leu Glu Asn Phe Leu Glu Asp Tyr Glu Asp
      500              505              510
Phe Leu Gln Tyr Glu Leu Gln Glu Arg Cys Glu Leu Tyr Pro Pro Phe
      515              520              525
Ser Arg Leu Cys Leu Leu Glu Phe Lys His Lys Asn Glu Glu Lys Ala
      530              535              540
Gln Gln Leu Ser Leu Lys Ala Ser Gln Thr Leu Ser Ser Cys Leu Glu
545              550              555              560
Lys Gly Val Thr Leu Ser Asn Phe Lys Ala Pro Ile Glu Lys Ile Ala
      565              570              575
Ser Ser Tyr Arg Tyr Leu Ile Leu Leu Arg Ser Lys Asn Pro Leu Ser
      580              585              590
Leu Ile Lys Ser Val His Ala Phe Leu Lys Ser Ala Pro Ser Ile Pro
      595              600              605
Cys Ser Val Asn Met Asp Pro Val Asp Ile Phe
      610              615

```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 82...2373
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

```

AAGATTAGCC ATGCTGACTT GCCAGATCAA TGATTTCGCG AGTTTCTTTG AAAGTGATTT      60
GAGAGTGTTG GAGAGCTTTT A ATG AAA CTG AGC ATT AAT GAT TTG AAT GTT      111
              Met Lys Leu Ser Ile Asn Asp Leu Asn Val
              1              5              10

TTT GTC AAT ACG CCT AAA GAT ATA GCC AAA CTC TGT GAG GAT TTG AGT      159
Phe Val Asn Thr Pro Lys Asp Ile Ala Lys Leu Cys Glu Asp Leu Ser
              15              20              25

CGC TTA GGT TTA GAA GTG GAA AGC TGT ATC CCT TGT ATC GCT CCT AAA      207
Arg Leu Gly Leu Glu Val Glu Ser Cys Ile Pro Cys Ile Ala Pro Lys

```

```

Met Phe Tyr His Leu Ile Ala Pro Leu Lys Asn Lys Thr Pro Pro Leu
 1          5          10          15
Thr Tyr Phe Ser Lys Glu Gln His Gln Lys Gly Ala Leu Val Asn Ile
 20          25          30
Pro Leu Arg Asn Lys Thr Leu Leu Gly Val Val Leu Glu Glu Val Ser
 35          40          45
Lys Pro Ser Phe Glu Cys Leu Glu Leu Glu Lys Thr Pro Tyr Phe Leu
 50          55          60
Leu Pro Phe Gln Met Glu Leu Ala Ile Phe Ile Ala Gln Tyr Tyr Ser
 65          70          75          80
Ala Asn Leu Ser Ser Val Leu Ser Leu Phe Ala Pro Phe Lys Glu Cys
 85          90          95
Asp Leu Val Gly Leu Glu Lys Ile Glu Pro Ile Leu Asn Ile Leu Ser
 100          105          110
Gln Thr Gln Thr Asn Ala Leu Lys Glu Leu Gln Lys His Ser Ala Ser
 115          120          125
Leu Leu Phe Gly Asp Thr Gly Ser Gly Lys Thr Glu Ile Tyr Met His
 130          135          140
Ala Ile Ala Gln Thr Leu Glu Gln Lys Lys Ser Ala Leu Leu Leu Val
 145          150          155          160
Pro Glu Ile Ala Leu Thr Pro Gln Met Gln Gln Arg Leu Lys Arg Val
 165          170          175
Phe Lys Glu Asn Leu Gly Leu Trp His Ser Lys Leu Ser Gln Asn Gln
 180          185          190
Lys Lys Gln Phe Leu Glu Lys Leu Tyr Ser Gln Glu Ile Lys Leu Val
 195          200          205
Val Gly Thr Arg Ser Ala Leu Phe Leu Pro Leu Lys Glu Leu Gly Leu
 210          215          220
Ile Ile Val Asp Glu Glu His Asp Phe Ser Tyr Lys Ser His Gln Ser
 225          230          235          240
Pro Met Tyr Asn Ala Arg Asp Leu Cys Leu Tyr Leu Ser His Lys Phe
 245          250          255
Pro Ile Gln Val Ile Leu Gly Ser Ala Thr Pro Ser Leu Asn Ser Tyr
 260          265          270
Lys Arg Phe Lys Asp Lys Ala Leu Val Arg Leu Lys Gly Arg Tyr Thr
 275          280          285
Pro Thr Gln Lys Asn Ile Ile Phe Glu Lys Thr Glu Arg Phe Ile Thr
 290          295          300
Pro Lys Leu Leu Glu Ala Leu Gln Gln Val Leu Asp Lys Asn Glu Gln
 305          310          315          320
Ala Ile Ile Phe Val Pro Thr Arg Ala Asn Phe Lys Thr Leu Leu Cys
 325          330          335
Gln Ser Cys Tyr Lys Ser Val Gln Cys Pro Phe Cys Ser Val Asn Met
 340          345          350
Ser Leu His Leu Lys Thr Asn Lys Leu Met Cys His Tyr Cys His Phe
 355          360          365
Ser Ser Pro Ile Pro Lys Ile Cys Ser Ala Cys Gln Ser Glu Val Leu
 370          375          380
Val Gly Lys Arg Ile Gly Thr Met Gln Val Leu Lys Glu Leu Glu Ser
 385          390          395          400
Leu Leu Glu Gly Ala Lys Ile Ala Ile Leu Asp Lys Asp His Thr Ser
 405          410          415
Thr Gln Lys Lys Leu His Asn Ile Leu Asn Asp Phe Asn Ala Gln Lys
 420          425          430
Thr Asn Ile Leu Ile Gly Thr Gln Met Ile Ser Lys Gly His Asp Tyr

```

AGT TAT AGG GCT TTA GAA GAA GGC GTG TCG TTA CTT TAT CAA ATC GCT	1496
Ser Tyr Arg Ala Leu Glu Glu Gly Val Ser Leu Leu Tyr Gln Ile Ala	
470 475 480	
GGG AGG AGC GCT AGG CAA ATT TCT GGC CAA GTG TTC ATT CAA AGC ACC	1544
Gly Arg Ser Ala Arg Gln Ile Ser Gly Gln Val Phe Ile Gln Ser Thr	
485 490 495	
GAA ACC GAT CTG TTA GAA AAT TTC TTA GAA GAT TAT GAA GAT TTT TTA	1592
Glu Thr Asp Leu Leu Glu Asn Phe Leu Glu Asp Tyr Glu Asp Phe Leu	
500 505 510	
CAA TAC GAA TTG CAA GAA AGG TGC GAA CTC TAC CCG CCT TTT TCT AGG	1640
Gln Tyr Glu Leu Gln Glu Arg Cys Glu Leu Tyr Pro Pro Phe Ser Arg	
515 520 525 530	
CTG TGT TTG TTG GAG TTT AAG CAT AAA AAC GAA GAA AAA GCC CAA CAA	1688
Leu Cys Leu Leu Glu Phe Lys His Lys Asn Glu Glu Lys Ala Gln Gln	
535 540 545	
TTG AGC CTA AAA GCC TCT CAA ACC CTT TCT TCG TGT TTA GAA AAG GGC	1736
Leu Ser Leu Lys Ala Ser Gln Thr Leu Ser Ser Cys Leu Glu Lys Gly	
550 555 560	
GTA ACG CTC TCT AAT TTC AAA GCC CCC ATT GAA AAA ATC GCT TCT TCT	1784
Val Thr Leu Ser Asn Phe Lys Ala Pro Ile Glu Lys Ile Ala Ser Ser	
565 570 575	
TAT CGC TAC CTT ATT TTA TTG CGT TCC AAA AAC CCT TTA AGC CTA ATC	1832
Tyr Arg Tyr Leu Ile Leu Leu Arg Ser Lys Asn Pro Leu Ser Leu Ile	
580 585 590	
AAA AGC GTG CAT GCG TTT TTA AAA TCC GCC CCT AGT ATC CCT TGC AGC	1880
Lys Ser Val His Ala Phe Leu Lys Ser Ala Pro Ser Ile Pro Cys Ser	
595 600 605 610	
GTG AAC ATG GAT CCT GTG GAT ATT TTT TAAAAAACTC ATGTTTTTATA TATTATT	1934
Val Asn Met Asp Pro Val Asp Ile Phe	
615	
TCAAAAAAACT TAAGTTTTTC TGGCGA	1960

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

TAT AAC GCT AGG GAT TTA TGC TTG TAT TTA TCT CAT AAA TTC CCT ATT	824
Tyr Asn Ala Arg Asp Leu Cys Leu Tyr Leu Ser His Lys Phe Pro Ile	
245 250 255	
CAA GTG ATC TTA GGC TCT GCT ACG CCA AGT TTG AAT AGT TAT AAA CGC	872
Gln Val Ile Leu Gly Ser Ala Thr Pro Ser Leu Asn Ser Tyr Lys Arg	
260 265 270	
TTT AAA GAT AAG GCT TTA GTG CGC TTA AAG GGG CGC TAC ACC CCC ACG	920
Phe Lys Asp Lys Ala Leu Val Arg Leu Lys Gly Arg Tyr Thr Pro Thr	
275 280 285 290	
CAA AAA AAC ATT ATT TTT GAA AAA ACC GAG CGT TTT ATC ACG CCC AAA	968
Gln Lys Asn Ile Ile Phe Glu Lys Thr Glu Arg Phe Ile Thr Pro Lys	
295 300 305	
CTC CTA GAA GCG CTA CAA CAA GTC CTA GAC AAA AAC GAG CAA GCC ATT	1016
Leu Leu Glu Ala Leu Gln Gln Val Leu Asp Lys Asn Glu Gln Ala Ile	
310 315 320	
ATT TTT GTG CCT ACA AGG GCT AAT TTC AAA ACC TTG CTG TGC CAA AGT	1064
Ile Phe Val Pro Thr Arg Ala Asn Phe Lys Thr Leu Leu Cys Gln Ser	
325 330 335	
TGT TAC AAA AGC GTT CAA TGC CCC TTT TGC AGC GTG AAT ATG AGC TTG	1112
Cys Tyr Lys Ser Val Gln Cys Pro Phe Cys Ser Val Asn Met Ser Leu	
340 345 350	
CAT TTA AAG ACC AAC AAA CTC ATG TGC CAT TAT TGC CAT TTT TCA AGC	1160
His Leu Lys Thr Asn Lys Leu Met Cys His Tyr Cys His Phe Ser Ser	
355 360 365 370	
CCT ATC CCT AAA ATT TGC AGC GCG TGT CAA AGC GAA GTC TTA GTG GGT	1208
Pro Ile Pro Lys Ile Cys Ser Ala Cys Gln Ser Glu Val Leu Val Gly	
375 380 385	
AAA AGG ATA GGC ACT ATG CAA GTG CTA AAG GAA TTA GAG AGC CTT TTA	1256
Lys Arg Ile Gly Thr Met Gln Val Leu Lys Glu Leu Glu Ser Leu Leu	
390 395 400	
GAG GGG GCT AAA ATA GCG ATT TTA GAT AAA GAT CAC ACT AGC ACG CAA	1304
Glu Gly Ala Lys Ile Ala Ile Leu Asp Lys Asp His Thr Ser Thr Gln	
405 410 415	
AAA AAA CTC CAC AAT ATT TTA AAC GAT TTC AAC GCT CAA AAA ACG AAT	1352
Lys Lys Leu His Asn Ile Leu Asn Asp Phe Asn Ala Gln Lys Thr Asn	
420 425 430	
ATC TTA ATC GGC ACT CAA ATG ATA AGC AAA GGG CAT GAT TAC GCT AAA	1400
Ile Leu Ile Gly Thr Gln Met Ile Ser Lys Gly His Asp Tyr Ala Lys	
435 440 445 450	
GTG AGT TTG GCG GTT GTT TTA GGC ATA GAC AAT ATC ATC AAA TCT AAT	1448
Val Ser Leu Ala Val Val Leu Gly Ile Asp Asn Ile Ile Lys Ser Asn	
455 460 465	

TTT TCT AAA GAG CAA CAC CAA AAA GGA GCG TTA GTC AAT ATC CCT TTA	152
Phe Ser Lys Glu Gln His Gln Lys Gly Ala Leu Val Asn Ile Pro Leu	
20 25 30	
AGG AAT AAA ACG CTT TTA GGC GTC GTC CTT GAA GAA GTT TCA AAA CCC	200
Arg Asn Lys Thr Leu Leu Gly Val Val Leu Glu Glu Val Ser Lys Pro	
35 40 45 50	
TCT TTT GAA TGC CTA GAG CTA GAA AAA ACC CCT TAT TTT TTA CTC CCC	248
Ser Phe Glu Cys Leu Glu Leu Glu Lys Thr Pro Tyr Phe Leu Leu Pro	
55 60 65	
TTT CAA ATG GAG CTC GCT ATT TTT ATC GCT CAA TAT TAC TCA GCT AAT	296
Phe Gln Met Glu Leu Ala Ile Phe Ile Ala Gln Tyr Tyr Ser Ala Asn	
70 75 80	
CTT TCT TCA GTT TTA AGC CTT TTT GCC CCT TTT AAA GAA TGC GAT TTA	344
Leu Ser Ser Val Leu Ser Leu Phe Ala Pro Phe Lys Glu Cys Asp Leu	
85 90 95	
GTG GGG TTA GAA AAA ATT GAG CCT ATT CTT AAT ATA TTA AGC CAA ACG	392
Val Gly Leu Glu Lys Ile Glu Pro Ile Leu Asn Ile Leu Ser Gln Thr	
100 105 110	
CAA ACA AAC GCT TTA AAA GAA TTG CAA AAA CAT TCA GCA AGC TTG CTC	440
Gln Thr Asn Ala Leu Lys Glu Leu Gln Lys His Ser Ala Ser Leu Leu	
115 120 125 130	
TTT GGC GAT ACG GGT AGC GGG AAA ACC GAG ATT TAT ATG CAT GCA ATC	488
Phe Gly Asp Thr Gly Ser Gly Lys Thr Glu Ile Tyr Met His Ala Ile	
135 140 145	
GCC CAA ACT TTA GAG CAA AAA AAA AGC GCT TTA TTG TTG GTG CCA GAA	536
Ala Gln Thr Leu Glu Gln Lys Lys Ser Ala Leu Leu Leu Val Pro Glu	
150 155 160	
ATC GCT CTC ACC CCT CAA ATG CAA CAA CGC CTT AAA AGG GTT TTT AAA	584
Ile Ala Leu Thr Pro Gln Met Gln Gln Arg Leu Lys Arg Val Phe Lys	
165 170 175	
GAA AAT TTA GGC TTG TGG CAT AGC AAA CTC TCT CAA AAT CAA AAA AAA	632
Glu Asn Leu Gly Leu Trp His Ser Lys Leu Ser Gln Asn Gln Lys Lys	
180 185 190	
CAA TTT TTA GAA AAG CTT TAT TCG CAA GAA ATC AAA TTA GTG GTA GGC	680
Gln Phe Leu Glu Lys Leu Tyr Ser Gln Glu Ile Lys Leu Val Val Gly	
195 200 205 210	
ACA CGA AGC GCG TTG TTT TTA CCC CTT AAA GAG CTG GGT TTA ATC ATT	728
Thr Arg Ser Ala Leu Phe Leu Pro Leu Lys Glu Leu Gly Leu Ile Ile	
215 220 225	
GTA GAT GAA GAG CAT GAC TTT TCT TAT AAA TCC CAT CAA AGC CCT ATG	776
Val Asp Glu Glu His Asp Phe Ser Tyr Lys Ser His Gln Ser Pro Met	
230 235 240	

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

```

Met Lys Asp Phe Tyr Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu
 1           5           10           15
His Thr Ile Ser Glu Met Val Ser Gly Leu Asn Leu Ile Glu Trp Met
          20           25           30
Ile Lys Ile Ala Gln Gly Glu Lys Leu Pro Lys Gln Glu Ser Phe Ser
          35           40           45
Leu Lys Gly His Ala Ile Glu Cys Arg Ile Thr Ala Glu Asp Pro Lys
          50           55           60
Lys Phe Tyr Pro Ser Pro Gly Lys Ile Thr Glu Trp Ile Ala Pro Gly
65           70           75           80
Gly Val Asn Val Arg Leu Asp Ser His Ala His Ala Asn Tyr Val Val
          85           90           95
Pro Thr His Tyr Asp Ser Met Ile Gly Lys Leu Ile Val Trp Gly Glu
          100          105          110
Asn Arg Glu Arg Ala Ile Ala Lys Met Lys Arg Ala Leu Lys Glu Phe
          115          120          125
Lys Val Glu Gly Ile Lys Thr Thr Ile Pro Phe His Leu Glu Met Leu
          130          135          140
Glu Asn Ala Asp Phe Arg Gln Ala Lys Ile His Thr Lys Tyr Leu Glu
145          150          155          160
Glu Asn Phe

```

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1907
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

```

AACGAGTATT TGCACAATGA ACTCCAAAAG CTTTtagAAA AAATCTCATC ATG TTC      56
                                     Met Phe
                                     1

TAT CAC TTA ATC GCT CCT TTA AAA AAT AAA ACC CCC CCT TTA ACC TAT      104
Tyr His Leu Ile Ala Pro Leu Lys Asn Lys Thr Pro Pro Leu Thr Tyr
          5           10           15

```

TTTTTGTGG ATTCTAAC ATG AAA GAT TTT TAT TTC ATG GAG ATG AAC ACT	171
Met Lys Asp Phe Tyr Phe Met Glu Met Asn Thr	
1 5 10	
CGT TTG CAA GTG GAA CAC ACC ATT AGC GAA ATG GTG AGC GGG TTA AAC	219
Arg Leu Gln Val Glu His Thr Ile Ser Glu Met Val Ser Gly Leu Asn	
15 20 25	
CTC ATT GAG TGG ATG ATT AAA ATC GCT CAA GGC GAA AAA TTG CCC AAG	267
Leu Ile Glu Trp Met Ile Lys Ile Ala Gln Gly Glu Lys Leu Pro Lys	
30 35 40	
CAA GAA AGC TTT TCT CTC AAA GGG CAT GCG ATA GAA TGC CGA ATC ACG	315
Gln Glu Ser Phe Ser Leu Lys Gly His Ala Ile Glu Cys Arg Ile Thr	
45 50 55	
GCA GAA GAT CCT AAA AAA TTC TAC CCA AGC CCG GGC AAA ATT ACC GAA	363
Ala Glu Asp Pro Lys Lys Phe Tyr Pro Ser Pro Gly Lys Ile Thr Glu	
60 65 70 75	
TGG ATC GCT CCT GGT GGG GTG AAT GTG CGC CTT GAT TCG CAC GCG CAT	411
Trp Ile Ala Pro Gly Gly Val Asn Val Arg Leu Asp Ser His Ala His	
80 85 90	
GCC AAT TAT GTC GTG CCT ACG CAC TAT GAT TCG ATG ATT GGC AAG CTC	459
Ala Asn Tyr Val Val Pro Thr His Tyr Asp Ser Met Ile Gly Lys Leu	
95 100 105	
ATT GTG TGG GGT GAA AAC AGA GAA AGA GCG ATC GCT AAG ATG AAA AGG	507
Ile Val Trp Gly Glu Asn Arg Glu Arg Ala Ile Ala Lys Met Lys Arg	
110 115 120	
GCT TTA AAG GAA TTT AAA GTA GAA GGC ATT AAA ACG ACC ATT CCT TTC	555
Ala Leu Lys Glu Phe Lys Val Glu Gly Ile Lys Thr Thr Ile Pro Phe	
125 130 135	
CAC CTT GAA ATG CTT GAA AAT GCG GAT TTC AGG CAA GCA AAA ATC CAC	603
His Leu Glu Met Leu Glu Asn Ala Asp Phe Arg Gln Ala Lys Ile His	
140 145 150 155	
ACG AAG TAT TTA GAA GAA AAT TTT TAAGTTTAA GGATTCTTTT AAGCATAGTT	657
Thr Lys Tyr Leu Glu Asn Phe	
160	
TAAGGGTTTT AAGCGATCAG AAAAAGTCAG CA	689

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

```

Ile Asp Asn Ile Asn Pro Phe Ile Thr Ser Pro Glu Ile Asn Leu Cys
      100                      105                      110
Leu Val Arg Gln Ala Tyr Glu Glu Ala Leu His Ser His Ala Tyr Ala
      115                      120                      125
Val Met Val Glu Ser Ile Ser Ala Asn Thr Glu Glu Ile Tyr Asp Met
      130                      135                      140
Trp Arg Asn Asp Met Gln Leu Lys Ser Lys Asn Asp Tyr Ile Ala Gln
      145                      150                      155                      160
Val Tyr Met Glu Leu Ala Lys Asn Pro Thr Glu Glu Asn Ile Leu Lys
      165                      170                      175
Ala Leu Phe Ala Asn Gln Ile Leu Glu Gly Ile Tyr Phe Tyr Ser Gly
      180                      185                      190
Phe Ser Tyr Phe Tyr Thr Leu Ala Arg Ser Gly Lys Met Leu Gly Ser
      195                      200                      205
Ala Gln Met Ile Arg Phe Ile Gln Arg Asp Glu Val Thr His Leu Ile
      210                      215                      220
Leu Phe Gln Asn Met Ile Asn Ala Leu Arg Asn Glu Arg Ala Asp Leu
      225                      230                      235                      240
Phe Thr Pro Gln Leu Ile Asn Glu Val Ile Gly Met Phe Lys Lys Ala
      245                      250                      255
Val Glu Ile Glu Ala Leu Trp Gly Asp Tyr Ile Thr Gln Gly Lys Ile
      260                      265                      270
Leu Gly Leu Thr Ser Ser Leu Ile Glu Gln Tyr Ile Gln Phe Leu Ala
      275                      280                      285
Asp Ser Arg Leu Ser Lys Val Gly Ile Ala Lys Val Tyr Gly Val Gln
      290                      295                      300
His Pro Ile Lys Trp Val Glu Ser Phe Ser Ser Phe Asn Glu Gln Arg
      305                      310                      315                      320
Ser Asn Phe Phe Glu Ala Arg Val Ser Asn Tyr Ala Lys Gly Ser Val
      325                      330                      335
Ser Phe Asp Asp Phe
      340

```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 139...627
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```

CAAAGCTCA TTGAAGAAAC CCCGGCAGTG GTTTTAGAAG AGGGCGTGCG TGACGTTTGC      60
TAGAAACAGC GATCAAGGCC GCTAAATATA TCGGCTRTTG TGGGGGCGGG GACTTTTGAA      120

```

AAC GCT TTA AGG AAT GAA AGA GCG GAT CTC TTC ACG CCG CAA TTG ATT	834
Asn Ala Leu Arg Asn Glu Arg Ala Asp Leu Phe Thr Pro Gln Leu Ile	
235 240 245	
AAT GAA GTC ATA GGA ATG TTT AAA AAA GCG GTA GAA ATT GAA GCT TTG	882
Asn Glu Val Ile Gly Met Phe Lys Lys Ala Val Glu Ile Glu Ala Leu	
250 255 260	
TGG GGG GAT TAT ATC ACG CAA GGC AAG ATT TTA GGG CTC ACT TCA AGC	930
Trp Gly Asp Tyr Ile Thr Gln Gly Lys Ile Leu Gly Leu Thr Ser Ser	
265 270 275	
TTG ATT GAG CAA TAC ATC CAG TTT TTA GCG GAT AGC CGT TTG AGT AAG	978
Leu Ile Glu Gln Tyr Ile Gln Phe Leu Ala Asp Ser Arg Leu Ser Lys	
280 285 290	
GTG GGC ATC GCT AAA GTT TAT GGC GTC CAA CAC CCC ATT AAA TGG GTA	1026
Val Gly Ile Ala Lys Val Tyr Gly Val Gln His Pro Ile Lys Trp Val	
295 300 305 310	
GAG AGC TTT TCA AGT TTC AAT GAG CAG CGC TCT AAT TTC TTT GAG GCT	1074
Glu Ser Phe Ser Ser Phe Asn Glu Gln Arg Ser Asn Phe Phe Glu Ala	
315 320 325	
AGG GTG AGC AAT TAC GCT AAA GGG AGC GTG AGT TTT GAT GAT TTT TAAGG	1124
Arg Val Ser Asn Tyr Ala Lys Gly Ser Val Ser Phe Asp Asp Phe	
330 335 340	
GGCTTGTTTG AATAGTATTA AAAACCATTT AATGTGTGAA GAAATC	1170

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

Met Glu Val Ser Arg Lys Lys Ile Tyr Asn Pro Asn Ser Thr Glu Ser	
1 5 10 15	
Val Asn Glu Arg Lys Ile Phe Gly Gly Asn Pro Thr Ser Met Phe Asp	
20 25 30	
Leu Asn Lys Ile Lys Tyr Gln Trp Ala Asp His Leu Trp Lys Thr Met	
35 40 45	
Leu Ala Asn Thr Trp Phe Ala Glu Glu Val Ser Met Asn Asp Asp Lys	
50 55 60	
Arg Asp Tyr Leu Lys Leu Ser Ala Glu Glu Lys Ile Gly Tyr Asp Arg	
65 70 75 80	
Ala Leu Ala Gln Leu Ile Phe Met Asp Ser Leu Gln Ala Asn Asn Leu	
85 90 95	

Lys	Ile	Tyr	Asn	Pro	Asn	Ser	Thr	Glu	Ser	Val	Asn	Glu	Arg	Lys	Ile		
			10					15					20				
TTT	GGG	GGC	AAT	CCT	ACA	AGC	ATG	TTT	GAT	TTG	AAT	AAG	ATC	AAG	TAT	210	
Phe	Gly	Gly	Asn	Pro	Thr	Ser	Met	Phe	Asp	Leu	Asn	Lys	Ile	Lys	Tyr		
		25					30					35					
CAA	TGG	GCG	GAT	CAT	TTG	TGG	AAA	ACG	ATG	CTC	GCT	AAC	ACC	TGG	TTT	258	
Gln	Trp	Ala	Asp	His	Leu	Trp	Lys	Thr	Met	Leu	Ala	Asn	Thr	Trp	Phe		
	40					45					50						
GCT	GAA	GAA	GTG	AGC	ATG	AAT	GAT	GAC	AAA	AGG	GAT	TAT	TTG	AAA	TTA	306	
Ala	Glu	Glu	Val	Ser	Met	Asn	Asp	Asp	Lys	Arg	Asp	Tyr	Leu	Lys	Leu		
55					60					65					70		
AGC	GCA	GAG	GAA	AAG	ATC	GGT	TAT	GAC	AGA	GCT	TTA	GCG	CAA	CTC	ATT	354	
Ser	Ala	Glu	Glu	Lys	Ile	Gly	Tyr	Asp	Arg	Ala	Leu	Ala	Gln	Leu	Ile		
				75					80					85			
TTT	ATG	GAC	AGC	TTG	CAA	GCG	AAT	AAT	TTA	ATT	GAC	AAT	ATC	AAT	CCC	402	
Phe	Met	Asp	Ser	Leu	Gln	Ala	Asn	Asn	Leu	Ile	Asp	Asn	Ile	Asn	Pro		
			90					95					100				
TTC	ATC	ACC	AGC	CCC	GAA	ATC	AAT	TTG	TGT	TTG	GTG	CGT	CAA	GCT	TAT	450	
Phe	Ile	Thr	Ser	Pro	Glu	Ile	Asn	Leu	Cys	Leu	Val	Arg	Gln	Ala	Tyr		
		105					110					115					
GAA	GAA	GCC	CTA	CAC	AGC	CAT	GCG	TAT	GCG	GTG	ATG	GTA	GAA	AGC	ATA	498	
Glu	Glu	Ala	Leu	His	Ser	His	Ala	Tyr	Ala	Val	Met	Val	Glu	Ser	Ile		
	120					125					130						
AGT	GCG	AAT	ACT	GAA	GAG	ATT	TAT	GAC	ATG	TGG	CGT	AAC	GAT	ATG	CAA	546	
Ser	Ala	Asn	Thr	Glu	Glu	Ile	Tyr	Asp	Met	Trp	Arg	Asn	Asp	Met	Gln		
135					140					145					150		
TTA	AAA	AGC	AAG	AAC	GAC	TAT	ATC	GCG	CAA	GTG	TAT	ATG	GAA	TTA	GCC	594	
Leu	Lys	Ser	Lys	Asn	Asp	Tyr	Ile	Ala	Gln	Val	Tyr	Met	Glu	Leu	Ala		
				155					160					165			
AAA	AAC	CCC	ACA	GAA	GAA	AAC	ATT	CTC	AAA	GCG	CTT	TTT	GCT	AAC	CAG	642	
Lys	Asn	Pro	Thr	Glu	Glu	Asn	Ile	Leu	Lys	Ala	Leu	Phe	Ala	Asn	Gln		
			170					175					180				
ATT	TTA	GAG	GGG	ATT	TAT	TTT	TAT	AGC	GGG	TTT	AGC	TAT	TTT	TAC	ACT	690	
Ile	Leu	Glu	Gly	Ile	Tyr	Phe	Tyr	Ser	Gly	Phe	Ser	Tyr	Phe	Tyr	Thr		
		185					190					195					
TTG	GCT	AGG	AGC	GGT	AAA	ATG	CTA	GGA	TCG	GCA	CAA	ATG	ATT	CGT	TTT	738	
Leu	Ala	Arg	Ser	Gly	Lys	Met	Leu	Gly	Ser	Ala	Gln	Met	Ile	Arg	Phe		
	200					205					210						
ATC	CAA	AGA	GAT	GAG	GTA	ACG	CAT	TTG	ATT	TTG	TTC	CAA	AAC	ATG	ATC	786	
Ile	Gln	Arg	Asp	Glu	Val	Thr	His	Leu	Ile	Leu	Phe	Gln	Asn	Met	Ile		
215					220					225					230		

```

Thr Ala Val Val Tyr Gly Glu Ser Ser Ser Ser Leu Asn Glu Glu Ser
 130                      135                      140
Pro Leu Asn Pro Ile Asn Pro Tyr Gly Ala Ser Lys Met Met Ser Glu
145                      150                      155                      160
Arg Ile Leu Leu Asp Thr Ser Lys Ile Ala Asp Phe Lys Cys Val Ile
                      165                      170                      175
Leu Arg Tyr Phe Asn Val Ala Gly Ala Cys Met His Asn Asp Tyr Thr
                      180                      185                      190
Thr Pro Tyr Thr Leu Gly Gln Arg Thr Leu Asn Ala Thr His Leu Ile
                      195                      200                      205
Lys Ile Ala Cys Glu Cys Ala Val Gly Lys Arg Lys Lys Met Gly Ile
210                      215                      220
Phe Gly Thr Asn Tyr Pro Thr Arg Asp Gly Thr Cys Ile Arg Asp Tyr
225                      230                      235                      240
Ile His Val Asp Asp Leu Ala Asn Ala His Leu Ala Ser Tyr Gln Thr
                      245                      250                      255
Leu Leu Glu Lys Asn Lys Ser Glu Ile Tyr Asn Val Gly Tyr Asn Gln
                      260                      265                      270
Gly His Ser Val Lys Glu Val Ile Glu Lys Val Lys Glu Ile Ser Asn
                      275                      280                      285
Asn Asp Phe Leu Val Glu Ile Leu Asp Lys Arg Gln Gly Asp Pro Ala
290                      295                      300
Ser Leu Ile Ala Asn Asn Ala Lys Ile Leu Gln Asn Thr Ser Phe Lys
305                      310                      315                      320
Pro Leu Tyr Asn Asn Leu Asp Thr Ile Ile Lys Ser Ala Leu Asp Trp
                      325                      330                      335
Glu Glu His Leu Leu Arg Phe Gln
                      340

```

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 97...1119
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

```

GGAGTTTTTT CTGGCTTTTA GGGGGTTTTTA AATTCTTTTA AGGTATTCTA ACAAGACTAT      60
ATCATTGAGA TAGTTTAAAG GAAATTAAGG AACAAA ATG GAA GTT TCA CGC AAG      114
                      Met Glu Val Ser Arg Lys
                      1                      5

AAA ATT TAC AAC CCC AAT TCT ACA GAA AGT GTG AAT GAA AGA AAG ATT      162

```

GAA AAA AAT AAG AGC GAG ATC TAT AAT GTC GGC TAC AAT CAA GGC CAT 872
 Glu Lys Asn Lys Ser Glu Ile Tyr Asn Val Gly Tyr Asn Gln Gly His
 260 265 270

AGC GTG AAA GAA GTG ATA GAA AAG GTC AAA GAA ATC TCA AAC AAC GAT 920
 Ser Val Lys Glu Val Ile Glu Lys Val Lys Glu Ile Ser Asn Asn Asp
 275 280 285 290

TTT TTA GTG GAA ATT TTA GAC AAA CGA CAG GGC GAT CCA GCA AGC CTT 968
 Phe Leu Val Glu Ile Leu Asp Lys Arg Gln Gly Asp Pro Ala Ser Leu
 295 300 305

ATT GCC AAT AAC GCT AAA ATC TTA CAA AAC ACC TCT TTC AAA CCC CTT 1016
 Ile Ala Asn Asn Ala Lys Ile Leu Gln Asn Thr Ser Phe Lys Pro Leu
 310 315 320

TAT AAC AAC CTA GAC ACC ATT ATC AAA AGC GCT CTA GAT TGG GAA GAA 1064
 Tyr Asn Asn Leu Asp Thr Ile Ile Lys Ser Ala Leu Asp Trp Glu Glu
 325 330 335

CAC CTT TTG AGG TTT CAA TAATACACCC TGTGCAAATA CAAGCCATTA GCCATTAT 1120
 His Leu Leu Arg Phe Gln
 340

GGGCGTTCTT ATAGT 1135

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

Met Ala Leu Leu Phe Thr Gly Ala Cys Gly Tyr Ile Gly Ser His Thr
 1 5 10 15
 Ala Arg Ala Phe Leu Glu Lys Thr Lys Glu Asn Ile Ile Ile Val Asp
 20 25 30
 Asp Leu Ser Thr Gly Phe Leu Glu His Leu Lys Ala Leu Glu His Tyr
 35 40 45
 Tyr Pro Asn Arg Val Val Phe Ile Gln Ala Asn Leu Asn Glu Thr His
 50 55 60
 Lys Leu Asp Ala Phe Leu Asn Lys Gln Gln Leu Lys Asp Pro Ile Glu
 65 70 75 80
 Ala Ile Leu His Phe Gly Ala Lys Ile Ser Val Glu Glu Ser Thr His
 85 90 95
 Leu Pro Leu Glu Tyr Tyr Thr Asn Asn Thr Leu Asn Thr Leu Glu Leu
 100 105 110
 Val Lys Leu Cys Leu Lys His Ala Ile Lys Arg Phe Ile Phe Ser Ser
 115 120 125

Ser	Thr	Gly	Phe	Leu	Glu	His	Leu	Lys	Ala	Leu	Glu	His	Tyr	Tyr	Pro	
35					40					45					50	
AAT	AGG	GTT	GTG	TTT	ATT	CAA	GCG	AAT	TTG	AAT	GAA	ACG	CAC	AAA	TTA	248
Asn	Arg	Val	Val	Phe	Ile	Gln	Ala	Asn	Leu	Asn	Glu	Thr	His	Lys	Leu	
				55					60					65		
GAC	GCC	TTT	TTG	AAT	AAG	CAG	CAG	CTA	AAA	GAT	CCC	ATT	GAA	GCC	ATC	296
Asp	Ala	Phe	Leu	Asn	Lys	Gln	Gln	Leu	Lys	Asp	Pro	Ile	Glu	Ala	Ile	
			70					75					80			
TTG	CAC	TTT	GGG	GCT	AAA	ATC	TCA	GTA	GAA	GAA	TCC	ACG	CAC	TTG	CCT	344
Leu	His	Phe	Gly	Ala	Lys	Ile	Ser	Val	Glu	Glu	Ser	Thr	His	Leu	Pro	
	85						90					95				
TTA	GAA	TAC	TAC	ACC	AAC	AAC	ACG	CTC	AAC	ACT	TTA	GAG	CTT	GTC	AAA	392
Leu	Glu	Tyr	Tyr	Thr	Asn	Asn	Thr	Leu	Asn	Thr	Leu	Glu	Leu	Val	Lys	
	100						105				110					
CTT	TGC	TTA	AAA	CAT	GCA	ATC	AAG	CGT	TTT	ATT	TTT	TCT	TCT	ACG	GCC	440
Leu	Cys	Leu	Lys	His	Ala	Ile	Lys	Arg	Phe	Ile	Phe	Ser	Ser	Thr	Ala	
	115				120					125					130	
GTG	GTT	TAT	GGC	GAA	TCT	AGT	TCA	AGT	TTG	AAT	GAA	GAA	AGC	CCC	TTA	488
Val	Val	Tyr	Gly	Glu	Ser	Ser	Ser	Ser	Leu	Asn	Glu	Glu	Ser	Pro	Leu	
			135						140				145			
AAC	CCC	ATT	AAT	CCT	TAT	GGA	GCG	TCT	AAA	ATG	ATG	AGC	GAA	AGA	ATC	536
Asn	Pro	Ile	Asn	Pro	Tyr	Gly	Ala	Ser	Lys	Met	Met	Ser	Glu	Arg	Ile	
			150					155					160			
TTG	TTA	GAC	ACT	TCT	AAA	ATA	GCG	GAT	TTT	AAA	TGC	GTT	ATT	TTG	CGC	584
Leu	Leu	Asp	Thr	Ser	Lys	Ile	Ala	Asp	Phe	Lys	Cys	Val	Ile	Leu	Arg	
	165						170					175				
TAT	TTC	AAT	GTG	GCT	GGG	GCA	TGC	ATG	CAC	AAT	GAT	TAT	ACC	ACC	CCT	632
Tyr	Phe	Asn	Val	Ala	Gly	Ala	Cys	Met	His	Asn	Asp	Tyr	Thr	Thr	Pro	
	180					185					190					
TAC	ACG	CTA	GGG	CAA	CGC	ACG	CTC	AAC	GCC	ACG	CAT	TTG	ATC	AAA	ATC	680
Tyr	Thr	Leu	Gly	Gln	Arg	Thr	Leu	Asn	Ala	Thr	His	Leu	Ile	Lys	Ile	
	195				200					205				210		
GCA	TGC	GAA	TGC	GCG	GTG	GGG	AAA	AGG	AAA	AAA	ATG	GGG	ATT	TTT	GGC	728
Ala	Cys	Glu	Cys	Ala	Val	Gly	Lys	Arg	Lys	Lys	Met	Gly	Ile	Phe	Gly	
			215						220				225			
ACT	AAC	TAC	CCC	ACA	AGA	GAT	GGC	ACT	TGC	ATT	AGG	GAT	TAT	ATC	CAT	776
Thr	Asn	Tyr	Pro	Thr	Arg	Asp	Gly	Thr	Cys	Ile	Arg	Asp	Tyr	Ile	His	
			230					235					240			
GTA	GAT	GAT	TTG	GCT	AAC	GCA	CAT	TTA	GCG	AGC	TAT	CAA	ACC	CTT	TTA	824
Val	Asp	Asp	Leu	Ala	Asn	Ala	His	Leu	Ala	Ser	Tyr	Gln	Thr	Leu	Leu	
	245						250					255				


```

      130              135              140
Ala Leu Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln
145              150              155              160
Ser Glu Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly
      165              170              175
Asn Gly Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys
      180              185              190
Asn Ile Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp
      195              200              205
Pro Asn Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe
      210              215              220
Ser Asp Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe
225              230              235              240
Leu Ser Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile
      245              250              255
Asp Glu Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu
      260              265              270
Gly Leu Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly
      275              280              285
Gln Glu Arg
      290

```

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1082
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

```

GGATTAAGAT GTTATAATAG TTGTTATTTT TTCATTTTAA AAGGGGTTTT ATG GCA      56
                                     Met Ala
                                     1

TTA TTA TTC ACA GGA GCG TGC GGG TAT ATA GGC TCG CAT ACC GCA AGG      104
Leu Leu Phe Thr Gly Ala Cys Gly Tyr Ile Gly Ser His Thr Ala Arg
      5              10              15

GCG TTT TTA GAA AAA ACC AAA GAA AAT ATC ATT ATT GTA GAT GAC TTA      152
Ala Phe Leu Glu Lys Thr Lys Glu Asn Ile Ile Ile Val Asp Asp Leu
      20              25              30

AGC ACC GGT TTT TTA GAG CAC CTC AAA GCG TTA GAG CAT TAT TAC CCT      200

```

TTA AGC GCG ATC GTT GCC CCT TAT CAA AAG CTC TAT GTT TTT AGC GAT	728
Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe Ser Asp	
215 220 225	
AAT TAC AAG CTT GGA GGG GTG GCT AGC GCG ATT TTA GAG TTT TTG AGC	776
Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe Leu Ser	
230 235 240	
GAA CAA AAT ATT TTA AAG CCT GTT AAA AGC TTT GAA ATC ATT GAT GAA	824
Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile Asp Glu	
245 250 255	
TTT ATC ATG CAT GGG AAC ACC GCT TTA GTG GAA AAA TCC TTA GGA TTA	872
Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu Gly Leu	
260 265 270	
GAC ACA GAG AGT TTG ACT GAC GCT ATT TTA AAA GAT TTA GGA CAA GAG	920
Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly Gln Glu	
275 280 285 290	
AGA TGAAAACAAA AGCGCCAATG AAAAATATCC GCAATTTTTC CATTATCGCT CAC	976
Arg	

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

Lys Asn Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp	
1 5 10 15	
Lys Leu Ile Asp Ala Xaa Pro Leu Arg Phe Phe Asp Val Ala Ile Ala	
20 25 30	
Glu Gln His Ala Leu Thr Ser Ser Ala Met Ala Lys Glu Gly Phe	
35 40 45	
Lys Pro Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp	
50 55 60	
Ser Ile Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala	
65 70 75 80	
Ile Asp Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly	
85 90 95	
Leu Leu Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe	
100 105 110	
Ala Pro Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn	
115 120 125	
Glu His Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe	

																Lys Asn	
																1	
CGT	AGG	CGT	AAC	CGC	GGC	GAT	GCT	AGC	GGC	ACA	GGA	TTA	GAC	AAA	CTC		104
Arg	Arg	Arg	Asn	Arg	Gly	Asp	Ala	Ser	Gly	Thr	Gly	Leu	Asp	Lys	Leu		
5				10				15									
ATT	GAC	GCT	TAN	CCT	TTG	CGC	TTT	TTT	GAT	GTC	GCT	ATC	GCT	GAG	CAA		152
Ile	Asp	Ala	Xaa	Pro	Leu	Arg	Phe	Phe	Asp	Val	Ala	Ile	Ala	Glu	Gln		
20				25				30									
CAC	GCT	TTA	ACT	TCT	AGC	AGC	GCT	ATG	GCT	AAA	GAG	GGG	TTT	AAA	CCT		200
His	Ala	Leu	Thr	Ser	Ser	Ser	Ala	Met	Ala	Lys	Glu	Gly	Phe	Lys	Pro		
35				40				45				50					
TTT	GTG	AGC	ATC	TAT	TCT	ACT	TTT	TTG	CAG	AGG	GCT	TAT	GAT	TCT	ATT		248
Phe	Val	Ser	Ile	Tyr	Ser	Thr	Phe	Leu	Gln	Arg	Ala	Tyr	Asp	Ser	Ile		
55				60				65									
GTG	CAT	GAC	GCT	TGT	ATT	TCT	AGC	TTG	CCG	ATT	AAA	TTA	GCC	ATT	GAC		296
Val	His	Asp	Ala	Cys	Ile	Ser	Ser	Leu	Pro	Ile	Lys	Leu	Ala	Ile	Asp		
70				75				80									
AGG	GCT	GGG	ATT	GTG	GGC	GAA	GAT	GGC	GAG	ACG	CAC	CAA	GGG	CTT	TTA		344
Arg	Ala	Gly	Ile	Val	Gly	Glu	Asp	Gly	Glu	Thr	His	Gln	Gly	Leu	Leu		
85				90				95									
GAC	GTG	TCG	TAT	TTG	CGC	TCT	ATC	CCT	AAC	ATG	GTC	ATT	TTT	GCC	CCA		392
Asp	Val	Ser	Tyr	Leu	Arg	Ser	Ile	Pro	Asn	Met	Val	Ile	Phe	Ala	Pro		
100				105				110									
CGA	GAC	AAT	GAG	ACT	TTA	AAA	AAC	GCC	GTG	CGT	TTT	GCC	AAT	GAA	CAC		440
Arg	Asp	Asn	Glu	Thr	Leu	Lys	Asn	Ala	Val	Arg	Phe	Ala	Asn	Glu	His		
115				120				125				130					
GAT	TCA	AGC	CCT	TGC	GCG	TTC	CGA	TAC	CCT	AGG	GGG	TCG	TTT	GCG	TTA		488
Asp	Ser	Ser	Pro	Cys	Ala	Phe	Arg	Tyr	Pro	Arg	Gly	Ser	Phe	Ala	Leu		
135				140				145									
AAA	GAG	GGG	GTT	TTT	GAG	CCT	AGC	GGT	TTT	GTT	TTA	GGC	CAA	AGC	GAA		536
Lys	Glu	Gly	Val	Phe	Glu	Pro	Ser	Gly	Phe	Val	Leu	Gly	Gln	Ser	Glu		
150				155				160									
TTG	TTG	AAA	AAA	GAG	GGC	GAA	ATT	TTA	CTC	ATA	GGC	TAT	GGT	AAT	GGC		584
Leu	Leu	Lys	Lys	Glu	Gly	Glu	Ile	Leu	Leu	Ile	Gly	Tyr	Gly	Asn	Gly		
165				170				175									
GTG	GGG	CGG	GCG	CAT	TTA	GTC	CAA	CTG	GCT	TTA	AAA	GAA	AAA	AAC	ATA		632
Val	Gly	Arg	Ala	His	Leu	Val	Gln	Leu	Ala	Leu	Lys	Glu	Lys	Asn	Ile		
180				185				190									
GAA	TGC	GCT	CTC	TTG	GAT	CTC	AGG	TTT	TTA	AAG	CCT	TTA	GAT	CCA	AAT		680
Glu	Cys	Ala	Leu	Leu	Asp	Leu	Arg	Phe	Leu	Lys	Pro	Leu	Asp	Pro	Asn		
195				200				205				210					

GGACTCTTTT CTTCATTGGC TTGAGTTGC

522

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

Met	Ser	Tyr	Phe	Phe	Lys	Ile	Ile	Leu	Gly	Thr	Ser	Val	Ile	Val	Gly
1				5				10					15		
Val	Leu	Leu	Gly	Leu	Trp	Arg	Leu	Thr	Tyr	Asp	Lys	Phe	Tyr	Phe	Ser
			20				25					30			
Leu	Val	Phe	Val	Leu	Leu	Ile	Leu	Gly	Ile	Val	Ala	Cys	Ser	Tyr	Ile
			35				40					45			
Ser	Leu	Lys	Met	His	Gln	Arg	Lys	Cys	Phe	Ala	Lys	Cys	Phe	Val	Asn
			50			55				60					
Ser	Glu	Ser	Phe	Leu	Ser	Lys	Met	Leu	His	Ser	Pro	Ile	Met	Val	Ile
					70					75				80	
Cys	Phe	Tyr	Phe	Ile	Phe	Ser	Ile	Phe	Thr	Ser	Ile	Ser	Ile	Val	Tyr
				85				90						95	
Ser	Val	Leu	Asp	Tyr	Asp	Gln	Met	Met	Trp	Gly	Phe	Val	Phe	Cys	Thr
			100					105					110		
Ile	Val	Val	Cys	Ala	Val	Val	Phe	Gly	Thr	Leu	Glu	Lys	Asn	Ala	Gln
			115				120					125			
Glu	Tyr	His	Gln	Arg	Arg	Leu	Phe	Asp	Ala	Asp	Val				
			130			135					140				

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...923
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

CCCACTGAAG CGTATTCTAA CACCCTTTTA GAATTAGCTA AAAAAGATGA AAA AAT

56

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...470
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

AAAGACAACC CTAACAAACG CTTCAAAAAC AACAAGAGGG ATAAAAAATA	ATG TCT	56
	Met Ser	
	1	
TAT TTT TTT AAA ATC ATT CTG GGC ACA AGC GTG ATC GTG GGG GTG TTG		104
Tyr Phe Phe Lys Ile Ile Leu Gly Thr Ser Val Ile Val Gly Val Leu		
5 10 15		
TTG GGC TTG TGG CGT TTG ACT TAC GAT AAG TTC TAT TTC TCG TTG GTC		152
Leu Gly Leu Trp Arg Leu Thr Tyr Asp Lys Phe Tyr Phe Ser Leu Val		
20 25 30		
TTT GTG TTG CTG ATA CTA GGG ATT GTC GCT TGT AGC TAT ATT TCT TTA		200
Phe Val Leu Leu Ile Leu Gly Ile Val Ala Cys Ser Tyr Ile Ser Leu		
35 40 45 50		
AAA ATG CAT CAG AGG AAA TGC TTC GCC AAG TGT TTC GTG AAT AGT GAA		248
Lys Met His Gln Arg Lys Cys Phe Ala Lys Cys Phe Val Asn Ser Glu		
55 60 65		
TCT TTT TTA TCC AAG ATG TTA CAC TCC CCA ATA ATG GTA ATT TGC TTT		296
Ser Phe Leu Ser Lys Met Leu His Ser Pro Ile Met Val Ile Cys Phe		
70 75 80		
TAT TTT ATT TTT TCA ATT TTC ACA TCC ATA TCC ATC GTC TAT AGC GTG		344
Tyr Phe Ile Phe Ser Ile Phe Thr Ser Ile Ser Ile Val Tyr Ser Val		
85 90 95		
CTG GAC TAT GAT CAG ATG ATG TGG GGG TTT GTT TTT TGC ACT ATC GTT		392
Leu Asp Tyr Asp Gln Met Met Trp Gly Phe Val Phe Cys Thr Ile Val		
100 105 110		
GTT TGC GCT GTG GTG TTT GGC ACG CTT GAA AAA AAT GCT CAA GAG TAC		440
Val Cys Ala Val Val Phe Gly Thr Leu Glu Lys Asn Ala Gln Glu Tyr		
115 120 125 130		
CAT CAA AGA AGA TTA TTT GAT GCT GAT GTC TAGAGAAGTG AGTGCTTTTG TGG		493
His Gln Arg Arg Leu Phe Asp Ala Asp Val		
135 140		

```

CAC CAG CAT GAG AAT AAA AAT CAG AAT ATT GAC TAT GAG CAA CCA AAC      154
His Gln His Glu Asn Lys Asn Gln Asn Ile Asp Tyr Glu Gln Pro Asn
20                               25                               30                               35

GAT AGA AGC AAA TTC CAC GCT CAC CCT TTC AAG AGC GTT TTA ACA ACC      202
Asp Arg Ser Lys Phe His Ala His Pro Phe Lys Ser Val Leu Thr Thr
                               40                               45                               50

CAA ACG CTA CCA CTT GGT TTT TTA GAG AGA GAA AGA GAG AGA AAG CAA      250
Gln Thr Leu Pro Leu Gly Phe Leu Glu Arg Glu Arg Glu Arg Lys Gln
                               55                               60                               65

AAT TTT AAG ATT GAT TCT CAA ATC TAT TCC TTT GCA AAA GTT AAG ATT      298
Asn Phe Lys Ile Asp Ser Gln Ile Tyr Ser Phe Ala Lys Val Lys Ile
                               70                               75                               80

GGG TGT TTT AAC ATG ATT TTT GGC CTG CTC GCA TCA AGC CCT TAT TTT T      347
Gly Cys Phe Asn Met Ile Phe Gly Leu Leu Ala Ser Ser Pro Tyr Phe
                               85                               90                               95

AACATTTCCG CTCCCTTGCT TTTTAAAGC CTCCTAAAT TACTACACCA CT      399

```

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

```

Asn Pro Gln Ser Phe Phe Arg Asn Thr Pro His Phe Leu Ile Ser Arg
1                               5                               10                               15
Ile Phe Ile His Gln His Glu Asn Lys Asn Gln Asn Ile Asp Tyr Glu
                               20                               25                               30
Gln Pro Asn Asp Arg Ser Lys Phe His Ala His Pro Phe Lys Ser Val
                               35                               40                               45
Leu Thr Thr Gln Thr Leu Pro Leu Gly Phe Leu Glu Arg Glu Arg Glu
                               50                               55                               60
Arg Lys Gln Asn Phe Lys Ile Asp Ser Gln Ile Tyr Ser Phe Ala Lys
65                               70                               75                               80
Val Lys Ile Gly Cys Phe Asn Met Ile Phe Gly Leu Leu Ala Ser Ser
                               85                               90                               95
Pro Tyr Phe

```

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

```

Val Asp Ser Glu Gly Phe Ser Pro Ser Ile Tyr Thr Asp Lys Thr Gly
 1          5          10          15
His Pro Thr Ile Gly Tyr Gly Tyr Asn Leu Ser Val Tyr Ser Tyr Glu
          20          25          30
Gly Lys Arg Ile Thr Lys Thr Tyr Gly Leu Leu Thr Asp Ile Leu Ser
          35          40          45
Tyr Gly Trp Tyr Lys Asn Leu Asp Ala Met Arg Arg Met Val Ile Leu
          50          55          60
Asp Leu Ser Tyr Asn Leu Gly Leu Asn Gly Leu Leu Lys Phe Lys Gln
          65          70          75          80
Phe Ile Lys Ala Ile Glu Asp Lys Asn Tyr Ala Leu Ala Val Glu Arg
          85          90          95
Leu Gln Lys Ser Pro Tyr Phe Asn Gln Val Lys Lys Glu Arg Gln Gly
          100          105          110
Ile Trp Lys Phe
          115

```

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...346
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

```

ACACAACCAT AGCGACCAAA AACCCGACAG ACCCGCCAAG GAGCGATAA AAC CCA CAA      58
                                     Asn Pro Gln
                                     1

AGC TTT TTC AGG AAT ACG CCA CAT TTT TTG ATC AGC CGA ATT TTT ATC      106
Ser Phe Phe Arg Asn Thr Pro His Phe Leu Ile Ser Arg Ile Phe Ile
 5          10          15

```

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...398
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GTGGAACGCT CTGTCTTAGC AAATTGATCT TAGCGGCGTC GTTTTTGATA	GTG GAT	56
	Val Asp	
	1	
TCA GAG GGG TTT TCG CCT TCT ATT TAT ACC GAC AAG ACA GGG CAT CCC		104
Ser Glu Gly Phe Ser Pro Ser Ile Tyr Thr Asp Lys Thr Gly His Pro		
5 10 15		
ACG ATT GGC TAT GGC TAT AAT TTG AGC GTT TAT TCT TAT GAG GGT AAG		152
Thr Ile Gly Tyr Gly Tyr Asn Leu Ser Val Tyr Ser Tyr Glu Gly Lys		
20 25 30		
CGT ATC ACC AAA ACA TAT GGC CTT TTA ACT GAC ATA CTC TCT TAT GGG		200
Arg Ile Thr Lys Thr Tyr Gly Leu Leu Thr Asp Ile Leu Ser Tyr Gly		
35 40 45 50		
TGG TAT AAA AAT TTG GAC GCA ATG AGG AGA ATG GTC ATC TTG GAT TTG		248
Trp Tyr Lys Asn Leu Asp Ala Met Arg Arg Met Val Ile Leu Asp Leu		
55 60 65		
AGC TAC AAT TTA GGC TTG AAC GGA CTG CTC AAA TTC AAG CAA TTC ATC		296
Ser Tyr Asn Leu Gly Leu Asn Gly Leu Leu Lys Phe Lys Gln Phe Ile		
70 75 80		
AAG GCC ATA GAG GAT AAA AAT TAT GCT TTG GCT GTG GAG AGA CTG CAA		344
Lys Ala Ile Glu Asp Lys Asn Tyr Ala Leu Ala Val Glu Arg Leu Gln		
85 90 95		
AAA AGC CCG TAT TTC AAT CAA GTG AAA AAA GAG CGT CAA GGA ATA TGG		392
Lys Ser Pro Tyr Phe Asn Gln Val Lys Lys Glu Arg Gln Gly Ile Trp		
100 105 110		
AAA TTT TGAAATTGGA GGGTTGCGAA AAACATTGTA AGAAAAAATA CGCAATAGAA AA		450
Lys Phe		
115		
G		451

(2) INFORMATION FOR SEQ ID NO:682:

TAC TAC TCT AAA GCT TGT GGA TTA AAT GAT CAA GAT GGG TGT TTA ATA 344
 Tyr Tyr Ser Lys Ala Cys Gly Leu Asn Asp Gln Asp Gly Cys Leu Ile
 85 90 95

CTA GGA TAT AAG CAA TAT GCT GGC AAG GGC GTA GTC AAA AAT GAA AAA 392
 Leu Gly Tyr Lys Gln Tyr Ala Gly Lys Gly Val Val Lys Asn Glu Lys
 100 105 110

CAA GCG GTG AAA ACC TTT GAA AAG GCT TGT AGG TTA GGA TCT GAA GAC 440
 Gln Ala Val Lys Thr Phe Glu Lys Ala Cys Arg Leu Gly Ser Glu Asp
 115 120 125 130

GCA TGT GGT ATT TTA AAC AAC TAC TAGATTTGAA ATAAATGCTG TTTTITAGCT 494
 Ala Cys Gly Ile Leu Asn Asn Tyr
 135

GGCTTTCATG TTTTGTGAAC CCC 517

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

Met Val Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln
 1 5 10 15
 Tyr Tyr Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser
 20 25 30
 Leu Val Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu
 35 40 45
 Ser Lys Ala Cys Glu Leu Asn Ser Gly Asn Gly Cys Arg Phe Leu Gly
 50 55 60
 Asp Phe Tyr Glu Asn Gly Lys Tyr Val Lys Lys Asp Leu Arg Lys Ala
 65 70 75 80
 Ala Gln Tyr Tyr Ser Lys Ala Cys Gly Leu Asn Asp Gln Asp Gly Cys
 85 90 95
 Leu Ile Leu Gly Tyr Lys Gln Tyr Ala Gly Lys Gly Val Val Lys Asn
 100 105 110
 Glu Lys Gln Ala Val Lys Thr Phe Glu Lys Ala Cys Arg Leu Gly Ser
 115 120 125
 Glu Asp Ala Cys Gly Ile Leu Asn Asn Tyr
 130 135

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid

```

Ile Thr Asn Ser Ser Ala Val Asp Asn Thr Ser Phe Gln Phe Leu Phe
145           150           155           160
Asn Phe Gly Leu Lys Ala Leu Phe Val Asp Glu His Glu Phe Glu Ile
           165           170           175
Gly Phe Lys Phe Pro Thr Ile Asn Asn Lys Tyr Tyr Thr Thr Asp Ala
           180           185           190
Leu Lys Val Gln Met Arg Arg Val Phe Ala Phe Tyr Val Gly Tyr Asn
           195           200           205
Tyr His Phe
210

```

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...464
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

```

AGATTTTCATT CGAGGTAGAA AATACATTGA AAAAGCGTGT GAATTAAACG  ATG GTA      56
                                     Met Val
                                     1

GGG GGT GGA ACG GTA AAA AAA GAC TTG AAG AAA GCC ATT CAA TAC TAT      104
Gly Gly Gly Thr Val Lys Lys Asp Leu Lys Lys Ala Ile Gln Tyr Tyr
      5              10              15

GTT AAA GCG TGT GAA TTG AAT GAA ATG TTT GGG TGT CTG TCA TTA GTT      152
Val Lys Ala Cys Glu Leu Asn Glu Met Phe Gly Cys Leu Ser Leu Val
      20              25              30

TCG AAC TCT CAA ATA AAC AAA CAA AAA CTC TTT CAA TAT CTC TCT AAA      200
Ser Asn Ser Gln Ile Asn Lys Gln Lys Leu Phe Gln Tyr Leu Ser Lys
      35              40              45              50

GCT TGT GAA TTA AAT AGT GGT AAT GGA TGT AGG TTT TTA GGG GAT TTT      248
Ala Cys Glu Leu Asn Ser Gly Asn Gly Cys Arg Phe Leu Gly Asp Phe
      55              60              65

TAT GAG AAT GGA AAA TAT GTA AAA AAG GAT TTA AGA AAA GCT GCT CAA      296
Tyr Glu Asn Gly Lys Tyr Val Lys Lys Asp Leu Arg Lys Ala Ala Gln
      70              75              80

```

120	125	130	135	
GGC AGT AAA GGG CAG GAA TTG TTA GGT ATC ACT AAC AGC AGC GCG GTT				547
Gly Ser Lys Gly Gln Glu Leu Leu Gly Ile Thr Asn Ser Ser Ala Val	140	145	150	
GAT AAC ACC TCT TTT CAA TTC CTC TTT AAC TTT GGC CTC AAG GCT TTA				595
Asp Asn Thr Ser Phe Gln Phe Leu Phe Asn Phe Gly Leu Lys Ala Leu	155	160	165	
TTT GTA GAT GAG CAT GAA TTT GAA ATC GGT TTT AAA TTC CCC ACC ATT				643
Phe Val Asp Glu His Glu Phe Glu Ile Gly Phe Lys Phe Pro Thr Ile	170	175	180	
AAT AAC AAA TAC TAC ACC ACT GAC GCG CTC AAG GTT CAA ATG CGT AGG				691
Asn Asn Lys Tyr Tyr Thr Thr Asp Ala Leu Lys Val Gln Met Arg Arg	185	190	195	
GTC TTT GCC TTT TAT GTG GGG TAT AAT TAC CAC TTC TAAAGGGCTT TTAAAA				743
Val Phe Ala Phe Tyr Val Gly Tyr Asn Tyr His Phe	200	205	210	
CCCAACGCAA CTCCTAACA TCTTTTGGTA ATAGCTCTTG GCTTTGAG				791

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Gly Val Asn Tyr Gln Thr Gly Ser Ile Asn Leu Met Thr Asn Ile	1	5	10	15
His Glu Val Arg Glu Val Thr Asn Tyr Gln Thr Gly Tyr Thr Asn Ile	20	25	30	
Ile Thr Ser Val Asn Ser Val Lys Lys Leu Thr Asn Met Gly Ser Asn	35	40	45	
Gly Ile Gly Leu Val Met Gly Tyr Asn His Phe Phe His Pro Asp Lys	50	55	60	
Ile Leu Gly Leu Arg Tyr Phe Ala Phe Leu Asp Trp Gln Gly Tyr Gly	65	70	75	80
Met Arg Tyr Pro Lys Gly Tyr Tyr Gly Gly Asn Asn Met Ile Thr Tyr	85	90	95	
Gly Val Gly Val Asp Ala Val Trp Asn Phe Phe Gln Gly Ser Phe Tyr	100	105	110	
Gln Asp Asp Ile Ser Val Asp Ile Gly Val Phe Gly Gly Ile Ala Ile	115	120	125	
Ala Gly Asn Ser Trp Tyr Ile Gly Ser Lys Gly Gln Glu Leu Leu Gly	130	135	140	

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 95...727
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

```

CCTTGTTAAA AATGTTAGTT GGTGCAAGCT TGCTGACACA CGCCTTAATA GCTAAAGAAG      60
AAAGCGCAGC NCTTCTTGGA CAAAAAATTT GTAT ATG GGA GTC AAT TAC CAA ACA      115
                               Met Gly Val Asn Tyr Gln Thr
                               1             5

GGT TCT ATC AAT TTA ATG ACT AAT ATC CAT GAA GTT AGA GAA GTT ACT      163
Gly Ser Ile Asn Leu Met Thr Asn Ile His Glu Val Arg Glu Val Thr
          10             15             20

AAC TAT CAA ACC GGT TAC ACC AAT ATT ATA ACT AGC GTT AAT AGC GTT      211
Asn Tyr Gln Thr Gly Tyr Thr Asn Ile Ile Thr Ser Val Asn Ser Val
          25             30             35

AAA AAG CTC ACC AAC ATG GGA TCT AAT GGG ATT GGA TTA GTC ATG GGT      259
Lys Lys Leu Thr Asn Met Gly Ser Asn Gly Ile Gly Leu Val Met Gly
          40             45             50             55

TAT AAC CAC TTT TTC CAT CCG GAT AAA ATC TTG GGC TTG CGC TAT TTC      307
Tyr Asn His Phe Phe His Pro Asp Lys Ile Leu Gly Leu Arg Tyr Phe
          60             65             70

GCT TTT TTA GAT TGG CAA GGC TAT GGC ATG AGA TAC CCT AAA GGC TAT      355
Ala Phe Leu Asp Trp Gln Gly Tyr Gly Met Arg Tyr Pro Lys Gly Tyr
          75             80             85

TAT GGC GGC AAT AAC ATG ATC ACT TAT GGC GTG GGC GTG GAT GCA GTG      403
Tyr Gly Gly Asn Asn Met Ile Thr Tyr Gly Val Gly Val Asp Ala Val
          90             95             100

TGG AAT TTC TTT CAA GGG AGT TTC TAT CAA GAT GAC ATT AGC GTG GAT      451
Trp Asn Phe Phe Gln Gly Ser Phe Tyr Gln Asp Asp Ile Ser Val Asp
          105             110             115

ATT GGC GTT TTT GGG GGG ATT GCG ATT GCG GGG AAT AGC TGG TAT ATT      499
Ile Gly Val Phe Gly Gly Ile Ala Ile Ala Gly Asn Ser Trp Tyr Ile

```

ATC ATG GAC GCT TTA GAT CCT AAA CGC ACC TCT TAAAAGGAGC TTGCATGATT 925
 Ile Met Asp Ala Leu Asp Pro Lys Arg Thr Ser
 275 280 285

TTAGAAGTTA AAGATTTAAA AACTTATTTT TTC 958

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

Met	Glu	Ser	Phe	Arg	Glu	Phe	Ile	Gln	Gln	Phe	Lys	Lys	Asn	Lys	Ala	1	5	10	15
Ala	Val	Val	Gly	Ala	Trp	Ile	Val	Leu	Leu	Leu	Val	Ile	Cys	Ala	Ile	20	25	30	
Phe	Ala	Pro	Leu	Leu	Ala	Pro	His	Asp	Pro	Tyr	Val	Gln	Asn	Ala	Gln	35	40	45	
Asp	Arg	Leu	Leu	Lys	Pro	Ile	Trp	Glu	His	Gly	Gly	Asn	Ala	Lys	Tyr	50	55	60	
Leu	Leu	Gly	Thr	Asp	Asp	Leu	Gly	Arg	Asp	Ile	Leu	Ser	Arg	Leu	Ile	65	70	75	80
Tyr	Gly	Ala	Arg	Ile	Ser	Leu	Thr	Ile	Gly	Ile	Val	Ser	Met	Gly	Ile	85	90	95	
Ala	Val	Phe	Phe	Gly	Thr	Ile	Leu	Gly	Leu	Ile	Ala	Gly	Tyr	Phe	Gly	100	105	110	
Gly	Lys	Thr	Asp	Ala	Ile	Ile	Met	Arg	Ile	Met	Asp	Ile	Met	Phe	Ala	115	120	125	
Leu	Pro	Ser	Ile	Leu	Leu	Ile	Val	Ile	Val	Val	Ala	Val	Leu	Gly	Pro	130	135	140	
Ser	Leu	Thr	Asn	Ala	Met	Leu	Ala	Ile	Gly	Phe	Val	Gly	Ile	Pro	Gly	145	150	155	160
Phe	Ala	Arg	Leu	Val	Arg	Ser	Ser	Val	Leu	Gly	Glu	Lys	Glu	Lys	Glu	165	170	175	
Tyr	Val	Ile	Ala	Ser	Lys	Ile	Asn	Gly	Ser	Ser	His	Leu	Arg	Leu	Met	180	185	190	
Cys	Lys	Val	Ile	Phe	Pro	Asn	Cys	Ile	Ile	Pro	Leu	Ile	Val	Gln	Thr	195	200	205	
Thr	Met	Gly	Phe	Ala	Ser	Thr	Val	Leu	Glu	Ala	Ala	Ala	Leu	Ser	Phe	210	215	220	
Leu	Gly	Leu	Gly	Ala	Gln	Pro	Pro	Lys	Pro	Glu	Trp	Gly	Ala	Met	Leu	225	230	235	240
Met	Asn	Ser	Met	Gln	Tyr	Ile	Ala	Thr	Ala	Pro	Trp	Met	Leu	Val	Phe	245	250	255	
Pro	Gly	Val	Met	Ile	Phe	Leu	Thr	Val	Met	Ser	Phe	Asn	Leu	Val	Gly	260	265	270	
Asp	Gly	Ile	Met	Asp	Ala	Leu	Asp	Pro	Lys	Arg	Thr	Ser				275	280	285	

CTT	TTG	AAG	CCT	ATA	TGG	GAG	CAT	GGA	GGG	AAT	GCT	AAA	TAC	CTT	TTA	248
Leu	Leu	Lys	Pro	Ile	Trp	Glu	His	Gly	Gly	Asn	Ala	Lys	Tyr	Leu	Leu	
				55					60					65		
GGC	ACC	GAT	GAT	TTG	GGG	CGC	GAT	ATT	TTG	AGC	CGC	TTG	ATC	TAT	GGG	296
Gly	Thr	Asp	Asp	Leu	Gly	Arg	Asp	Ile	Leu	Ser	Arg	Leu	Ile	Tyr	Gly	
			70					75					80			
GCC	AGG	ATT	TCT	TTA	ACC	ATA	GGG	ATT	GTT	TCT	ATG	GGG	ATT	GCG	GTG	344
Ala	Arg	Ile	Ser	Leu	Thr	Ile	Gly	Ile	Val	Ser	Met	Gly	Ile	Ala	Val	
		85					90					95				
TTT	TTT	GGC	ACG	ATA	CTA	GGG	CTA	ATA	GCG	GGG	TAT	TTT	GGG	GGG	AAA	392
Phe	Phe	Gly	Thr	Ile	Leu	Gly	Leu	Ile	Ala	Gly	Tyr	Phe	Gly	Gly	Lys	
	100					105					110					
ACA	GAT	GCA	ATT	ATC	ATG	CGT	ATC	ATG	GAC	ATC	ATG	TTC	GCT	TTG	CCC	440
Thr	Asp	Ala	Ile	Ile	Met	Arg	Ile	Met	Asp	Ile	Met	Phe	Ala	Leu	Pro	
115					120				125						130	
TCT	ATT	TTA	TTG	ATC	GTG	ATT	GTG	GTC	GCG	GTG	TTA	GGG	CCT	TCA	CTC	488
Ser	Ile	Leu	Leu	Ile	Val	Ile	Val	Val	Ala	Val	Leu	Gly	Pro	Ser	Leu	
				135				140						145		
ACT	AAC	GCC	ATG	CTC	GCT	ATT	GGG	TTT	GTG	GGG	ATT	CCT	GGG	TTT	GCA	536
Thr	Asn	Ala	Met	Leu	Ala	Ile	Gly	Phe	Val	Gly	Ile	Pro	Gly	Phe	Ala	
		150					155					160				
AGA	TTG	GTG	CGC	AGT	TCC	GTG	CTA	GGT	GAA	AAA	GAA	AAA	GAA	TAC	GTG	584
Arg	Leu	Val	Arg	Ser	Ser	Val	Leu	Gly	Glu	Lys	Glu	Lys	Glu	Tyr	Val	
		165					170					175				
ATC	GCT	TCT	AAA	ATC	AAT	GGC	TCT	TCG	CAT	CTT	CGT	TTG	ATG	TGT	AAG	632
Ile	Ala	Ser	Lys	Ile	Asn	Gly	Ser	Ser	His	Leu	Arg	Leu	Met	Cys	Lys	
	180					185					190					
GTG	ATT	TTC	CCT	AAT	TGC	ATT	ATC	CCT	TTA	ATC	GTT	CAA	ACG	ACA	ATG	680
Val	Ile	Phe	Pro	Asn	Cys	Ile	Ile	Pro	Leu	Ile	Val	Gln	Thr	Thr	Met	
195					200				205						210	
GGT	TTT	GCT	TCC	ACG	GTT	TTA	GAA	GCG	GCT	GCA	CTG	AGC	TTC	TTA	GGT	728
Gly	Phe	Ala	Ser	Thr	Val	Leu	Glu	Ala	Ala	Ala	Leu	Ser	Phe	Leu	Gly	
				215					220					225		
CTT	GGG	GCC	CAA	CCT	CCC	AAA	CCC	GAA	TGG	GGA	GCG	ATG	TTG	ATG	AAT	776
Leu	Gly	Ala	Gln	Pro	Pro	Lys	Pro	Glu	Trp	Gly	Ala	Met	Leu	Met	Asn	
			230					235						240		
TCC	ATG	CAA	TAC	ATC	GCT	ACC	GCT	CCT	TGG	ATG	CTT	GTT	TTC	CCT	GGG	824
Ser	Met	Gln	Tyr	Ile	Ala	Thr	Ala	Pro	Trp	Met	Leu	Val	Phe	Pro	Gly	
		245					250					255				
GTG	ATG	ATT	TTT	TTA	ACG	GTC	ATG	AGT	TTT	AAT	CTG	GTA	GGC	GAT	GGC	872
Val	Met	Ile	Phe	Leu	Thr	Val	Met	Ser	Phe	Asn	Leu	Val	Gly	Asp	Gly	
	260					265					270					

```

          405          410          415
Val Leu Leu Asn Lys Lys Gly Lys Leu Ile Lys Glu Tyr Lys Thr Leu
          420          425          430
Glu Pro Leu Lys Ser Leu Glu Ile Arg Leu Ser Glu Ala Pro Ile Asp
          435          440          445
Lys Arg Asn Asp Phe Leu Tyr His Lys Thr Thr Tyr Ala Pro Phe Tyr
          450          455          460
Gln Lys Ala Arg Ala Leu Ile Lys Lys Gly Val Met Phe Asp Glu Ile
          465          470          475          480
Phe Tyr Asn Gln Asp Leu Glu Leu Thr Glu Gly Ala Arg Ser Asn Leu
          485          490          495
Val Leu Glu Ile His Asn Arg Leu Leu Thr Pro Tyr Phe Ser Ala Gly
          500          505          510
Ala Leu Asn Gly Thr Gly Val Val Gly Leu Leu Lys Lys Gly Leu Val
          515          520          525
Gly His Ala Pro Leu Lys Leu Gln Asp Leu Gln Lys Ala Ser Lys Ile
          530          535          540
Tyr Cys Ile Asn Ala Leu Tyr Gly Leu Val Glu Val Lys Ile Lys
          545          550          555

```

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...905
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

```

TTAGTGGATA TTTTATACGC TTTTATTGAT CCTAGAATAA GGTTGTCATA  ATG GAG      56
                                     Met Glu
                                     1

TCT TTT AGA GAG TTT ATC CAA CAA TTC AAA AAA AAT AAG GCA GCG GTC      104
Ser Phe Arg Glu Phe Ile Gln Gln Phe Lys Lys Asn Lys Ala Ala Val
      5              10              15

GTT GGG GCT TGG ATT GTG CTT TTA TTG GTA ATT TGC GCG ATT TTT GCG      152
Val Gly Ala Trp Ile Val Leu Leu Leu Val Ile Cys Ala Ile Phe Ala
      20              25              30

CCC CTT TTA GCC CCG CAT GAT CCT TAT GTC CAA AAC GCG CAA GAT CGC      200
Pro Leu Leu Ala Pro His Asp Pro Tyr Val Gln Asn Ala Gln Asp Arg
      35              40              45              50

```

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

```

Met Ile Phe Gly Asp Phe Lys Tyr Gln Lys Ser Val Lys Lys Leu Thr
 1           5           10           15
Ala Thr Asn Leu Asn Glu Leu Lys Asn Ala Leu Asp Phe Ile Ser Gln
           20           25           30
Asn Arg Gly Asn Gly Tyr Phe Val Gly Tyr Leu Leu Tyr Glu Ala Arg
           35           40           45
Leu Ala Phe Leu Asp Glu Asn Phe Gln Ser Gln Thr Pro Phe Leu Tyr
           50           55           60
Phe Glu Gln Phe Leu Glu Arg Lys Lys Tyr Ser Leu Glu Pro Leu Lys
65           70           75           80
Glu His Ala Phe Tyr Pro Lys Ile His Ser Ser Leu Asp Gln Lys Thr
           85           90           95
Tyr Phe Lys Gln Phe Lys Ala Val Lys Glu Arg Leu Lys Asn Gly Asp
           100          105          110
Thr Tyr Gln Val Asn Leu Thr Met Asp Leu Phe Leu Asp Thr Lys Ala
           115          120          125
Lys Pro Lys Arg Val Phe Lys Glu Val Val His Asn Gln Asn Thr Pro
           130          135          140
Phe Lys Ala Phe Ile Glu Asn Glu Phe Gly Ser Val Leu Ser Phe Ser
145          150          155          160
Pro Glu Leu Phe Phe Glu Leu Glu Phe Leu Asp Thr Ala Ile Lys Ile
           165          170          175
Ile Thr Lys Pro Met Lys Gly Thr Ile Ala Arg Ser Lys Asn Pro Leu
           180          185          190
Ile Asp Glu Lys Asn Arg Leu Phe Leu Gln Asn Asp Asp Lys Asn Arg
           195          200          205
Ser Glu Asn Val Met Ile Val Asp Leu Leu Arg Asn Asp Leu Ser Arg
           210          215          220
Leu Ala Leu Lys Asn Ser Val Lys Val Asn Gln Leu Phe Glu Ile Ile
225          230          235          240
Ser Leu Pro Ser Val Tyr Gln Met Ile Ser Glu Ile Glu Ala Lys Leu
           245          250          255
Pro Leu Lys Thr Ser Leu Phe Glu Ile Phe Lys Ala Leu Phe Pro Cys
           260          265          270
Gly Ser Val Thr Gly Cys Pro Lys Ile Lys Thr Met Gln Ile Ile Glu
           275          280          285
Ser Leu Glu Lys Arg Pro Arg Gly Val Tyr Cys Gly Ala Ile Gly Met
           290          295          300
Val Glu Glu Lys Lys Ala Leu Phe Ser Val Pro Ile Arg Thr Leu Glu
305          310          315          320
Lys Arg Val His Glu Asn Phe Leu His Leu Gly Val Gly Ser Gly Val
           325          330          335
Thr Tyr Lys Ser Lys Ala Pro Lys Glu Tyr Glu Glu Ser Phe Leu Lys
           340          345          350
Ser Phe Phe Val Met Pro Lys Ile Glu Phe Glu Ile Val Glu Thr Met
           355          360          365
Lys Ile Ile Lys Lys Asp Gln Lys Leu Glu Ile Asn Asn Lys Asn Ala
           370          375          380
His Lys Glu Arg Leu Met Asn Ser Thr Arg Tyr Phe Asn Phe Lys Tyr
385          390          395          400
Asp Glu Asn Leu Leu Asp Phe Glu Leu Glu Lys Glu Gly Val Leu Arg

```


GAA CGC TTA ATG AAT AGC ACT CGA TAT TTT AAC TTT AAA TAC GAT GAA	1256
Glu Arg Leu Met Asn Ser Thr Arg Tyr Phe Asn Phe Lys Tyr Asp Glu	
390 395 400	
AAT CTT TTA GAT TTT GAA TTA GAA AAA GAA GGG GTT TTA AGG GTT TTA	1304
Asn Leu Leu Asp Phe Glu Leu Glu Lys Glu Gly Val Leu Arg Val Leu	
405 410 415	
CTC AAT AAA AAG GGC AAG CTC ATT AAA GAA TAC AAA ACC TTA GAG CCT	1352
Leu Asn Lys Lys Gly Lys Leu Ile Lys Glu Tyr Lys Thr Leu Glu Pro	
420 425 430	
TTA AAA AGC CTA GAA ATC CGT TTG AGT GAA GCC CCC ATT GAT AAA CGC	1400
Leu Lys Ser Leu Glu Ile Arg Leu Ser Glu Ala Pro Ile Asp Lys Arg	
435 440 445 450	
AAT GAT TTT TTA TAC CAT AAG ACC ACT TAT GCC CCT TTT TAT CAA AAG	1448
Asn Asp Phe Leu Tyr His Lys Thr Thr Tyr Ala Pro Phe Tyr Gln Lys	
455 460 465	
GCT CGA GCG CTC ATT AAA AAG GGC GTT ATG TTT GAT GAA ATC TTT TAT	1496
Ala Arg Ala Leu Ile Lys Lys Gly Val Met Phe Asp Glu Ile Phe Tyr	
470 475 480	
AAC CAG GAT TTG GAA CTC ACT GAG GGC GCT AGG AGC AAT CTT GTT TTA	1544
Asn Gln Asp Leu Glu Leu Thr Glu Gly Ala Arg Ser Asn Leu Val Leu	
485 490 495	
GAA ATC CAT AAC AGG CTT TTA ACC CCT TAT TTT AGC GCG GGC GCG TTA	1592
Glu Ile His Asn Arg Leu Leu Thr Pro Tyr Phe Ser Ala Gly Ala Leu	
500 505 510	
AAC GGG ACG GGT GTT GTG GGG TTG TTA AAA AAG GGT CTT GTT GGG CAT	1640
Asn Gly Thr Gly Val Val Gly Leu Leu Lys Lys Gly Leu Val Gly His	
515 520 525 530	
GCA CCT TTG AAA TTG CAA GAT TTG CAA AAA GCG TCT AAA ATC TAT TGT	1688
Ala Pro Leu Lys Leu Gln Asp Leu Gln Lys Ala Ser Lys Ile Tyr Cys	
535 540 545	
ATT AAC GCG CTA TAT GGC TTA GTG GAA GTG AAA ATA AAA TAACTATAAA AA	1739
Ile Asn Ala Leu Tyr Gly Leu Val Glu Val Lys Ile Lys	
550 555	
CAGAGCGGCT AAAACCTCAT TTTTAGAAAT AGGTTACCCA A	1780

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

TTG TTT TTT GAA TTA GAG TTT TTA GAT ACA GCG ATT AAG ATT ATT ACA	584
Leu Phe Phe Glu Leu Glu Phe Leu Asp Thr Ala Ile Lys Ile Ile Thr	
165 170 175	
AAA CCC ATG AAA GGC ACG ATC GCT CGC TCA AAA AAC CCC TTA ATA GAT	632
Lys Pro Met Lys Gly Thr Ile Ala Arg Ser Lys Asn Pro Leu Ile Asp	
180 185 190	
GAA AAA AAC CGA TTG TTT TTG CAA AAT GAT GAC AAA AAC AGA AGC GAA	680
Glu Lys Asn Arg Leu Phe Leu Gln Asn Asp Asp Lys Asn Arg Ser Glu	
195 200 205 210	
AAT GTG ATG ATT GTG GAT TTA TTG CGT AAC GAT TTG AGC CGC TTG GCC	728
Asn Val Met Ile Val Asp Leu Leu Arg Asn Asp Leu Ser Arg Leu Ala	
215 220 225	
TTA AAA AAT AGC GTG AAA GTC AAT CAA TTG TTT GAA ATC ATC AGC TTG	776
Leu Lys Asn Ser Val Lys Val Asn Gln Leu Phe Glu Ile Ile Ser Leu	
230 235 240	
CCT AGC GTG TAT CAA ATG ATA AGC GAG ATT GAA GCG AAA TTG CCC CTA	824
Pro Ser Val Tyr Gln Met Ile Ser Glu Ile Glu Ala Lys Leu Pro Leu	
245 250 255	
AAA ACC AGC TTG TTT GAG ATT TTT AAG GCG TTG TTC CCT TGC GGC TCT	872
Lys Thr Ser Leu Phe Glu Ile Phe Lys Ala Leu Phe Pro Cys Gly Ser	
260 265 270	
GTG ACC GGA TGC CCT AAA ATC AAA ACC ATG CAA ATC ATT GAA AGT TTA	920
Val Thr Gly Cys Pro Lys Ile Lys Thr Met Gln Ile Ile Glu Ser Leu	
275 280 285 290	
GAA AAA CGC CCT AGG GGG GTG TAT TGC GGG GCG ATA GGC ATG GTT GAA	968
Glu Lys Arg Pro Arg Gly Val Tyr Cys Gly Ala Ile Gly Met Val Glu	
295 300 305	
GAA AAA AAA GCC CTT TTT AGC GTG CCT ATC CGC ACT TTA GAA AAA AGA	1016
Glu Lys Lys Ala Leu Phe Ser Val Pro Ile Arg Thr Leu Glu Lys Arg	
310 315 320	
GTG CAC GAA AAT TTT TTG CAT TTA GGG GTA GGG AGT GGG GTA ACT TAT	1064
Val His Glu Asn Phe Leu His Leu Gly Val Gly Ser Gly Val Thr Tyr	
325 330 335	
AAA AGT AAA GCG CCA AAA GAA TAT GAA GAA AGC TTT TTG AAA TCC TTT	1112
Lys Ser Lys Ala Pro Lys Glu Tyr Glu Glu Ser Phe Leu Lys Ser Phe	
340 345 350	
TTT GTG ATG CCC AAA ATA GAA TTT GAG ATT GTA GAA ACG ATG AAA ATT	1160
Phe Val Met Pro Lys Ile Glu Phe Glu Ile Val Glu Thr Met Lys Ile	
355 360 365 370	
ATC AAA AAG GAT CAA AAA TTA GAG ATT AAT AAT AAA AAC GCC CAT AAA	1208
Ile Lys Lys Asp Gln Lys Leu Glu Ile Asn Asn Lys Asn Ala His Lys	
375 380 385	

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1727
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

ATAACCCGGT GTTTTTGATA GACAAATACG AAGCCGTTGC TAAAAATTAA	ATG ATT	56
	Met Ile	
	1	
TTT GGG GAT TTT AAA TAT CAA AAA AGC GTT AAA AAA CTC ACA GCC ACC		104
Phe Gly Asp Phe Lys Tyr Gln Lys Ser Val Lys Lys Leu Thr Ala Thr		
5 10 15		
AAT CTT AAT GAG CTT AAA AAC GCC CTG GAT TTC ATC TCT CAA AAT AGG		152
Asn Leu Asn Glu Leu Lys Asn Ala Leu Asp Phe Ile Ser Gln Asn Arg		
20 25 30		
GGG AAT GGG TAT TTT GTG GGG TAT CTT TTA TAT GAA GCG CGC TTA GCG		200
Gly Asn Gly Tyr Phe Val Gly Tyr Leu Leu Tyr Glu Ala Arg Leu Ala		
35 40 45 50		
TTT TTA GAT GAA AAT TTT CAA AGC CAA ACC CCT TTT TTG TAT TTT GAA		248
Phe Leu Asp Glu Asn Phe Gln Ser Gln Thr Pro Phe Leu Tyr Phe Glu		
55 60 65		
CAA TTT TTA GAA AGA AAA AAA TAT TCT TTA GAG CCT TTA AAA GAG CAT		296
Gln Phe Leu Glu Arg Lys Lys Tyr Ser Leu Glu Pro Leu Lys Glu His		
70 75 80		
GCG TTT TAC CCT AAA ATC CAT AGT TCT TTA GAT CAA AAA ACT TAT TTC		344
Ala Phe Tyr Pro Lys Ile His Ser Ser Leu Asp Gln Lys Thr Tyr Phe		
85 90 95		
AAG CAG TTT AAA GCC GTT AAA GAG CGT CTC AAA AAC GGC GAC ACC TAT		392
Lys Gln Phe Lys Ala Val Lys Glu Arg Leu Lys Asn Gly Asp Thr Tyr		
100 105 110		
CAA GTG AAT CTC ACA ATG GAT TTA TTT TTA GAC ACT AAA GCC AAA CCA		440
Gln Val Asn Leu Thr Met Asp Leu Phe Leu Asp Thr Lys Ala Lys Pro		
115 120 125 130		
AAG CGC GTT TTT AAG GAG GTG GTA CAC AAC CAA AAC ACG CCT TTT AAG		488
Lys Arg Val Phe Lys Glu Val Val His Asn Gln Asn Thr Pro Phe Lys		
135 140 145		
GCT TTT ATA GAA AAT GAG TTT GGG AGC GTT TTA AGC TTT TCG CCG GAA		536
Ala Phe Ile Glu Asn Glu Phe Gly Ser Val Leu Ser Phe Ser Pro Glu		
150 155 160		

Ala Gly Glu Ala Ala Leu Gln Ser Ala Glu Phe Ala Arg Ser His Ala
 115 120 125 130

CAA AGC GAA TGG TTG TTT AAG GAA TTG TTT GTG CTG GTG TGC GCT TTG 488
 Gln Ser Glu Trp Leu Phe Lys Glu Leu Phe Val Leu Val Cys Ala Leu
 135 140 145

TTT TTT TGG CGT TTG CTT GGA AAA AAT GTG CTT TAGTCCCTTT GATTTAATCA 541
 Phe Phe Trp Arg Leu Leu Gly Lys Asn Val Leu
 150 155

AATGAGAGAG TTTTGGCTA CTATCTAGGA AAT 574

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

Met Lys Lys Phe Gly Leu Gly Val Tyr Leu Leu Leu Leu Gly Ile Leu
 1 5 10 15
 Gly Gly Ser Leu Ile Ile Leu Gly Ala Ile Val Ala Pro Ile Val Phe
 20 25 30
 Lys Ala Ser Ser Val Leu Pro Glu Leu His Leu Thr Pro Phe Glu Ser
 35 40 45
 Gly Lys Leu Met Ala Gln Ile Phe Val Arg Phe Asn Tyr Val Leu Gly
 50 55 60
 Ala Ile Gly Phe Val Val Leu Leu Tyr Glu Ile Ile Ser Phe Ile Tyr
 65 70 75 80
 Tyr Lys Arg Ser Leu Val Tyr Leu Ile Leu Gly Val Ala Ile Gly Ala
 85 90 95
 Leu Cys Leu Leu Phe Val Phe Tyr Tyr Thr Pro Tyr Ile Leu Asn Ala
 100 105 110
 Gln Lys Ala Gly Glu Ala Ala Leu Gln Ser Ala Glu Phe Ala Arg Ser
 115 120 125
 His Ala Gln Ser Glu Trp Leu Phe Lys Glu Leu Phe Val Leu Val Cys
 130 135 140
 Ala Leu Phe Phe Trp Arg Leu Leu Gly Lys Asn Val Leu
 145 150 155

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...521
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```

AGTTTAAGGA TTGCAACCAT TTGTTGCAAA AATCTTAAAA AAGGTGGAAG  ATG AAA      56
                                     Met Lys
                                     1

AAA TTT GGT TTG GGG GTG TAT TTG CTT CTT TTA GGT ATT TTG GGC GGC      104
Lys Phe Gly Leu Gly Val Tyr Leu Leu Leu Leu Gly Ile Leu Gly Gly
      5              10              15

TCT TTG ATC ATT CTA GGA GCG ATA GTC GCG CCC ATT GTT TTC AAA GCT      152
Ser Leu Ile Ile Leu Gly Ala Ile Val Ala Pro Ile Val Phe Lys Ala
      20              25              30

TCA AGC GTT TTA CCT GAA TTG CAT CTG ACT CCC TTT GAG AGC GGG AAA      200
Ser Ser Val Leu Pro Glu Leu His Leu Thr Pro Phe Glu Ser Gly Lys
      35              40              45              50

CTC ATG GCG CAA ATC TTT GTG CGT TTC AAT TAT GTT TTA GGC GCG ATC      248
Leu Met Ala Gln Ile Phe Val Arg Phe Asn Tyr Val Leu Gly Ala Ile
              55              60              65

GGT TTT GTA GTG TTA CTT TAT GAA ATC ATT TCG TTT ATT TAT TAC AAA      296
Gly Phe Val Val Leu Leu Tyr Glu Ile Ile Ser Phe Ile Tyr Tyr Lys
      70              75              80

AGA TCG TTA GTG TAT TTG ATC CTT GGC GTG GCG ATA GGG GCG TTG TGT      344
Arg Ser Leu Val Tyr Leu Ile Leu Gly Val Ala Ile Gly Ala Leu Cys
      85              90              95

TTG CTC TTT GTT TTT TAT TAC ACG CCT TAT ATT TTA AAC GCT CAA AAA      392
Leu Leu Phe Val Phe Tyr Tyr Thr Pro Tyr Ile Leu Asn Ala Gln Lys
      100              105              110

GCG GGC_GAA GCC GCG CTT CAA AGT GCT GAA TTT GCC CGC TCG CAC GCT      440

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

```

Met Lys Lys Val Tyr Phe Lys Thr Phe Gly Cys Arg Thr Asn Leu Phe
 1      5      10      15
Asp Thr Gln Val Met Ser Glu Asn Leu Lys Asp Phe Ser Thr Thr Leu
      20      25      30
Glu Glu Gln Glu Ala Asp Ile Ile Ile Ile Asn Ser Cys Thr Val Thr
      35      40      45
Asn Gly Ala Asp Ser Ala Val Arg Ser Tyr Ala Lys Lys Met Ala Arg
      50      55      60
Leu Asp Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly
65      70      75      80
Lys Glu Leu Phe Glu Lys Gly Phe Leu Lys Gly Val Phe Gly His Asp
      85      90      95
Asn Lys Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe
      100      105      110
Ile Asp Asp Asn Leu Glu Asn Lys His Leu Asp Thr Thr Met Val Ser
      115      120      125
Glu Phe Val Gly Lys Thr Arg Ala Phe Ile Lys Ile Gln Glu Gly Cys
      130      135      140
Asp Phe Asp Cys Asn Tyr Cys Ile Ile Pro Ser Val Arg Gly Arg Ala
145      150      155      160
Arg Ser Phe Glu Glu Arg Lys Ile Leu Glu Gln Val Gly Leu Leu Cys
      165      170      175
Ser Lys Gly Val Gln Glu Val Val Leu Thr Gly Thr Asn Val Gly Ser
      180      185      190
Tyr Gly Lys Asp Arg Gly Ser Asn Ile Ala Arg Leu Ile Lys Lys Leu
      195      200      205
Ser Gln Ile Ala Gly Leu Lys Arg Ile Arg Ile Gly Ser Leu Glu Pro
      210      215      220
Asn Gln Ile Asn Asp Glu Phe Leu Glu Leu Leu Glu Glu Asp Phe Leu
225      230      235      240
Glu Lys His Leu His Ile Ala Leu Gln His Ser His Asp Leu Met Leu
      245      250      255
Glu Arg Met Asn Arg Arg Asn Arg Thr Lys Ser Asp Arg Glu Leu Leu
      260      265      270
Glu Thr Ile Ala Ser Lys Asn Phe Ala Ile Gly Thr Asp Phe Ile Val
      275      280      285
Gly His Pro Gly Glu Ser Gly Ser Val Phe Glu Lys Ala Phe Lys Asn
      290      295      300
Leu Glu Ser Leu Pro Leu Thr His Ile His Pro Phe Ile Tyr Ser Lys
305      310      315      320
Arg Lys Asp Thr Pro Ser Ser Leu Met Thr Asp Ser Val Ser Leu Glu
      325      330      335
Asp Ser Lys Lys Arg Leu Asn Ala Ile Lys Asp Leu Ile Phe His Lys
      340      345      350
Asn Lys Ala Phe Arg Gln Leu Gln Leu Lys Leu Asn Thr Pro Leu Lys
      355      360      365
Ala Leu Val Glu Val Gln Lys Asp Gly Glu Phe Lys Ala Leu Asp Gln
      370      375      380
Phe Phe Asn Pro Ile Lys Ile Lys Ser Asp Lys Pro Leu Arg Ala Ser
385      390      395      400
Phe Leu Glu Ile Lys Glu Tyr Glu Ile Lys Glu Arg Glu Asn His Ala
      405      410      415
Val Phe

```

His	Leu	His	Ile	Ala	Leu	Gln	His	Ser	His	Asp	Leu	Met	Leu	Glu	Arg	
		245					250					255				
ATG	AAT	CGA	AGA	AAC	CGC	ACT	AAA	AGC	GAT	AGG	GAA	TTA	TTA	GAA	ACA	872
Met	Asn	Arg	Arg	Asn	Arg	Thr	Lys	Ser	Asp	Arg	Glu	Leu	Leu	Glu	Thr	
	260					265					270					
ATC	GCT	TCT	AAG	AAT	TTT	GCT	ATT	GGC	ACG	GAT	TTT	ATT	GTG	GGG	CAT	920
Ile	Ala	Ser	Lys	Asn	Phe	Ala	Ile	Gly	Thr	Asp	Phe	Ile	Val	Gly	His	
275					280					285					290	
CCG	GGC	GAG	AGC	GGA	AGC	GTT	TTT	GAA	AAA	GCG	TTT	AAA	AAT	TTA	GAA	968
Pro	Gly	Glu	Ser	Gly	Ser	Val	Phe	Glu	Lys	Ala	Phe	Lys	Asn	Leu	Glu	
				295					300					305		
AGC	TTG	CCT	TTA	ACG	CAC	ATC	CAC	CCT	TTT	ATT	TAC	AGC	AAA	CGA	AAA	1016
Ser	Leu	Pro	Leu	Thr	His	Ile	His	Pro	Phe	Ile	Tyr	Ser	Lys	Arg	Lys	
		310						315					320			
GAC	ACC	CCC	TCT	AGC	TTG	ATG	ACT	GAT	AGC	GTG	AGT	TTG	GAA	GAT	TCT	1064
Asp	Thr	Pro	Ser	Ser	Leu	Met	Thr	Asp	Ser	Val	Ser	Leu	Glu	Asp	Ser	
		325					330					335				
AAA	AAG	CGT	TTG	AAT	GCG	ATT	AAA	GAT	TTG	ATT	TTT	CAT	AAA	AAT	AAG	1112
Lys	Lys	Arg	Leu	Asn	Ala	Ile	Lys	Asp	Leu	Ile	Phe	His	Lys	Asn	Lys	
	340					345					350					
GCG	TTC	AGG	CAA	TTG	CAG	CTC	AAG	CTC	AAT	ACG	CCT	CTA	AAA	GCC	TTA	1160
Ala	Phe	Arg	Gln	Leu	Gln	Leu	Lys	Leu	Asn	Thr	Pro	Leu	Lys	Ala	Leu	
355					360				365						370	
GTG	GAA	GTG	CAA	AAA	GAC	GGC	GAA	TTT	AAA	GCC	TTA	GAT	CAA	TTT	TTC	1208
Val	Glu	Val	Gln	Lys	Asp	Gly	Glu	Phe	Lys	Ala	Leu	Asp	Gln	Phe	Phe	
				375					380					385		
AAC	CCC	ATT	AAA	ATC	AAA	AGC	GAT	AAG	CCT	CTA	AGG	GCT	AGT	TTT	TTA	1256
Asn	Pro	Ile	Lys	Ile	Lys	Ser	Asp	Lys	Pro	Leu	Arg	Ala	Ser	Phe	Leu	
		390						395					400			
GAA	ATC	AAA	GAG	TAT	GAA	ATT	AAG	GAG	AGG	GAA	AAT	CAT	GCC	GTT	TTC	T 1305
Glu	Ile	Lys	Glu	Tyr	Glu	Ile	Lys	Glu	Arg	Glu	Asn	His	Ala	Val	Phe	
	405					410					415					
AAAAATTTAG	AAAATCTTAC	CGCTCCCTTC	AAACGCATTA	AAAACCGCTC	GC											1357

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

20	25	30	
CAA GAA GCC GAT ATT ATT ATC ATC AAT TCT TGC ACC GTG ACC AAT GGG			200
Gln Glu Ala Asp Ile Ile Ile Ile Asn Ser Cys Thr Val Thr Asn Gly			
35	40	45	50
GCC GAT AGC GCG GTA AGG AGT TAC GCT AAA AAA ATG GCA CGG TTG GAT			248
Ala Asp Ser Ala Val Arg Ser Tyr Ala Lys Lys Met Ala Arg Leu Asp			
	55	60	65
AAG GAA GTG CTA TTT ACT GGT TGC GGG GTG AAA ACC CAA GGC AAA GAG			296
Lys Glu Val Leu Phe Thr Gly Cys Gly Val Lys Thr Gln Gly Lys Glu			
	70	75	80
CTT TTT GAA AAA GGG TTT TTA AAG GGC GTT TTT GGG CAT GAC AAT AAA			344
Leu Phe Glu Lys Gly Phe Leu Lys Gly Val Phe Gly His Asp Asn Lys			
	85	90	95
GAA AAG ATT AAC GCG CTT TTA CAA GAA AAA AAG CGT TTT TTT ATA GAT			392
Glu Lys Ile Asn Ala Leu Leu Gln Glu Lys Lys Arg Phe Phe Ile Asp			
	100	105	110
GAC AAT TTA GAA AAC AAG CAC TTA GAC ACC ACG ATG GTG AGC GAG TTT			440
Asp Asn Leu Glu Asn Lys His Leu Asp Thr Thr Met Val Ser Glu Phe			
	115	120	125
GTG GGA AAA ACT AGG GCG TTT ATT AAG ATC CAA GAA GGC TGT GAT TTT			488
Val Gly Lys Thr Arg Ala Phe Ile Lys Ile Gln Glu Gly Cys Asp Phe			
	135	140	145
GAT TGC AAT TAT TGC ATT ATC CCA AGC GTG AGA GGG AGG GCT AGG AGT			536
Asp Cys Asn Tyr Cys Ile Ile Pro Ser Val Arg Gly Arg Ala Arg Ser			
	150	155	160
TTT GAA GAG AGA AAA ATT TTA GAG CAA GTG GGC CTT TTA TGC TCT AAA			584
Phe Glu Glu Arg Lys Ile Leu Glu Gln Val Gly Leu Leu Cys Ser Lys			
	165	170	175
GGG GTT CAA GAA GTG GTT TTA ACC GGC ACC AAT GTG GGG AGC TAT GGG			632
Gly Val Gln Glu Val Val Leu Thr Gly Thr Asn Val Gly Ser Tyr Gly			
	180	185	190
AAA GAT AGA GGA AGC AAT ATC GCG CGA TTG ATT AAA AAA TTA AGC CAG			680
Lys Asp Arg Gly Ser Asn Ile Ala Arg Leu Ile Lys Lys Leu Ser Gln			
	195	200	205
ATC GCT GGA TTA AAA CGC ATA AGG ATT GGG AGC TTA GAA CCT AAT CAA			728
Ile Ala Gly Leu Lys Arg Ile Arg Ile Gly Ser Leu Glu Pro Asn Gln			
	215	220	225
ATT AAC GAT GAA TTT TTA GAG CTT TTA GAA GAG GAT TTT TTA GAA AAA			776
Ile Asn Asp Glu Phe Leu Glu Leu Leu Glu Glu Asp Phe Leu Glu Lys			
	230	235	240
CAT TTG_CAT ATC GCT TTA CAG CAC AGC CAT GAT CTC ATG CTA GAG AGG			824


```

His Leu Lys Met Arg Ser Leu Ser Val Gly Leu Thr His Glu Gly Phe
    195                                200                205
Asp Gly Tyr Ala Ile Gly Gly Leu Ala Val Gly Glu Ser Ala Asp Glu
    210                                215                220
Met Leu Glu Thr Ile Ala His Thr Ala Pro Leu Leu Pro Lys Asp Lys
    225                                230                235                240
Pro Arg Tyr Leu Met Gly Val Gly Thr Pro Glu Asn Ile Leu Asp Ala
    245                                250                255
Ile Ser Leu Gly Val Asp Met Phe Asp Cys Val Met Pro Thr Arg Asn
    260                                265                270
Ala Arg Asn Ala Thr Leu Phe Thr His Ser Gly Lys Ile Ser Ile Lys
    275                                280                285
Asn Ala Pro Tyr Lys Leu Asp Asn Thr Pro Ile Glu Glu Asn Cys Ala
    290                                295                300
Cys Tyr Ala Cys Lys Arg Tyr Ser Lys Ala Tyr Leu His His Leu Phe
    305                                310                315                320
Arg Ala Lys Glu Leu Thr Tyr Ala Arg Leu Ala Ser Leu His Asn Leu
    325                                330                335
His Phe Tyr Leu Glu Leu Val Lys Asn Ala Arg Asn Ala Ile Leu Glu
    340                                345                350
Lys Arg Phe Leu Ser Phe Lys Lys Glu Phe Leu Glu Lys Tyr Asn Ser
    355                                360                365
Arg Ser His
    370

```

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1304
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

```

GTGGATGCTG ATTTTATTAGG CGATGGTTTT GGAATAAAAA GGGAACAAAA  ATG AAA      56
                                     Met Lys
                                     1

AAA GTC TAT TTC AAA ACT TTT GGG TGC AGG ACG AAT CTT TTT GAC ACG      104
Lys Val Tyr Phe Lys Thr Phe Gly Cys Arg Thr Asn Leu Phe Asp Thr
    5                                10                15

CAA GTG ATG AGC GAG AAT TTG AAG GAC TTT AGC ACG ACC TTA GAA GAA      152
Gln Val Met Ser Glu Asn Leu Lys Asp Phe Ser Thr Thr Leu Glu Glu

```

GCT AAA GAA CTC ACT TAC GCT CGT TTG GCC AGC TTG CAC AAT TTG CAT 1068
 Ala Lys Glu Leu Thr Tyr Ala Arg Leu Ala Ser Leu His Asn Leu His
 325 330 335

TTT TAT TTA GAG CTG GTG AAG AAC GCC AGA AAC GCC ATT TTA GAA AAG 1116
 Phe Tyr Leu Glu Leu Val Lys Asn Ala Arg Asn Ala Ile Leu Glu Lys
 340 345 350

CGG TTT TTG AGT TTT AAA AAA GAA TTT TTG GAG AAA TAC AAC TCC CGC 1164
 Arg Phe Leu Ser Phe Lys Lys Glu Phe Leu Glu Lys Tyr Asn Ser Arg
 355 360 365

TCT CAT TGAATGATGG AATGCAAAAA TACTAAAAAG CGTTTTTTTAC CATCAATAAA AG 1222
 Ser His
 370

TTTTCTTAAA A 1233

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

Met Asp Phe Gln Leu Gln Ala Thr Asp Asn Asn Ala Arg Ala Gly Leu
 1 5 10 15
 Leu Asn Leu Ala His Ser Gln Val Ala Thr Pro Val Phe Met Pro Val
 20 25 30
 Gly Thr Gln Gly Cys Ile Lys Ser Leu Asp Ala Thr Asp Ala Gln Glu
 35 40 45
 Ile Leu Gly Ala Lys Leu Ile Leu Ala Asn Thr Tyr His Met Tyr Leu
 50 55 60
 Arg Pro Gly Glu Lys Val Val Glu Glu Leu Gly Gly Leu His Arg Phe
 65 70 75 80
 Ala Gln Phe Tyr Gly Ser Phe Leu Thr Asp Ser Gly Gly Phe Gln Ala
 85 90 95
 Phe Ser Leu Ser Asp Asn Val Lys Leu Gln Glu Asp Gly Ile Val Phe
 100 105 110
 Lys Ser His Ile Asp Gly Ser Lys His Leu Phe Thr Pro Ala Lys Val
 115 120 125
 Leu Asp Ile Gln Tyr Ser Leu Asn Ser Asp Ile Met Met Val Leu Asp
 130 135 140
 Asp Leu Val Gly Leu Pro Ala Pro Leu Lys Arg Leu Glu Glu Ser Ile
 145 150 155 160
 Lys Arg Ser Ala Lys Trp Ala Asn Met Ser Leu Glu Tyr His Lys Glu
 165 170 175
 Lys Asn Arg Pro Ser Asn Asn Leu Phe Ala Ile Ile Gln Gly Gly Thr
 180 185 190

AGT	TTG	AGC	GAT	AAT	GTC	AAA	TTG	CAA	GAA	GAT	GGG	ATC	GTT	TTT	AAA	396
Ser	Leu	Ser	Asp	Asn	Val	Lys	Leu	Gln	Glu	Asp	Gly	Ile	Val	Phe	Lys	
		100					105					110				
TCC	CAT	ATT	GAT	GGG	AGC	AAG	CAT	CTA	TTC	ACG	CCC	GCT	AAA	GTT	TTG	444
Ser	His	Ile	Asp	Gly	Ser	Lys	His	Leu	Phe	Thr	Pro	Ala	Lys	Val	Leu	
	115					120					125					
GAC	ATT	CAA	TAT	TCT	TTG	AAT	AGC	GAT	ATT	ATG	ATG	GTT	TTA	GAC	GAT	492
Asp	Ile	Gln	Tyr	Ser	Leu	Asn	Ser	Asp	Ile	Met	Met	Val	Leu	Asp	Asp	
130					135				140					145		
TTA	GTG	GGC	TTG	CCC	GCT	CCC	TTA	AAA	CGC	CTT	GAA	GAA	TCC	ATT	AAA	540
Leu	Val	Gly	Leu	Pro	Ala	Pro	Leu	Lys	Arg	Leu	Glu	Glu	Ser	Ile	Lys	
			150						155					160		
AGA	AGT	GCT	AAA	TGG	GCG	AAT	ATG	AGC	CTA	GAA	TAC	CAC	AAA	GAA	AAA	588
Arg	Ser	Ala	Lys	Trp	Ala	Asn	Met	Ser	Leu	Glu	Tyr	His	Lys	Glu	Lys	
		165					170						175			
AAC	CGC	CCG	AGC	AAC	AAC	CTT	TTT	GCC	ATT	ATC	CAG	GGC	GGG	ACG	CAT	636
Asn	Arg	Pro	Ser	Asn	Asn	Leu	Phe	Ala	Ile	Ile	Gln	Gly	Gly	Thr	His	
	180					185						190				
TTG	AAA	ATG	CGC	AGC	CTT	AGC	GTG	GGA	TTA	ACG	CAT	GAG	GGT	TTT	GAT	684
Leu	Lys	Met	Arg	Ser	Leu	Ser	Val	Gly	Leu	Thr	His	Glu	Gly	Phe	Asp	
	195				200						205					
GGC	TAC	GCT	ATA	GGC	GGT	TTA	GCG	GTG	GGG	GAA	AGC	GCT	GAT	GAA	ATG	732
Gly	Tyr	Ala	Ile	Gly	Gly	Leu	Ala	Val	Gly	Glu	Ser	Ala	Asp	Glu	Met	
210				215					220					225		
CTA	GAA	ACC	ATC	GCG	CAC	ACC	GCC	CCC	TTG	CTC	CCC	AAA	GAC	AAG	CCT	780
Leu	Glu	Thr	Ile	Ala	His	Thr	Ala	Pro	Leu	Leu	Pro	Lys	Asp	Lys	Pro	
			230						235					240		
CGC	TAC	TTA	ATG	GGC	GTA	GGC	ACG	CCT	GAA	AAT	ATC	CTA	GAC	GCT	ATC	828
Arg	Tyr	Leu	Met	Gly	Val	Gly	Thr	Pro	Glu	Asn	Ile	Leu	Asp	Ala	Ile	
		245						250					255			
AGT	TTG	GGG	GTG	GAT	ATG	TTT	GAT	TGC	GTG	ATG	CCC	ACC	AGA	AAC	GCC	876
Ser	Leu	Gly	Val	Asp	Met	Phe	Asp	Cys	Val	Met	Pro	Thr	Arg	Asn	Ala	
	260					265						270				
AGA	AAC	GCC	ACC	CTT	TTC	ACG	CAT	TCT	GGC	AAA	ATT	TCT	ATC	AAA	AAC	924
Arg	Asn	Ala	Thr	Leu	Phe	Thr	His	Ser	Gly	Lys	Ile	Ser	Ile	Lys	Asn	
	275					280					285					
GCG	CCC	TAT	AAA	TTG	GAT	AAT	ACC	CCT	ATT	GAA	GAA	AAT	TGC	GCA	TGT	972
Ala	Pro	Tyr	Lys	Leu	Asp	Asn	Thr	Pro	Ile	Glu	Glu	Asn	Cys	Ala	Cys	
290				295					300					305		
TAT	GCT	TGC	AAA	CGC	TAT	TCT	AAA	GCC	TAT	TTG	CAC	CAT	TTA	TTT	AGG	1020
Tyr	Ala	Cys	Lys	Arg	Tyr	Ser	Lys	Ala	Tyr	Leu	His	His	Leu	Phe	Arg	
			310					315						320		

Gln Lys Ala Leu Met His Leu Gln Glu Thr Leu Met Ile Glu Val Asp
 290 295 300
 Arg Leu Asp Phe Ser Leu Val Glu Arg Leu Asn Ile Leu Ala Arg Met
 305 310 315 320
 Glu Asn Glu Lys His Ala Phe
 325

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...1170
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

ATTCCAAACT TCCTAAAAAA TGATTACGCC ATTATATCCA AGATTAAGGC TTAAACG ATG 60
 Met
 1

GAT TTT CAA CTC CAA GCG ACT GAC AAT AAC GCG CGA GCT GGT CTT TTA 108
 Asp Phe Gln Leu Gln Ala Thr Asp Asn Asn Ala Arg Ala Gly Leu Leu
 5 10 15

AAT TTA GCC CAT TCT CAA GTG GCA ACG CCT GTT TTT ATG CCC GTA GGC 156
 Asn Leu Ala His Ser Gln Val Ala Thr Pro Val Phe Met Pro Val Gly
 20 25 30

ACG CAA GGC TGC ATC AAA TCT TTA GAC GCT ACA GAT GCG CAA GAA ATT 204
 Thr Gln Gly Cys Ile Lys Ser Leu Asp Ala Thr Asp Ala Gln Glu Ile
 35 40 45

TTA GGC GCT AAA CTC ATT TTA GCC AAC ACC TAT CAC ATG TAT TTA AGG 252
 Leu Gly Ala Lys Leu Ile Leu Ala Asn Thr Tyr His Met Tyr Leu Arg
 50 55 60 65

CCG GGT GAA AAG GTC GTT GAG GAG TTA GGG GGC TTG CAT CGT TTC GCT 300
 Pro Gly Glu Lys Val Val Glu Glu Leu Gly Gly Leu His Arg Phe Ala
 70 75 80

CAA TTT TAT GGG AGT TTT TTA ACC GAT AGT GGA GGG TTT CAA GCC TTT 348
 Gln Phe Tyr Gly Ser Phe Leu Thr Asp Ser Gly Gly Phe Gln Ala Phe
 85 90 95

GAA AAG CAT GCG TTT TAGTTACATT GAGCCAAGAG CGAAATACCT TATCAGCAAG C 1072
Glu Lys His Ala Phe
325

TTTCTAAAAT T

1083

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:666:

Val 1	Leu	Lys	Gly	Leu 5	Lys	Lys	Ala	Phe	Lys 10	Glu	Arg	Phe	Cys	Ser 15	Gln
Val	Tyr	Ile	Ser	Phe	Asn	Val	Asp	His	Asn	Leu	Leu	Ser	Thr	Gln	Val
			20					25					30		
Ile	Arg	Ile	Lys	Asn	Asp	Arg	Ile	Lys	Glu	Lys	Phe	Phe	Lys	Thr	Phe
			35				40					45			
Glu	Thr	Lys	Val	Glu	Thr	Lys	Asn	Gly	Glu	Val	Pro	Ile	Gln	Ala	Leu
			50			55					60				
Lys	Ile	Ala	Arg	Thr	Tyr	Ser	Gln	Lys	Tyr	Pro	Tyr	Thr	Tyr	Phe	Ser
65					70					75				80	
Ala	Met	Ser	Lys	Ala	Lys	Glu	Val	Leu	Cys	Glu	Lys	Gln	Ala	Phe	Glu
				85					90					95	
Gln	Ile	Lys	Gln	Glu	Asn	Gln	Asp	Tyr	His	Ala	Cys	Glu	Val	Asn	Gln
			100					105					110		
Lys	Tyr	Cys	Val	Tyr	Val	Glu	Ser	Lys	Asp	Phe	Leu	Lys	Asp	Phe	Lys
			115				120					125			
Arg	Phe	Lys	Ile	Gln	Asp	Val	Asp	Phe	Leu	Phe	Ser	Pro	Phe	Ser	Leu
			130			135					140				
Ile	Tyr	Asp	Phe	Val	Arg	Asp	Asn	Leu	Glu	Asn	Lys	Pro	Leu	Leu	Tyr
145					150					155				160	
Leu	Leu	Leu	Glu	Arg	Ser	Arg	Phe	Tyr	Phe	Leu	Ile	Ala	Asp	Lys	Lys
				165					170					175	
Glu	Ile	Phe	Leu	Ala	Lys	Ser	Val	Phe	Leu	Glu	Glu	Gln	Pro	Glu	Glu
			180					185					190		
Phe	Ile	Glu	Ser	Lys	Glu	Glu	Asp	Phe	Met	Gly	Met	Asp	Asn	Glu	Ala
			195				200					205			
Val	Asp	Leu	Phe	Leu	Ser	Glu	Ile	Gln	Glu	Asp	Ile	Asp	Ser	Leu	Glu
			210			215					220				
Glu	Ala	Ile	Gly	Leu	Asp	Ser	Ser	Lys	Asp	Asn	Ser	Glu	Lys	Ile	Thr
225					230					235				240	
Glu	Asp	Ala	Tyr	Ser	Leu	Ile	Glu	Gly	Met	Thr	Asn	Ile	Pro	Leu	Ile
				245					250					255	
Ala	Asp	Val	Leu	Gln	Glu	Gly	Leu	Arg	Gly	Val	Tyr	His	Ser	Arg	Glu
			260					265					270		
Ile	Asp	Phe	Val	Glu	Lys	Val	Val	Val	Leu	Asp	Ser	Cys	Gln	Ile	His
			275				280					285			

AAA CAA GAA AAT CAA GAT TAT CAT GCT TGT GAA GTC AAT CAA AAG TAT	392
Lys Gln Glu Asn Gln Asp Tyr His Ala Cys Glu Val Asn Gln Lys Tyr	
100 105 110	
TGC GTT TAT GTG GAA TCT AAG GAT TTT TTA AAG GAT TTT AAG CGT TTT	440
Cys Val Tyr Val Glu Ser Lys Asp Phe Leu Lys Asp Phe Lys Arg Phe	
115 120 125 130	
AAA ATC CAG GAT GTG GAT TTT TTG TTT TCG CCT TTT AGC CTT ATT TAT	488
Lys Ile Gln Asp Val Asp Phe Leu Phe Ser Pro Phe Ser Leu Ile Tyr	
135 140 145	
GAT TTT GTG CGC GAT AAT TTA GAA AAT AAG CCG TTG TTG TAT TTG CTT	536
Asp Phe Val Arg Asp Asn Leu Glu Asn Lys Pro Leu Leu Tyr Leu Leu	
150 155 160	
TTG GAG CGT TCA AGA TTT TAT TTT TTG ATT GCG GAT AAA AAA GAG ATT	584
Leu Glu Arg Ser Arg Phe Tyr Phe Leu Ile Ala Asp Lys Lys Glu Ile	
165 170 175	
TTT TTA GCC AAA TCC GTG TTT TTA GAA GAA CAA CCT GAA GAG TTT ATA	632
Phe Leu Ala Lys Ser Val Phe Leu Glu Glu Gln Pro Glu Glu Phe Ile	
180 185 190	
GAG AGC AAA GAA GAA GAT TTT ATG GGA ATG GAT AAT GAG GCT GTG GAT	680
Glu Ser Lys Glu Glu Asp Phe Met Gly Met Asp Asn Glu Ala Val Asp	
195 200 205 210	
TTG TTT TTG AGT GAA ATC CAA GAA GAT ATT GAC AGC CTT GAA GAA GCG	728
Leu Phe Leu Ser Glu Ile Gln Glu Asp Ile Asp Ser Leu Glu Glu Ala	
215 220 225	
ATA GGC CTA GAC AGC AGT AAG GAT AAT AGC GAA AAA ATA ACA GAG GAC	776
Ile Gly Leu Asp Ser Ser Lys Asp Asn Ser Glu Lys Ile Thr Glu Asp	
230 235 240	
GCT TAT AGT TTG ATT GAA GGC ATG ACG AAT ATC CCC TTA ATT GCA GAT	824
Ala Tyr Ser Leu Ile Glu Gly Met Thr Asn Ile Pro Leu Ile Ala Asp	
245 250 255	
GTT TTG CAA GAG GGA TTG CGT GGC GTC TAT CAT TCT AGA GAG ATA GAC	872
Val Leu Gln Glu Gly Leu Arg Gly Val Tyr His Ser Arg Glu Ile Asp	
260 265 270	
TTT GTA GAA AAA GTG GTT GTT TTA GAC AGC TGT CAA ATC CAC CAA AAA	920
Phe Val Glu Lys Val Val Leu Asp Ser Cys Gln Ile His Gln Lys	
275 280 285 290	
GCG TTA ATG CAT TTG CAA GAA ACT TTG ATG ATA GAA GTG GAT AGG CTT	968
Ala Leu Met His Leu Gln Glu Thr Leu Met Ile Glu Val Asp Arg Leu	
295 300 305	
GAT TTT TCT TTA GTG GAG CGC TTG AAC ATT TTA GCG CGC ATG GAG AAT	1016
Asp Phe Ser Leu Val Glu Arg Leu Asn Ile Leu Ala Arg Met Glu Asn	
310 315 320	

Lys Asn Asn Gln Ala Ile Glu Leu Glu Ala Leu Lys Arg Gly Asp Lys
 385 390 395 400
 Ile Glu Leu Ser Asn Glu Lys Thr Arg Ala Ser Ala Glu Ile Leu Ser
 405 410 415
 Val Asp Arg Val
 420

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1031
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

AAAGACGCGC ATGGATTCTG TTGGGTTTGA AGAACCTCAA AGGGGTTTGG	GTG CTT	56
	Val Leu	
	1	
AAG GGG TTA AAA AAA GCG TTT AAG GAG AGG TTT TGC TCT CAA GTG TAT		104
Lys Gly Leu Lys Lys Ala Phe Lys Glu Arg Phe Cys Ser Gln Val Tyr		
5 10 15		
ATC TCT TTT AAT GTG GAT CAC AAT CTT TTA TCC ACT CAA GTC ATA AGG		152
Ile Ser Phe Asn Val Asp His Asn Leu Leu Ser Thr Gln Val Ile Arg		
20 25 30		
ATC AAA AAC GAT CGC ATT AAA GAG AAA TTT TTT AAA ACT TTT GAG ACT		200
Ile Lys Asn Asp Arg Ile Lys Glu Lys Phe Phe Lys Thr Phe Glu Thr		
35 40 45 50		
AAA GTG GAG ACT AAA AAT GGT GAA GTC CCT ATT CAA GCC TTA AAA ATC		248
Lys Val Glu Thr Lys Asn Gly Glu Val Pro Ile Gln Ala Leu Lys Ile		
55 60 65		
GCC AGA ACT TAT AGC CAA AAA TAC CCC TAC ACT TAT TTT AGC GCG ATG		296
Ala Arg Thr Tyr Ser Gln Lys Tyr Pro Tyr Thr Tyr Phe Ser Ala Met		
70 75 80		
AGT AAA GCT AAA GAG GTT TTA TGC GAA AAG CAG GCG TTT GAA CAA ATC		344
Ser Lys Ala Lys Glu Val Leu Cys Glu Lys Gln Ala Phe Glu Gln Ile		
85 90 95		

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

```

Val Asp Val Leu Ser Val Ser Glu Ile Asn Ala Gln Ile Lys Ala Leu
 1           5           10           15
Leu Glu Ala Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn
 20           25           30
Leu Thr Ile His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp
 35           40           45
Ser Gln Ser Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg
 50           55           60
Leu Lys Phe Ala Leu Lys Glu Gly Gln Glu Val Val Val Phe Gly Gly
 65           70           75           80
Ile Ser Val Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu
 85           90           95
Ile Glu Pro Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu
 100          105          110
Lys Glu Lys Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu
 115          120          125
Pro Lys Pro His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn
 130          135          140
Ser Ala Ala Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro
 145          150          155          160
Met Cys Glu Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys
 165          170          175
Val Gln Ser Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp
 180          185          190
Thr Lys Asn Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser
 195          200          205
Met Glu Asp Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu
 210          215          220
Tyr Leu Ala Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp
 225          230          235          240
Phe Leu Leu Ser Asp Leu Val Ala Asp Leu Arg Ala Ser Thr Pro Ser
 245          250          255
Asn Ala Met Glu Ile Leu Leu Pro Ser Ser Asp Glu Trp Leu Gln Arg
 260          265          270
Leu Asp Gly Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu
 275          280          285
His Gln Lys Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg
 290          295          300
Leu Ser Phe Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys
 305          310          315          320
Leu Lys Ile Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys
 325          330          335
Lys Thr Leu Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe
 340          345          350
Leu Gln Thr Lys Thr Glu Arg Leu Asn Arg Leu Glu Asn Ala Leu Lys
 355          360          365
Leu Ala His Ala Asn Leu Lys Leu Pro Gln Phe Gly Ala Leu Val Ser
 370          375          380

```


Leu Ser Asp	Leu Val Ala Asp	Leu Arg Ala Ser Thr	Pro Ser Asn Ala	
245		250	255	
ATG GAA ATT TTA CTC CCC AGC	AGC GAT GAA TGG TTG CAA AGA CTT GAT	872		
Met Glu Ile Leu Leu Pro Ser	Ser Asp Glu Trp Leu Gln Arg Leu Asp			
260	265	270		
GGG TTT AAT GTG AAA TTG CAC CGC TCG TTT AAA ACT TTG CTC CAC CAA	920			
Gly Phe Asn Val Lys Leu His Arg Ser Phe Lys Thr Leu Leu His Gln				
275	280	285	290	
AAA AAG GCG CAT TTA GAG CAT TTA GTG GCT TCT TTA AAA CGA TTG AGT	968			
Lys Lys Ala His Leu Glu His Leu Val Ala Ser Leu Lys Arg Leu Ser				
295	300	305		
TTT GAA AAC AAG CAC CAT TTA AAC GCT TTA AAA CTA GAA AAA TTA AAA	1016			
Phe Glu Asn Lys His His Leu Asn Ala Leu Lys Leu Glu Lys Leu Lys				
310	315	320		
ATC GCC CTA GAA AAT AAA ACT CTA GAA TTT TTA CGC TTT AAA AAA ACG	1064			
Ile Ala Leu Glu Asn Lys Thr Leu Glu Phe Leu Arg Phe Lys Lys Thr				
325	330	335		
CTT TTA GAA AAA ATC TCT ACT CAA ACA TTA ACA AGC CCT TTT TTA CAA	1112			
Leu Leu Glu Lys Ile Ser Thr Gln Thr Leu Thr Ser Pro Phe Leu Gln				
340	345	350		
ACT AAA ACA GAG CGA TTG AAC AGG CTA GAA AAC GCC CTT AAA CTC GCT	1160			
Thr Lys Thr Glu Arg Leu Asn Arg Leu Glu Asn Ala Leu Lys Leu Ala				
355	360	365	370	
CAT GCT AAT TTG AAA TTA CCC CAA TTC GGG GCG TTG GTG AGC AAA AAT	1208			
His Ala Asn Leu Lys Leu Pro Gln Phe Gly Ala Leu Val Ser Lys Asn				
375	380	385		
AAT CAA GCG ATA GAA TTA GAG GCA TTA AAA AGG GGC GAT AAA ATT GAA	1256			
Asn Gln Ala Ile Glu Leu Glu Ala Leu Lys Arg Gly Asp Lys Ile Glu				
390	395	400		
TTA AGT AAT GAA AAA ACC AGA GCG AGC GCT GAA ATT TTG AGC GTG GAT	1304			
Leu Ser Asn Glu Lys Thr Arg Ala Ser Ala Glu Ile Leu Ser Val Asp				
405	410	415		
AGG GTG TAGGGGTTTG AAAAAATAATA TTAAACGC TATTTGTTTT ATCTTAAAT TT	1362			
Arg Val				
420				
C				1363

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

20	25	30	
ATC CAT AAG GTG AGC GGC CAT GCG TAT TTT TCG CTC AAA GAC AGC CAG			200
Ile His Lys Val Ser Gly His Ala Tyr Phe Ser Leu Lys Asp Ser Gln			
35	40	45	50
TCG GTT ATT AAA TGC GTG CTG TTT AAA GGG AAC GCT AAC AGG CTC AAA			248
Ser Val Ile Lys Cys Val Leu Phe Lys Gly Asn Ala Asn Arg Leu Lys			
	55	60	65
TTC GCT TTA AAA GAA GGG CAG GAA GTG GTT GTT TTT GGG GGT ATT AGC			296
Phe Ala Leu Lys Glu Gly Gln Glu Val Val Val Phe Gly Gly Ile Ser			
	70	75	80
GTG TAT GTC CCA AGG GGG GAT TAT CAA ATC AAT TGC TTT GAA ATA GAG			344
Val Tyr Val Pro Arg Gly Asp Tyr Gln Ile Asn Cys Phe Glu Ile Glu			
	85	90	95
CCT AAG GAT ATA GGT TCA TTA ACT TTA GCT TTA GAG CAA TTG AAA GAA			392
Pro Lys Asp Ile Gly Ser Leu Thr Leu Ala Leu Glu Gln Leu Lys Glu			
	100	105	110
AAA TTA CGC CTT AAA GGC TAT TTT GAT GAA GAA AAT AAA TTA CCC AAA			440
Lys Leu Arg Leu Lys Gly Tyr Phe Asp Glu Glu Asn Lys Leu Pro Lys			
	115	120	125
CCG CAT TTT CCT AAA CGA GTG GCA GTC ATC ACT TCT CAA AAT TCA GCC			488
Pro His Phe Pro Lys Arg Val Ala Val Ile Thr Ser Gln Asn Ser Ala			
	135	140	145
GCT TGG GCG GAC ATG AAA AAG ATC GCT TCC AAA CGA TGG CCG ATG TGT			536
Ala Trp Ala Asp Met Lys Lys Ile Ala Ser Lys Arg Trp Pro Met Cys			
	150	155	160
GAA TTA GTT TGT ATC AAC ACC TTA ATG CAA GGG GAG GGC TGC GTT CAA			584
Glu Leu Val Cys Ile Asn Thr Leu Met Gln Gly Glu Gly Cys Val Gln			
	165	170	175
AGC GTG GTG GAA AGC ATC GTT TAT GCG GAT AGT TTT CAT GAC ACA AAA			632
Ser Val Val Glu Ser Ile Val Tyr Ala Asp Ser Phe His Asp Thr Lys			
	180	185	190
AAC GCT TTT GAT GCG ATT GTA GTG GCT AGG GGT GGG GGG AGC ATG GAG			680
Asn Ala Phe Asp Ala Ile Val Val Ala Arg Gly Gly Gly Ser Met Glu			
	195	200	205
GAT TTG TAT TCT TTC AAT GAT GAA AAA ATC GCT GAT GCT CTG TAT TTG			728
Asp Leu Tyr Ser Phe Asn Asp Glu Lys Ile Ala Asp Ala Leu Tyr Leu			
	215	220	225
GCC AAA ACC TTC AGC ATG TCA GCT ATT GGG CAT GAG AGC GAT TTT TTA			776
Ala Lys Thr Phe Ser Met Ser Ala Ile Gly His Glu Ser Asp Phe Leu			
	230	235	240
TTG AGC GAT TTA GTG GCG GAT TTA AGG GCT TCT ACG CCT TCA AAC GCG			824

```

Thr Tyr Pro Phe Val Thr Ser Ser Asn Thr Thr Ser Ala Ser Ala Cys
225                230                235                240
Val Ser Thr Gly Leu Asn Pro Lys Ala Ile Asn Glu Val Ile Gly Ile
                245                250                255
Thr Lys Ala Tyr Ser Thr Arg Val Gly Asn Gly Pro Phe Pro Ser Glu
                260                265                270
Asp Thr Thr Pro Met Gly Asp His Leu Arg Thr Lys Gly Ala Glu Phe
                275                280                285
Gly Thr Thr Thr Lys Arg Pro Arg Arg Cys Gly Trp Leu Asp Leu Val
                290                295                300
Ala Leu Lys Tyr Ala Cys Ala Leu Asn Gly Cys Thr Gln Leu Ala Leu
305                310                315                320
Met Lys Leu Asp Val Leu Asp Gly Ile Asp Ala Ile Lys Val Cys Val
                325                330                335
Ala Tyr Glu Arg Lys Gly Glu Arg Leu Glu Ile Phe Pro Ser Asp Leu
                340                345                350
Lys Asp Cys Val Pro Ile Tyr Gln Thr Phe Lys Gly Trp Glu Lys Ser
                355                360                365
Val Gly Val Arg Lys Leu Asp Asp Leu Glu Pro Asn Val Arg Glu Tyr
                370                375                380
Ile Arg Phe Ile Glu Lys Glu Val Gly Val Lys Ile Arg Leu Ile Ser
385                390                395                400
Thr Ser Pro Glu Arg Glu Asp Thr Ile Phe Leu
                405                410

```

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1310
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

```

TTTTAGGGCT TTTCAATGAT CTCACTCGTT TGCTATAAAA GGGGGAGCTG  GTG GAT      56
                                   Val Asp
                                   1

GTA TTG AGC GTG AGC GAA ATC AAT GCG CAA ATC AAA GCC CTT TTA GAA      104
Val Leu Ser Val Ser Glu Ile Asn Ala Gln Ile Lys Ala Leu Leu Glu
      5                10                15

GCG ACT TTT TTG CAA GTT AGG GTT CAA GGG GAA GTG AGT AAT TTG ACT      152
Ala Thr Phe Leu Gln Val Arg Val Gln Gly Glu Val Ser Asn Leu Thr

```

GAA AAA AGC GTG GGC GTG AGA AAA TTA GAC GAT TTA GAG CCA AAC GTT 1215
 Glu Lys Ser Val Gly Val Arg Lys Leu Asp Asp Leu Glu Pro Asn Val
 370 375 380

AGA GAG TAT ATC CGT TTT ATT GAA AAA GAA GTG GGG GTA AAA ATC CGC 1263
 Arg Glu Tyr Ile Arg Phe Ile Glu Lys Glu Val Gly Val Lys Ile Arg
 385 390 395

CTT ATT TCT ACA AGC CCT GAA AGA GAA GAC ACG ATT TTT CTA TGAAAAAAT 1314
 Leu Ile Ser Thr Ser Pro Glu Arg Glu Asp Thr Ile Phe Leu
 400 405 410

TCGCTTCTGT ATTGGTGCAA TTAAAAACCC TTGCGT 1350

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Met Ala Asp Val Val Val Gly Ile Gln Trp Gly Asp Glu Gly Lys Gly
 1 5 10 15
 Lys Ile Val Asp Arg Ile Ala Lys Asp Tyr Asp Phe Val Val Arg Tyr
 20 25 30
 Gln Gly Gly His Asn Ala Gly His Thr Ile Val His Lys Gly Val Lys
 35 40 45
 His Ser Leu His Leu Met Pro Ser Gly Val Leu Tyr Pro Lys Cys Lys
 50 55 60
 Asn Ile Ile Ser Ser Ala Val Val Val Ser Val Lys Asp Leu Cys Glu
 65 70 75 80
 Glu Ile Ser Ala Phe Glu Asp Leu Glu Asn Arg Leu Phe Val Ser Asp
 85 90 95
 Arg Ala His Val Ile Leu Pro Tyr His Ala Lys Lys Asp Ala Phe Lys
 100 105 110
 Glu Lys Ser Gln Asn Ile Gly Thr Thr Lys Lys Gly Ile Gly Pro Cys
 115 120 125
 Tyr Glu Asp Lys Met Ala Arg Ser Gly Ile Arg Met Gly Asp Leu Leu
 130 135 140
 Asp Asp Lys Ile Leu Glu Lys Leu Asn Ala His Phe Lys Ala Ile
 145 150 155 160
 Glu Pro Phe Lys Lys Ala Tyr Asp Leu Gly Glu Asn Tyr Glu Lys Asp
 165 170 175
 Leu Met Gly Tyr Phe Lys Thr Tyr Ala Pro Lys Ile Cys Pro Phe Ile
 180 185 190
 Lys Asp Thr Thr Ser Met Leu Ile Glu Ala Asn Gln Lys Gly Glu Lys
 195 200 205
 Ile Leu Leu Glu Gly Ala Gln Gly Thr Leu Leu Asp Ile Asp Leu Gly
 210 215 220

GAT TTA TTA GAC GAT AAA ATC TTA GAA GAA AAG CTA AAC GCT CAT TTC	543
Asp Leu Leu Asp Asp Lys Ile Leu Glu Glu Lys Leu Asn Ala His Phe	
145 150 155	
AAA GCC ATT GAG CCT TTT AAA AAA GCG TAT GAT TTG GGC GAG AAT TAC	591
Lys Ala Ile Glu Pro Phe Lys Lys Ala Tyr Asp Leu Gly Glu Asn Tyr	
160 165 170	
GAA AAA GAT TTG ATG GGG TAT TTT AAA ACT TAC GCT CCA AAA ATT TGC	639
Glu Lys Asp Leu Met Gly Tyr Phe Lys Thr Tyr Ala Pro Lys Ile Cys	
175 180 185	
CCC TTT ATC AAA GAC ACG ACA AGC ATG CTG ATA GAA GCG AAT CAA AAG	687
Pro Phe Ile Lys Asp Thr Thr Ser Met Leu Ile Glu Ala Asn Gln Lys	
190 195 200 205	
GGT GAA AAA ATC CTA TTA GAA GGG GCA CAA GGC ACG CTT TTA GAC ATT	735
Gly Glu Lys Ile Leu Leu Glu Gly Ala Gln Gly Thr Leu Leu Asp Ile	
210 215 220	
GAT TTA GGG ACT TAC CCT TTT GTA ACA AGC TCT AAC ACC ACG AGC GCT	783
Asp Leu Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Thr Thr Ser Ala	
225 230 235	
AGC GCA TGC GTG AGC ACC GGC TTA AAC CCT AAA GCG ATC AAT GAA GTC	831
Ser Ala Cys Val Ser Thr Gly Leu Asn Pro Lys Ala Ile Asn Glu Val	
240 245 250	
ATA GGT ATC ACA AAA GCC TAC TCC ACT CGT GTG GGT AAT GGG CCT TTC	879
Ile Gly Ile Thr Lys Ala Tyr Ser Thr Arg Val Gly Asn Gly Pro Phe	
255 260 265	
CCT AGC GAA GAC ACT ACA CCC ATG GGC GAT CAT TTA AGG ACT AAG GGT	927
Pro Ser Glu Asp Thr Thr Pro Met Gly Asp His Leu Arg Thr Lys Gly	
270 275 280 285	
GCG GAG TTT GGC ACG ACA ACC AAG CGC CCA AGG CGT TGC GGG TGG CTG	975
Ala Glu Phe Gly Thr Thr Thr Lys Arg Pro Arg Arg Cys Gly Trp Leu	
290 295 300	
GAT TTG GTG GCT TTG AAA TAC GCT TGC GCT TTG AAT GGT TGC ACG CAA	1023
Asp Leu Val Ala Leu Lys Tyr Ala Cys Ala Leu Asn Gly Cys Thr Gln	
305 310 315	
TTA GCC TTA ATG AAA TTA GAC GTT TTA GAC GGG ATT GAT GCG ATT AAG	1071
Leu Ala Leu Met Lys Leu Asp Val Leu Asp Gly Ile Asp Ala Ile Lys	
320 325 330	
GTG TGC GTG GCT TAT GAA AGA AAG GGC GAA AGA TTG GAG ATT TTC CCT	1119
Val Cys Val Ala Tyr Glu Arg Lys Gly Glu Arg Leu Glu Ile Phe Pro	
335 340 345	
AGC GAT TTG AAA GAT TGC GTG CCG ATC TAT CAA ACT TTT AAA GGT TGG	1167
Ser Asp Leu Lys Asp Cys Val Pro Ile Tyr Gln Thr Phe Lys Gly Trp	
350 355 360 365	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...1305
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

```

TTTTACTTTT TTTTGGTAT TCTAACAAGC TTTTAAATAA TCCAATCTAC TTTGTTTAA      60
GGATAATATT TT ATG GCA GAT GTC GTT GTG GGG ATC CAG TGG GGA GAT GAG      111
      Met Ala Asp Val Val Val Gly Ile Gln Trp Gly Asp Glu
        1              5              10

GGG AAG GGA AAA ATT GTT GAT AGG ATC GCT AAA GAT TAT GAC TTT GTG      159
Gly Lys Gly Lys Ile Val Asp Arg Ile Ala Lys Asp Tyr Asp Phe Val
      15              20              25

GTG CGC TAT CAG GGC GGG CAT AAT GCT GGG CAT ACC ATT GTG CAT AAG      207
Val Arg Tyr Gln Gly Gly His Asn Ala Gly His Thr Ile Val His Lys
      30              35              40              45

GGG GTT AAG CAT TCT TTG CAT TTA ATG CCT TCA GGG GTT TTA TAC CCC      255
Gly Val Lys His Ser Leu His Leu Met Pro Ser Gly Val Leu Tyr Pro
              50              55              60

AAA TGC AAG AAC ATC ATT TCT AGC GCG GTG GTC GTG AGC GTT AAG GAT      303
Lys Cys Lys Asn Ile Ile Ser Ser Ala Val Val Val Ser Val Lys Asp
              65              70              75

TTG TGC GAA GAA ATC AGC GCG TTT GAG GAT TTA GAA AAT CGT TTG TTT      351
Leu Cys Glu Glu Ile Ser Ala Phe Glu Asp Leu Glu Asn Arg Leu Phe
              80              85              90

GTC AGC GAC AGA GCC CAT GTG ATC TTG CCC TAT CAT GCC AAA AAA GAC      399
Val Ser Asp Arg Ala His Val Ile Leu Pro Tyr His Ala Lys Lys Asp
      95              100              105

GCT TTT AAA GAA AAA TCT CAA AAC ATC GGC ACG ACT AAA AAA GGC ATA      447
Ala Phe Lys Glu Lys Ser Gln Asn Ile Gly Thr Thr Lys Lys Gly Ile
      110              115              120              125

GGC CCT TGC TAT GAG GAT AAA ATG GCC AGG AGC GGG ATA AGA ATG GGG      495
Gly Pro Cys Tyr Glu Asp Lys Met Ala Arg Ser Gly Ile Arg Met Gly
              130              135              140

```

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...212
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

```

TAAGCGCTTT GCGTGTTTAA AAATTCCTTA TCCAAGCTCT CAGCGTCTTC  ATG AAA      56
                                     Met Lys
                                     1

GCT GTA ACC ATC TTT CAT GAT AAA TTC CCT CGC TCT CAC CAG CCC AAA      104
Ala Val Thr Ile Phe His Asp Lys Phe Pro Arg Ser His Gln Pro Lys
      5              10              15

TCT TGG GCG GAT TTC ATC ACG GAA TTT CGT GTG GAT TTG ATA GAG ATG      152
Ser Trp Ala Asp Phe Ile Thr Glu Phe Arg Val Asp Leu Ile Glu Met
      20              25              30

GAC GGG CAA TTG CTT GTA ACT TTT AAT GAA ATT AGC GGC AAT TTC GGT      200
Asp Gly Gln Leu Leu Val Thr Phe Asn Glu Ile Ser Gly Asn Phe Gly
      35              40              45              50

GAT ATT TTC TTC TAAAGTGGGG CTAAAACAA AATCATTGTC TTTTCGGTCT TTAAA      257
Asp Ile Phe Phe

AACCAATA      265
  
```

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

```

Met Lys Ala Val Thr Ile Phe His Asp Lys Phe Pro Arg Ser His Gln
 1              5              10              15
Pro Lys Ser Trp Ala Asp Phe Ile Thr Glu Phe Arg Val Asp Leu Ile
      20              25              30
Glu Met Asp Gly Gln Leu Leu Val Thr Phe Asn Glu Ile Ser Gly Asn
      35              40              45
Phe Gly Asp Ile Phe Phe
      50
  
```

(2) INFORMATION FOR SEQ ID NO:661:

Ile Leu Glu Lys Ala Gln Leu Phe
190

TTTGGTGGTG GTTAAGCTTG AACGCT

1020

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

Met	Ser	Leu	Pro	Lys	Gly	Ala	Lys	Val	Gly	Thr	Thr	Ser	Leu	Arg	Arg	1	5	10	15
Ser	Met	Gln	Ile	Lys	Leu	Lys	Arg	Gln	Asp	Leu	Asp	Thr	Glu	Ser	Leu	20	25	30	
Arg	Gly	Asn	Val	Gln	Thr	Arg	Leu	Lys	Lys	Leu	Glu	Cys	Gly	Glu	Phe	35	40	45	
Asp	Ala	Ile	Ile	Leu	Ala	Glu	Ala	Gly	Leu	Cys	Arg	Leu	Glu	Ile	Gln	50	55	60	
Gly	Ala	Lys	Tyr	Arg	Lys	Ala	Phe	Ser	Val	Glu	Glu	Met	Ile	Pro	Ser	65	70	75	80
Met	Gly	Gln	Gly	Ala	Leu	Gly	Val	Glu	Met	Leu	Lys	Asn	His	Lys	His	85	90	95	
Phe	Ala	Thr	Leu	Gln	Lys	Leu	Asn	Asp	Glu	Lys	Ser	Ala	Phe	Cys	Cys	100	105	110	
Arg	Leu	Glu	Arg	Glu	Phe	Ile	Lys	Gly	Leu	Asn	Gly	Gly	Cys	Gln	Ile	115	120	125	
Pro	Ile	Gly	Val	His	Ala	Ser	Leu	Met	Gly	Asp	Arg	Val	Lys	Ile	Gln	130	135	140	
Ala	Val	Leu	Gly	Leu	Pro	Asn	Gly	Lys	Glu	Val	Ile	Thr	Lys	Glu	Lys	145	150	155	160
Gln	Gly	Asp	Lys	Thr	Lys	Ala	Phe	Asp	Leu	Val	Gln	Glu	Leu	Leu	Glu	165	170	175	
Glu	Phe	Leu	Gln	Ser	Gly	Ala	Lys	Glu	Ile	Leu	Glu	Lys	Ala	Gln	Leu	180	185	190	
Phe																			

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

GAAGAAAAAA	TTTTAGAAAT	GTTAGAAAGC	GAATAAGGGG	GAGTGAGTGG	GAAATTTAGT	60
GATTGGCTCT	AGGGGGAGCG	AATTAGCCTT	ATGGCAAGCG	AATCACATTA	AAGAACGCCT	120
GAAAAAAGAA	TGCTTGATAG	AAAGCGAAAT	TCAAATCGTT	AAGACTAAGG	GCGATAAAAT	180
CTTAGACACC	CCTTTAAATA	AGATCGGCGG	TAAGGGGCTA	TTCACATAAGG	AATTAGAAGA	240
ATTGCTTTTA	AAGGGCGCAA	TTGATTGGC	GGTGCATTCT	TTAAAAGACG	TGCCGGTCGT	300
GTTTGAAAAG	GGGTTAGACT	TGGCATGCAT	CACCAAAGG	GCTGATGTGA	GGGACACTTT	360
TTTAAGCGTG	AAATTCCTG	ATTG ATG	AGT TTG	CCT AAA	GGG GCA	AAG GTT 412
		Met Ser Leu Pro	Lys Gly Ala Lys Val			
		1	5			
GGC ACG ACT TCT TTA AGG CGC TCT ATG CAG ATC AAA TTA AAG CGC CAG	460					
Gly Thr Thr Ser Leu Arg Arg Ser Met Gln Ile Lys Leu Lys Arg Gln						
10 15 20 25						
GAT TTG GAC ACA GAA AGC TTG AGA GGG AAT GTC CAA ACC CGT TTG AAA	508					
Asp Leu Asp Thr Glu Ser Leu Arg Gly Asn Val Gln Thr Arg Leu Lys						
30 35 40						
AAG CTT GAA TGC GGA GAA TTT GAC GCT ATC ATT TTA GCT GAA GCC GGG	556					
Lys Leu Glu Cys Gly Glu Phe Asp Ala Ile Ile Leu Ala Glu Ala Gly						
45 50 55						
TTG TGC CGC CTA GAA ATT CAA GGA GCG AAA TAC CGC AAG GCT TTT AGC	604					
Leu Cys Arg Leu Glu Ile Gln Gly Ala Lys Tyr Arg Lys Ala Phe Ser						
60 65 70						
GTA GAA GAA ATG ATT CCT AGC ATG GGT CAG GGG GCT TTA GGG GTA GAA	652					
Val Glu Glu Met Ile Pro Ser Met Gly Gln Gly Ala Leu Gly Val Glu						
75 80 85						
ATG CTC AAA AAC CAC AAG CAT TTT GCC ACG CTT CAA AAA CTC AAC GAC	700					
Met Leu Lys Asn His Lys His Phe Ala Thr Leu Gln Lys Leu Asn Asp						
90 95 100 105						
GAG AAA AGC GCG TTT TGC TGC CGT TTA GAA AGG GAG TTT ATC AAG GGG	748					
Glu Lys Ser Ala Phe Cys Cys Arg Leu Glu Arg Glu Phe Ile Lys Gly						
110 115 120						
CTT AAT GGA GGG TGT CAG ATC CCT ATA GGC GTG CAT GCG AGT TTA ATG	796					
Leu Asn Gly Gly Cys Gln Ile Pro Ile Gly Val His Ala Ser Leu Met						
125 130 135						
GGC GAT AGG GTT AAA ATC CAG GCG GTT TTA GGC TTG CCT AAC GGG AAA	844					
Gly Asp Arg Val Lys Ile Gln Ala Val Leu Gly Leu Pro Asn Gly Lys						
140 145 150						
GAA GTC ATT ACT AAA GAA AAA CAA GGG GAT AAA ACT AAA GCG TTT GAT	892					
Glu Val Ile Thr Lys Glu Lys Gln Gly Asp Lys Thr Lys Ala Phe Asp						
155 160 165						
TTA GTT CAA GAG CTT TTA GAA GAA TTT TTG CAA AGC GGG GCT AAA GAG	940					
Leu Val Gln Glu Leu Leu Glu Glu Phe Leu Gln Ser Gly Ala Lys Glu						
170 175 180 185						
ATT TTA GAA AAG GCG CAG TTG TTT TAATGCGTTT GTTTATCGCG CTAGTTTTGT	994					

```

Val Asn Ala Leu Gly Ile Leu Leu Leu Met Glu Gln Phe Lys Phe Leu
  130          135          140
Gln Asn Gln Asn Leu Gly Val Phe Val Leu Leu Ala Ile Gly Ile Leu
  145          150          155          160
Ile Ile Tyr Leu Phe Pro Leu Ile Thr Lys Lys Ile Pro Ser Asn Leu
          165          170          175
Ile Cys Ile Leu Ile Val Ser Ala Ile Ala Leu Ile Phe Asp Met His
          180          185          190
Ala Pro Asn Leu Gly Ser Ile Glu Gln Gly Val Ser Gly Phe His Phe
          195          200          205
Ile Ile Ile Pro Lys Asn Leu Asp Phe Lys Ile Met Ile Glu Leu Leu
          210          215          220
Pro Tyr Ala Leu Ser Leu Ala Leu Val Gly Thr Ile Glu Ser Leu Leu
          225          230          235          240
Thr Ala Lys Thr Leu Asp Val Ile Leu Lys Asp Gly Val Ser Asp Lys
          245          250          255
Asn Lys Glu Thr Lys Ala Gln Gly Leu Gly Asn Ile Ile Ser Gly Leu
          260          265          270
Leu Gly Gly Met Thr Gly Cys Ala Leu Val Gly Gln Ser Ile Ile Asn
          275          280          285
Ala Lys Ser Gly Ala Lys Thr Arg Leu Ser Thr Phe Phe Ala Gly Phe
          290          295          300
Ser Leu Met Val Leu Ile Leu Val Phe Asn Glu Tyr Val Val Lys Ile
          305          310          315          320
Pro Ile Val Ala Val Val Ala Val Met Val Met Ile Ser Phe Thr Thr
          325          330          335
Phe Asn Phe Gln Ser Ile Ile Asn Ile Lys Lys Ile Lys Leu Tyr Asp
          340          345          350
Thr Leu Asn Met Leu Leu Val Val Ala Val Val Leu Tyr Thr His Asn
          355          360          365
Leu Ala Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile
          370          375          380
Lys Ser Lys Gly Ile Ala
          385          390

```

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 386...964
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

ATG GTG CTC ATA TTA GTG TTT AAT GAA TAT GTG GTT AAG ATC CCC ATT	1016
Met Val Leu Ile Leu Val Phe Asn Glu Tyr Val Val Lys Ile Pro Ile	
310 315 320	
GTG GCG GTT GTG GCG GTA ATG GTG ATG ATT TCT TTC ACC ACT TTT AAT	1064
Val Ala Val Val Ala Val Met Val Met Ile Ser Phe Thr Thr Phe Asn	
325 330 335	
TTC CAA TCC ATT ATT AAC ATT AAA AAA ATC AAG CTC TAT GAC ACG CTC	1112
Phe Gln Ser Ile Ile Asn Ile Lys Lys Ile Lys Leu Tyr Asp Thr Leu	
340 345 350	
AAC ATG CTC TTA GTC GTG GCG GTG GTT TTA TAC ACG CAT AAT TTA GCG	1160
Asn Met Leu Leu Val Val Ala Val Val Leu Tyr Thr His Asn Leu Ala	
355 360 365 370	
ATA GGG GTT GTG GTG GGG GTT TTA GTC AAT GCG TTA TGG ATC AAA TCT	1208
Ile Gly Val Val Val Gly Val Leu Val Asn Ala Leu Trp Ile Lys Ser	
375 380 385	
AAA GGG ATT GCA TGAAATTTTA TTTTAAAAAG TTGGGTAGCT AGAGATATGG CTCCA	1265
Lys Gly Ile Ala	
390	
GATGTAGG	1273

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

Met Arg Lys Lys Gly Met Phe Glu Lys Ile Gln Lys Glu Trp Leu Ser	
1 5 10 15	
Asn Ile Gln Lys Asp Leu Leu Ser Gly Phe Val Val Gly Leu Ser Val	
20 25 30	
Ile Pro Glu Thr Ala Gly Phe Ala Ile Met Val Gly Leu Asp Val Gly	
35 40 45	
Val Ala Phe Tyr Thr Thr Phe Tyr Met Ala Phe Val Leu Ser Leu Phe	
50 55 60	
Gly Ala Arg Lys Ala Met Ile Ser Ala Ala Ala Gly Ser Val Ala Leu	
65 70 75 80	
Ile Leu Val Gly Val Val Lys Asn Tyr Gly Leu Glu Tyr Ala Gly Val	
85 90 95	
Ala Thr Leu Met Ala Gly Val Leu Gln Ile Leu Leu Gly Tyr Leu Lys	
100 105 110	
Ile Gly Asn Leu Leu Arg Phe Ile Pro Gln Ser Val Met Tyr Gly Phe	
115 120 125	

GTG GGC GTG GTT AAA AAC TAT GGG CTT GAA TAC GCG GGC GTG GCG ACT	344
Val Gly Val Val Lys Asn Tyr Gly Leu Glu Tyr Ala Gly Val Ala Thr	
85 90 95	
CTT ATG GCA GGG GTG TTG CAA ATT CTT TTA GGC TAT TTG AAA ATA GGG	392
Leu Met Ala Gly Val Leu Gln Ile Leu Leu Gly Tyr Leu Lys Ile Gly	
100 105 110	
AAT CTT TTG AGG TTT ATC CCC CAA TCA GTG ATG TAT GGC TTT GTG AAC	440
Asn Leu Leu Arg Phe Ile Pro Gln Ser Val Met Tyr Gly Phe Val Asn	
115 120 125 130	
GCG CTA GGC ATT TTG CTT TTA ATG GAG CAA TTC AAA TTC CTT CAA AAC	488
Ala Leu Gly Ile Leu Leu Leu Met Glu Gln Phe Lys Phe Leu Gln Asn	
135 140 145	
CAA AAT TTG GGG GTG TTT GTC TTG CTC GCT ATT GGG ATA CTC ATC ATT	536
Gln Asn Leu Gly Val Phe Val Leu Leu Ala Ile Gly Ile Leu Ile Ile	
150 155 160	
TAT CTT TTT CCT CTA ATC ACT AAA AAA ATC CCC TCT AAT CTG ATT TGT	584
Tyr Leu Phe Pro Leu Ile Thr Lys Lys Ile Pro Ser Asn Leu Ile Cys	
165 170 175	
ATC CTT ATA GTG AGC GCG ATC GCT TTA ATT TTT GAT ATG CAT GCG CCG	632
Ile Leu Ile Val Ser Ala Ile Ala Leu Ile Phe Asp Met His Ala Pro	
180 185 190	
AAT TTG GGG AGC ATT GAG CAA GGG GTT TCA GGC TTT CAT TTC ATC ATT	680
Asn Leu Gly Ser Ile Glu Gln Gly Val Ser Gly Phe His Phe Ile Ile	
195 200 205 210	
ATC CCC AAA AAT TTG GAT TTT AAA ATA ATG ATA GAG TTG TTG CCT TAC	728
Ile Pro Lys Asn Leu Asp Phe Lys Ile Met Ile Glu Leu Leu Pro Tyr	
215 220 225	
GCT CTT TCT TTA GCA CTA GTG GGA ACG ATA GAA AGC TTA TTG ACG GCT	776
Ala Leu Ser Leu Ala Leu Val Gly Thr Ile Glu Ser Leu Leu Thr Ala	
230 235 240	
AAA ACT TTA GAT GTG ATT TTA AAA GAC GGC GTG AGC GAT AAA AAT AAA	824
Lys Thr Leu Asp Val Ile Leu Lys Asp Gly Val Ser Asp Lys Asn Lys	
245 250 255	
GAA ACT AAA GCG CAA GGC TTG GGG AAT ATC ATC TCA GGG CTT TTG GGG	872
Glu Thr Lys Ala Gln Gly Leu Gly Asn Ile Ile Ser Gly Leu Leu Gly	
260 265 270	
GGA ATG ACA GGG TGC GCT TTA GTG GGG CAG TCT ATC ATT AAC GCA AAA	920
Gly Met Thr Gly Cys Ala Leu Val Gly Gln Ser Ile Ile Asn Ala Lys	
275 280 285 290	
TCC GGG GCT AAA ACA AGG CTT TCT ACT TTT TTT GCC GGC TTT TCT TTA	968
Ser Gly Ala Lys Thr Arg Leu Ser Thr Phe Phe Ala Gly Phe Ser Leu	
295 300 305	

```

Met Leu Trp Asp Leu Asn Arg Ser Asn Ile Ala Ala Ser Thr Gly Ser
 290                               295                               300
Ala Cys Ala Ser Glu Asp Leu Glu Ala Asn Pro Val Met Val Ala Ile
305                               310                               315                               320
Gly Ala Ser Lys Glu Leu Ala His Thr Ala Ile Arg Leu Ser Leu Ser
                               325                               330                               335
Arg Phe Asn Thr Glu Ala Glu Ile Asp Lys Thr Ile Glu Val Phe Ser
                               340                               345                               350
Gln Ala Ala Val Arg Leu Arg Asn Ile Ser Ser Ser Tyr
      355                               360                               365

```

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1220
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

```

TCCGGTTTGA AGTTGGTTTT TAAATCTTTG GCTATAATCA AGCCATTCTA ATG AGA      56
                                     Met Arg
                                     1

AAG AAA GGC ATG TTT GAA AAG ATA CAA AAA GAA TGG CTG AGC AAC ATT      104
Lys Lys Gly Met Phe Glu Lys Ile Gln Lys Glu Trp Leu Ser Asn Ile
      5                               10                               15

CAA AAG GAT TTG TTG TCT GGT TTT GTG GTG GGG CTT TCT GTG ATC CCA      152
Gln Lys Asp Leu Leu Ser Gly Phe Val Val Gly Leu Ser Val Ile Pro
      20                               25                               30

GAG ACG GCC GGC TTT GCG ATC ATG GTG GGT TTA GAT GTG GGC GTG GCG      200
Glu Thr Ala Gly Phe Ala Ile Met Val Gly Leu Asp Val Gly Val Ala
      35                               40                               45                               50

TTT TAT ACG ACC TTT TAC ATG GCT TTT GTT TTG TCT CTT TTT GGG GCT      248
Phe Tyr Thr Thr Phe Tyr Met Ala Phe Val Leu Ser Leu Phe Gly Ala
                               55                               60                               65

AGA AAG GCG ATG ATT AGC GCA GCG GCC GGC TCA GTG GCG CTC ATT TTA      296
Arg Lys Ala Met Ile Ser Ala Ala Ala Gly Ser Val Ala Leu Ile Leu
      70                               75                               80

```

GCT GTA AGG TTG AGA AAT ATT TCA AGC TCT TAT TAAAAAGAAT ATAAAGGAAT 1165
 Ala Val Arg Leu Arg Asn Ile Ser Ser Ser Tyr
 355 360 365

CAAAATGGCA AAACATGATT TAGTGGGTTC GGT 1198

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

Met	Asp	Pro	Phe	Leu	Arg	Asp	His	Tyr	Gly	Asn	Pro	Ser	Ser	Leu	His	1	5	10	15
Gln	Phe	Gly	Thr	Glu	Thr	His	Pro	Ala	Ile	Ala	Glu	Ala	Leu	Asp	Lys	20	25	30	
Leu	Tyr	Lys	Gly	Ile	Asn	Ala	Arg	Asp	Ile	Asp	Asp	Val	Ile	Ile	Thr	35	40	45	
Ser	Cys	Ala	Thr	Glu	Ser	Asn	Trp	Val	Leu	Lys	Gly	Val	Tyr	Phe		50	55	60	
Asp	Glu	Cys	Leu	Lys	Lys	Gly	Lys	Asn	His	Ile	Val	Thr	Thr	Val	Ala	65	70	75	80
Glu	His	Pro	Ala	Val	Arg	Ser	Thr	Cys	Asn	Phe	Leu	Glu	Ser	Leu	Gly	85	90	95	
Val	Glu	Val	Thr	Tyr	Leu	Pro	Ile	Asn	Glu	His	Gly	Ser	Ile	Thr	Ala	100	105	110	
Glu	Gln	Val	Lys	Glu	Ala	Ile	Thr	Glu	Lys	Thr	Ala	Leu	Val	Ser	Val	115	120	125	
Met	Trp	Ala	Asn	Asn	Glu	Thr	Gly	Leu	Ile	Phe	Pro	Ile	Glu	Glu	Ile	130	135	140	
Gly	Ala	Ile	Cys	Lys	Glu	Lys	Gly	Val	Leu	Phe	His	Thr	Asp	Ala	Val	145	150	155	160
Gln	Ala	Ile	Gly	Lys	Ile	Pro	Val	Asp	Val	Leu	Lys	Ala	Asn	Ala	Asp	165	170	175	
Phe	Leu	Ser	Phe	Ser	Ala	His	Lys	Phe	His	Gly	Pro	Lys	Gly	Ile	Gly	180	185	190	
Gly	Leu	Tyr	Ile	Arg	Ser	Gly	Val	Gly	Leu	Thr	Pro	Leu	Phe	His	Gly	195	200	205	
Gly	Glu	His	Met	Asn	Gly	Arg	Arg	Ser	Gly	Thr	Leu	Asn	Val	Pro	Tyr	210	215	220	
Ile	Val	Gly	Met	Gly	Glu	Ala	Met	Lys	Leu	Ala	Val	Glu	His	Leu	Asp	225	230	235	240
Tyr	Glu	Lys	Glu	Val	Val	Gly	Lys	Leu	Arg	Asp	Lys	Leu	Glu	Glu	Ala	245	250	255	
Leu	Leu	Lys	Ile	Pro	Asp	Val	Met	Val	Val	Gly	Asp	Arg	Ile	His	Arg	260	265	270	
Val	Pro	Asn	Thr	Thr	Leu	Val	Ser	Val	Arg	Gly	Ile	Glu	Gly	Glu	Ala	275	280	285	

GCG AAT AAT GAA ACC GGT CTC ATT TTC CCT ATT GAA GAA ATT GGG GCT	488
Ala Asn Asn Glu Thr Gly Leu Ile Phe Pro Ile Glu Glu Ile Gly Ala	
135 140 145	
ATT TGT AAA GAA AAG GGC GTG TTG TTC CAT ACC GAT GCC GTG CAA GCG	536
Ile Cys Lys Glu Lys Gly Val Leu Phe His Thr Asp Ala Val Gln Ala	
150 155 160	
ATT GGT AAA ATC CCT GTA GAT GTG TTA AAA GCG AAT GCA GAT TTC CTT	584
Ile Gly Lys Ile Pro Val Asp Val Leu Lys Ala Asn Ala Asp Phe Leu	
165 170 175	
TCT TTT AGC GCG CAC AAG TTT CAT GGG CCT AAA GGC ATT GGG GGG TTG	632
Ser Phe Ser Ala His Lys Phe His Gly Pro Lys Gly Ile Gly Gly Leu	
180 185 190	
TAT ATT AGA AGT GGG GTG GGA TTG ACC CCT CTT TTT CAT GGC GGG GAG	680
Tyr Ile Arg Ser Gly Val Gly Leu Thr Pro Leu Phe His Gly Gly Glu	
195 200 205 210	
CAT ATG AAT GGC AGG CGC AGC GGG ACT TTG AAT GTG CCT TAT ATT GTG	728
His Met Asn Gly Arg Arg Ser Gly Thr Leu Asn Val Pro Tyr Ile Val	
215 220 225	
GGA ATG GGC GAA GCG ATG AAA TTA GCC GTA GAG CAT TTA GAC TAT GAA	776
Gly Met Gly Glu Ala Met Lys Leu Ala Val Glu His Leu Asp Tyr Glu	
230 235 240	
AAA GAA GTG GTG GGG AAA TTG CGC GAC AAA TTA GAA GAA GCG CTT TTG	824
Lys Glu Val Val Gly Lys Leu Arg Asp Lys Leu Glu Glu Ala Leu Leu	
245 250 255	
AAA ATC CCT GAT GTG ATG GTG GTG GGC GAT AGA ATC CAT CGT GTG CCT	872
Lys Ile Pro Asp Val Met Val Val Gly Asp Arg Ile His Arg Val Pro	
260 265 270	
AAC ACG ACT TTA GTC AGC GTG AGA GGG ATT GAA GGA GAG GCC ATG CTG	920
Asn Thr Thr Leu Val Ser Val Arg Gly Ile Glu Gly Glu Ala Met Leu	
275 280 285 290	
TGG GAT TTA AAC CGC TCT AAT ATC GCC GCT TCC ACA GGG AGC GCG TGC	968
Trp Asp Leu Asn Arg Ser Asn Ile Ala Ala Ser Thr Gly Ser Ala Cys	
295 300 305	
GCG AGT GAG GAT TTA GAG GCT AAT CCG GTG ATG GTA GCG ATT GGA GCG	1016
Ala Ser Glu Asp Leu Glu Ala Asn Pro Val Met Val Ala Ile Gly Ala	
310 315 320	
AGT AAG GAA TTG GCT CAT ACC GCT ATC AGG CTT TCA TTG AGC CGT TTT	1064
Ser Lys Glu Leu Ala His Thr Ala Ile Arg Leu Ser Leu Ser Arg Phe	
325 330 335	
AAC ACG GAA GCT GAA ATT GAC AAA ACG ATT GAA GTT TTC TCT CAA GCG	1112
Asn Thr Glu Ala Glu Ile Asp Lys Thr Ile Glu Val Phe Ser Gln Ala	
340 345 350	

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1145
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

ATTTAGACAA TAACGCTACA ACTAGGATTG ACCCTAAAGT CAAAGAGATC	ATG GAT	56
	Met Asp	
	1	
CCT TTT TTA AGG GAT CAT TAT GGG AAT CCT AGC TCG TTG CAC CAG TTT		104
Pro Phe Leu Arg Asp His Tyr Gly Asn Pro Ser Ser Leu His Gln Phe		
5 10 15		
GGC ACA GAA ACC CAC CCA GCC ATT GCA GAA GCG CTA GAT AAG CTT TAT		152
Gly Thr Glu Thr His Pro Ala Ile Ala Glu Ala Leu Asp Lys Leu Tyr		
20 25 30		
AAG GGC ATT AAC GCT AGG GAT ATA GAT GAT GTG ATC ATC ACT TCT TGT		200
Lys Gly Ile Asn Ala Arg Asp Ile Asp Asp Val Ile Ile Thr Ser Cys		
35 40 45 50		
GCG ACA GAA AGC AAT AAT TGG GTT TTA AAG GGC GTG TAT TTT GAT GAA		248
Ala Thr Glu Ser Asn Asn Trp Val Leu Lys Gly Val Tyr Phe Asp Glu		
55 60 65		
TGC TTG AAA AAA GGC AAA AAC CAT ATT GTA ACC ACG GTT GCA GAG CAT		296
Cys Leu Lys Lys Gly Lys Asn His Ile Val Thr Thr Val Ala Glu His		
70 75 80		
CCG GCG GTG CGA TCC ACT TGC AAT TTT TTA GAA AGC TTG GGG GTG GAG		344
Pro Ala Val Arg Ser Thr Cys Asn Phe Leu Glu Ser Leu Gly Val Glu		
85 90 95		
GTT ACT TAC TTG CCC ATT AAT GAG CAT GGG AGC ATC ACC GCA GAG CAA		392
Val Thr Tyr Leu Pro Ile Asn Glu His Gly Ser Ile Thr Ala Glu Gln		
100 105 110		
GTC AAA GAA GCG ATC ACA GAA AAA ACC GCT CTA GTG AGC GTG ATG TGG		440
Val Lys Glu Ala Ile Thr Glu Lys Thr Ala Leu Val Ser Val Met Trp		
115 120 125 130		

CAA AAA GTG AAG CGA CTG ATT AAA AGG GTT TTT TAAAACCCTT TTAAACTAA 1230
 Gln Lys Val Lys Arg Leu Ile Lys Arg Val Phe
 275 280

TGCGAGCAAG CATGGGTTTG TGTGGGCTGG ATGTCCTTAT T 1271

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

Met	Ile	Met	Cys	Arg	Phe	Phe	Phe	Ala	Ser	Leu	Phe	Pro	Gln	Tyr	Asp	1	5	10	15
Lys	Met	Ile	Met	Phe	Asp	Val	Asp	Thr	Leu	Phe	Val	Asn	Asp	Ile	Ser	20	25	30	
Glu	Ser	Phe	Phe	Ile	Pro	Leu	Glu	Thr	His	Tyr	Phe	Gly	Ala	Val	Arg	35	40	45	
Glu	Lys	Asp	Leu	Ile	Ala	Ile	Asn	Arg	Asn	Ser	Ala	Lys	Asp	Leu	Tyr	50	55	60	
Glu	Leu	Arg	Gln	Met	His	Ala	Lys	Ser	Ile	Gly	Ile	Ala	Asn	Ala	Phe	65	70	75	80
Pro	Asn	Leu	Glu	Glu	Ala	Gln	Ile	Leu	Phe	Asp	Asn	Tyr	Phe	Asn	Ala	85	90	95	
Gly	Phe	Leu	Ala	Leu	Asn	Leu	Lys	Ser	Trp	Arg	Lys	Glu	Asn	Leu	Glu	100	105	110	
Asn	Gln	Leu	Ile	Thr	Phe	Phe	Ile	Leu	Lys	Asn	Glu	Lys	Leu	Leu	Phe	115	120	125	
Asn	Asp	Gln	Asp	Ala	Leu	Cys	Phe	Val	Cys	Arg	Gly	Arg	Ile	Leu	Glu	130	135	140	
Leu	Pro	Tyr	Pro	Tyr	Asn	Ala	His	Pro	Ser	Phe	Leu	Asp	Thr	Leu	Ser	145	150	155	160
Phe	Pro	Ser	Ile	Lys	Glu	Ala	Arg	Met	Leu	His	Phe	Trp	Gly	Asp	Lys	165	170	175	
Pro	Trp	Lys	Leu	Leu	Ser	Val	Ile	Gly	Ala	Lys	Lys	Trp	His	Glu	Ala	180	185	190	
Leu	Ile	Gln	Thr	Pro	Phe	Lys	Asp	Ala	Tyr	Phe	Asn	Ala	Ser	Phe	Leu	195	200	205	
Asp	His	Leu	Phe	Glu	Ser	Leu	Gln	Asn	Lys	Asp	Asn	Glu	Ile	Lys	Arg	210	215	220	
Arg	Asp	Glu	Arg	Ile	Ile	Glu	Ala	Leu	Gln	Ala	Arg	Asp	Lys	Ile	Leu	225	230	235	240
Ser	Phe	Ser	Asp	Lys	Arg	His	Ser	Phe	Glu	Ser	Leu	Leu	Pro	Lys	Leu	245	250	255	
Ser	Ser	Lys	Leu	Leu	Ile	Glu	Phe	Leu	Leu	Phe	Lys	Ala	Lys	Gln	Lys	260	265	270	
Val	Lys	Arg	Leu	Ile	Lys	Arg	Val	Phe								275	280		

Val	Arg	Glu	Lys	Asp	Leu	Ile	Ala	Ile	Asn	Arg	Asn	Ser	Ala	Lys	Asp	
			50					55					60			
TTA	TAC	GAA	TTG	CGC	CAA	ATG	CAT	GCA	AAA	TCT	ATC	GGC	ATC	GCC	AAC	601
Leu	Tyr	Glu	Leu	Arg	Gln	Met	His	Ala	Lys	Ser	Ile	Gly	Ile	Ala	Asn	
		65				70					75					
GCT	TTC	CCT	AAT	TTA	GAA	GAA	GCT	CAA	ATC	CTT	TTT	GAC	AAC	TAC	TTT	649
Ala	Phe	Pro	Asn	Leu	Glu	Glu	Ala	Gln	Ile	Leu	Phe	Asp	Asn	Tyr	Phe	
	80				85					90						
AAC	GCC	GGG	TTT	TTA	GCC	TTA	AAT	TTA	AAA	TCA	TGG	CGT	AAA	GAA	AAT	697
Asn	Ala	Gly	Phe	Leu	Ala	Leu	Asn	Leu	Lys	Ser	Trp	Arg	Lys	Glu	Asn	
95					100				105					110		
CTT	GAA	AAC	CAA	TTG	ATT	ACC	TTT	TTC	ATT	TTG	AAA	AAT	GAA	AAA	CTT	745
Leu	Glu	Asn	Gln	Leu	Ile	Thr	Phe	Phe	Ile	Leu	Lys	Asn	Glu	Lys	Leu	
			115					120					125			
TTA	TTT	AAC	GAT	CAA	GAT	GCT	TTG	TGT	TTT	GTG	TGC	CGT	GGG	AGG	ATT	793
Leu	Phe	Asn	Asp	Gln	Asp	Ala	Leu	Cys	Phe	Val	Cys	Arg	Gly	Arg	Ile	
			130					135					140			
TTA	GAA	TTG	CCT	TAT	CCA	TAC	AAT	GCC	CAC	CCT	AGT	TTC	CTT	GAT	ACG	841
Leu	Glu	Leu	Pro	Tyr	Pro	Tyr	Asn	Ala	His	Pro	Ser	Phe	Leu	Asp	Thr	
	145					150						155				
CTC	TCA	TTC	CCT	AGC	ATC	AAA	GAA	GCG	CGC	ATG	CTG	CAT	TTT	TGG	GGC	889
Leu	Ser	Phe	Pro	Ser	Ile	Lys	Glu	Ala	Arg	Met	Leu	His	Phe	Trp	Gly	
	160					165				170						
GAT	AAA	CCC	TGG	AAA	CTC	TTA	AGC	GTC	ATT	GGC	GCG	AAA	AAA	TGG	CAT	937
Asp	Lys	Pro	Trp	Lys	Leu	Leu	Ser	Val	Ile	Gly	Ala	Lys	Lys	Trp	His	
175					180				185					190		
GAA	GCG	TTG	ATC	CAA	ACG	CCT	TTT	AAA	GAC	GCC	TAT	TTC	AAC	GCT	TCT	985
Glu	Ala	Leu	Ile	Gln	Thr	Pro	Phe	Lys	Asp	Ala	Tyr	Phe	Asn	Ala	Ser	
				195				200					205			
TTT	TTA	GAT	CAC	CTC	TTT	GAA	TCC	CTT	CAA	AAC	AAG	GAT	AAT	GAG	ATC	1033
Phe	Leu	Asp	His	Leu	Phe	Glu	Ser	Leu	Gln	Asn	Lys	Asp	Asn	Glu	Ile	
			210					215					220			
AAA	AGA	AGA	GAT	GAA	AGG	ATC	ATT	GAA	GCA	CTT	CAA	GCA	AGG	GAT	AAA	1081
Lys	Arg	Arg	Asp	Glu	Arg	Ile	Ile	Glu	Ala	Leu	Gln	Ala	Arg	Asp	Lys	
	225					230						235				
ATC	CTG	TCT	TTT	TCA	GAC	AAG	CGA	CAT	TCT	TTT	GAA	TCT	CTT	CTG	CCC	1129
Ile	Leu	Ser	Phe	Ser	Asp	Lys	Arg	His	Ser	Phe	Glu	Ser	Leu	Leu	Pro	
	240					245					250					
AAG	CTT	TCT	TCT	AAA	CTC	CTT	ATA	GAA	TTT	TTG	CTT	TTT	AAA	GCC	AAA	1177
Lys	Leu	Ser	Ser	Lys	Leu	Leu	Ile	Glu	Phe	Leu	Leu	Phe	Lys	Ala	Lys	
255					260					265				270		

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

```

Met Asp Leu Leu Phe Ala Thr Pro Thr Ile Ser Pro Phe Leu Pro Phe
 1           5           10           15
Lys Asn Pro Met Ile Phe Leu Tyr Lys Asn Glu Met Ile Val Leu Lys
          20           25           30
Phe Ser Asn Ser Gln Asp Ala Leu Pro Ile Asn Lys Pro Ser Thr Leu
        35           40           45
Ser Ile Pro Lys Ile Ser Leu Ala Phe Cys Val Phe Thr Leu Pro Pro
      50           55           60
Tyr Asn Lys Gly Val Phe
65           70

```

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 368...1210
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

```

TTTAAGGACT ATGCATGCAA GAGATTATCC CTATTGTCGT GGCTTTTGAT AACAACTATT      60
GTATCCCTGC TGGCGTGAGC TTATTTTCCA TGCTAGCAAA CGCCAAACGA GAGAGAGAGA      120
GAGAGAGAGA GTAAAACTCT TTTATCAAAT CCATTGTTTG GTGGAGAGTT TAACCCGAGA      180
GAATATAGCC AAATTAGAAG AAACGATCGC TCCTTTTAGA GCTTTTTCTA GCATAGAGTT      240
TTTGATATT ACCGATAAAG AATTAGAACC ACGCCACAAT TATAATAAGC TTGATCCTTT      300
AATAGCGAGT GAAATTAAAA AATTGTATTT AAAACTCAAT GCTTTTTTCGC AAAAACGCTT      360
TTCTAAA ATG ATC ATG TGC CGT TTC TTT TTT GCC TCC CTT TTC CCC CAA      409
      Met Ile Met Cys Arg Phe Phe Phe Ala Ser Leu Phe Pro Gln
        1           5           10

TAC GAT AAG ATG ATC ATG TTT GAT GTG GAC ACT TTG TTT GTG AAT GAT      457
Tyr Asp Lys Met Ile Met Phe Asp Val Asp Thr Leu Phe Val Asn Asp
15           20           25           30

ATT AGC GAG AGC TTT TTT ATC CCC CTT GAA ACG CAT TAT TTT GGG GCT      505
Ile Ser Glu Ser Phe Phe Ile Pro Leu Glu Thr His Tyr Phe Gly Ala
          35           40           45

GTG AGG GAA AAA GAT TTG ATC GCT ATA AAT AGG AAT TCG GCT AAG GAT      553

```

210

215

220

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...262
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

```

GAAAGCCAAA GTAGCCCCTT GATTGAAACA AGATTGAGCG ATCCCATAG CG ATG GAT      58
                                   Met Asp
                                   1

TTA TTG TTC GCC ACC CCT ACA ATA AGC CCT TTT TTA CCT TTT AAA AAT      106
Leu Leu Phe Ala Thr Pro Thr Ile Ser Pro Phe Leu Pro Phe Lys Asn
      5                      10                      15

CCC ATG ATT TTC CTT TAT AAA AAT GAA ATG ATT GTT TTA AAA TTT TCT      154
Pro Met Ile Phe Leu Tyr Lys Asn Glu Met Ile Val Leu Lys Phe Ser
      20                      25                      30

AAT TCC CAA GAC GCG CTC CCG ATC AAC AAG CCA TCC ACG CTA TCA ATC      202
Asn Ser Gln Asp Ala Leu Pro Ile Asn Lys Pro Ser Thr Leu Ser Ile
      35                      40                      45                      50

CCT AAA ATT TCT TTA GCG TTT TGT GTG TTC ACG CTC CCC CCA TAC AAC      250
Pro Lys Ile Ser Leu Ala Phe Cys Val Phe Thr Leu Pro Pro Tyr Asn
      55                      60                      65

AAG GGC GTT TTT TGATTTAAGA TTTGCTTTAA AAAACCATGC GTGAGATAAA TATCT      307
Lys Gly Val Phe
      70

TCTAAAGAAG CGCTTTTTTTT GGTGCCAATC GCCCAAATAG GCTC      351

```

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

TTGCAAAGCA GTATCGCCAC TTTGCGTAAC AGGATGTTGA AAGTGGGTAA AAGCCGCTAA 791
TTTCTTTTTA GTGGGTCGTT TTTGAAAATC TTTTTAGTCT TTTTAAGCG 840

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

CAATGTCCAT GAGTTATTGG ACCAACACAA CGCTAACCTA AAAGGAGAAC ACC ATG	56
Met	
1	
AGT GAT AAT GAA CGA ACG ATT GTA GTT AGA GTG CTA AAA TTT GAC CCT	104
Ser Asp Asn Glu Arg Thr Ile Val Val Arg Val Leu Lys Phe Asp Pro	
5 10 15	
CAA AGC GCG GTG AGT AAG CCG CAT TTT AAA GAG TAT CAG TTG AAA GAA	152
Gln Ser Ala Val Ser Lys Pro His Phe Lys Glu Tyr Gln Leu Lys Glu	
20 25 30	
ACG CCA TCC ATG ACG CTT TTT ATC GCT TTG AAC CTC ATT AGA GAG CAT	200
Thr Pro Ser Met Thr Leu Phe Ile Ala Leu Asn Leu Ile Arg Glu His	
35 40 45	
CAA GAT CCG GAT TTG AGT TTT GAT TTT GTG TGC CGC GCT GGG ATT TGC	248
Gln Asp Pro Asp Leu Ser Phe Asp Phe Val Cys Arg Ala Gly Ile Cys	
50 55 60 65	
GGC TCT TGC GCG ATG ATG GTT AAT GGG AGA CCG AGG CTA GCT TGT AAA	296
Gly Ser Cys Ala Met Met Val Asn Gly Arg Pro Arg Leu Ala Cys Lys	
70 75 80	
ACC CTA ACT TCT AGC TTT GAA AGC GGG GTG ATC ACG CTC ATG CCC ATG	344
Thr Leu Thr Ser Ser Phe Glu Ser Gly Val Ile Thr Leu Met Pro Met	
85 90 95	
CCC AGT TTT ACG CTC ATT AAA GAT TTG AGC GTG AAT ACG GGC GAT TGG	392
Pro Ser Phe Thr Leu Ile Lys Asp Leu Ser Val Asn Thr Gly Asp Trp	
100 105 110	
TTT TTG GAT ATG ACT AAA AGG GTG GAG AGT TGG GCG CAT TCT AAA GAA	440
Phe Leu Asp Met Thr Lys Arg Val Glu Ser Trp Ala His Ser Lys Glu	
115 120 125	
GAA GTG GAT ATT ACT AGA CCG GAA AAA AGG GTT GAG CCT GAC GAA GCC	488
Glu Val Asp Ile Thr Arg Pro Glu Lys Arg Val Glu Pro Asp Glu Ala	
130 135 140 145	
CAA GAA GTC TTT GAA CTA GAC AGG TGT ATT GAA TGC GGG TGT TGT ATC	536
Gln Glu Val Phe Glu Leu Asp Arg Cys Ile Glu Cys Gly Cys Cys Ile	
150 155 160	
GCT TCT TGC GGG ACT AAA CTC ATG CGC CCT AAT TTC ATT GGA GCT GCT	584
Ala Ser Cys Gly Thr Lys Leu Met Arg Pro Asn Phe Ile Gly Ala Ala	
165 170 175	

40	45	50	
GGG GAA TTA AAA TTA GAA GTC GCC CCC AAA AAC CAA AGC TTC TTC AAA			308
Gly Glu Leu Lys Leu Glu Val Ala Pro Lys Asn Gln Ser Phe Phe Lys			
55	60	65	
ACG CTC TTG GAA GCG GCA GAA AAG GAG AAT ATC AGC CAG AAA AAG ATG			356
Thr Leu Leu Glu Ala Ala Glu Lys Glu Asn Ile Ser Gln Lys Lys Met			
70	75	80	
CAG ACA CCG AGG GCA AGC AAA ATC TTT TTG AAG TTT TGAAGGCTAT CTTGGA			408
Gln Thr Pro Arg Ala Ser Lys Ile Phe Leu Lys Phe			
85	90	95	
TAAGGTCAGC AAATTGAGTG AAGAAGAAGT GAATGAGCGT TTG			451

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

Met	Val	Val	Ala	Lys	Asn	Glu	Asp	Asn	Lys	Lys	Leu	Tyr	Asp	Ile	Ile
1				5					10					15	
Asp	Gly	Gln	Gln	Arg	Thr	Thr	Thr	Ile	Phe	Met	Leu	Leu	His	Val	Leu
			20					25					30		
Ala	Asn	Lys	Gln	Asn	Glu	Lys	Asp	Lys	Gln	Glu	Thr	Arg	Lys	Tyr	Leu
		35					40					45			
Tyr	Gln	Lys	Gly	Glu	Leu	Lys	Leu	Glu	Val	Ala	Pro	Lys	Asn	Gln	Ser
		50				55					60				
Phe	Phe	Lys	Thr	Leu	Leu	Glu	Ala	Ala	Glu	Lys	Glu	Asn	Ile	Ser	Gln
65				70					75					80	
Lys	Lys	Met	Gln	Thr	Pro	Arg	Ala	Ser	Lys	Ile	Phe	Leu	Lys	Phe	
			85						90					95	

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 54...718

(2) INFORMATION FOR SEQ ID NO:645:

(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 108...392
(D) OTHER INFORMATION:

ATCAGAGGGA	TTACGCCTGG	AAGGATAAGA	ATTTTAGGGA	TCTGTAAGAA	GATCTAGAAG		60
AAGCGATAGA	ATACAACAAA	AAGGGTCAGG	GGCATTTTAT	AGGCACC	ATG GTT GTC		116
					Met Val Val		
					1		
GCT AAG AAT GAA GAC AAC AAA AAA TTG TAT GAC ATC ATT GAC GGC CAG							164
Ala Lys Asn Glu Asp Asn Lys Lys Leu Tyr Asp Ile Ile Asp Gly Gln							
5					10	15	
CAA CGA ACG ACT ACC ATC TTC ATG CTC TTG CAT GTC TTG GCG AAC AAA							212
Gln Arg Thr Thr Thr Ile Phe Met Leu Leu His Val Leu Ala Asn Lys							
20				25		30	35
CAA AAC GAG AAA GAC AAG CAA GAA ACA AGA AAA TAT CTA TAC CAA AAG							260
Gln Asn Glu Lys Asp Lys Gln Glu Thr Arg Lys Tyr Leu Tyr Gln Lys							

TTT AAC CGA AAA AGC GTG TTT GAA TGC TTG AAA AAT GAA GTG GAA AAT	488
Phe Asn Arg Lys Ser Val Phe Glu Cys Leu Lys Asn Glu Val Glu Asn	
135 140 145	
TTA AAA CTC AGT CTA GAA GAT TTA GAA TTC GCT CTC ATT GAT TAT GGT	536
Leu Lys Leu Ser Leu Glu Asp Leu Glu Phe Ala Leu Ile Asp Tyr Gly	
150 155 160	
TTG GAA GAA TTA GAA GAA GTG GAA GAC AAG ATC ATT ATT AGG GGG GAT	584
Leu Glu Glu Leu Glu Glu Val Glu Asp Lys Ile Ile Ile Arg Gly Asp	
165 170 175	
TAT AAC AGC TTC AAG CTT TTA AAT GAG GGG TTT GAA AGC TTG AAA TTA	632
Tyr Asn Ser Phe Lys Leu Leu Asn Glu Gly Phe Glu Ser Leu Lys Leu	
180 185 190	
CCC ATT TTA AAA GCG AGT TTG CAA CGC ATC GCC ACA ACG CCC ATT GAA	680
Pro Ile Leu Lys Ala Ser Leu Gln Arg Ile Ala Thr Thr Pro Ile Glu	
195 200 205 210	
TTG AAT GAC GAA CAA ATG GAG CTT ACC GAA AAA TTA CTG GAC AGG ATT	728
Leu Asn Asp Glu Gln Met Glu Leu Thr Glu Lys Leu Leu Asp Arg Ile	
215 220 225	
GAA GAC GAT GAT GAT GTG GTC GCG CTT TAT ACC AAT ATT GAG TGAAATGCA	779
Glu Asp Asp Asp Asp Val Val Ala Leu Tyr Thr Asn Ile Glu	
230 235 240	
AAAAGACTCA AAGTATTTTT TTAACCACC CAAGCATTCA TCCCAATAGG GAATGCGTTG	839
GAGA	843

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

Met Gly Arg Ala Phe Glu Tyr Arg Arg Ala Ala Lys Glu Lys Arg Trp	
1 5 10 15	
Asp Lys Met Ser Lys Val Phe Pro Lys Leu Ala Lys Ala Ile Thr Leu	
20 25 30	
Ala Ala Lys Asp Gly Gly Ser Glu Pro Asp Thr Asn Ala Lys Leu Arg	
35 40 45	
Thr Ala Ile Leu Asn Ala Lys Ala Gln Asn Met Pro Lys Asp Asn Ile	
50 55 60	
Asp Ala Ala Ile Lys Arg Ala Ser Ser Lys Glu Gly Asn Leu Ser Glu	
65 70 75 80	
Ile Thr Tyr Glu Gly Lys Ala Asn Phe Gly Val Leu Ile Ile Met Glu	

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...770
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

TTATTAGCTA TCATGCTAAA GAAGTGGCTA ACTTATTACA AAGGAATTGA	ATG GGA	56
	Met Gly	
	1	
CGA GCG TTT GAA TAC AGA AGA GCG GCT AAA GAA AAA CGA TGG GAT AAG		104
Arg Ala Phe Glu Tyr Arg Arg Ala Ala Lys Glu Lys Arg Trp Asp Lys		
5 10 15		
ATG AGT AAG GTT TTC CCA AAG CTC GCT AAA GCG ATC ACT CTA GCG GCA		152
Met Ser Lys Val Phe Pro Lys Leu Ala Lys Ala Ile Thr Leu Ala Ala		
20 25 30		
AAA GAT GGC GGG AGC GAA CCG GAC ACG AAC GCC AAA CTA CGA ACA GCG		200
Lys Asp Gly Gly Ser Glu Pro Asp Thr Asn Ala Lys Leu Arg Thr Ala		
35 40 45 50		
ATT TTA AAC GCT AAA GCG CAA AAC ATG CCT AAA GAC AAT ATT GAC GCA		248
Ile Leu Asn Ala Lys Ala Gln Asn Met Pro Lys Asp Asn Ile Asp Ala		
55 60 65		
GCG ATT AAA AGA GCG AGC AGT AAA GAA GGG AAT TTG AGT GAA ATC ACT		296
Ala Ile Lys Arg Ala Ser Ser Lys Glu Gly Asn Leu Ser Glu Ile Thr		
70 75 80		
TAT GAA GGT AAG GCG AAT TTT GGC GTG CTA ATC ATC ATG GAA TGC ATG		344
Tyr Glu Gly Lys Ala Asn Phe Gly Val Leu Ile Ile Met Glu Cys Met		
85 90 95		
ACT GAT AAC CCC ACC AGA ACC ATT GCC AAC CTT AAA AGC TAT TTC AAT		392
Thr Asp Asn Pro Thr Arg Thr Ile Ala Asn Leu Lys Ser Tyr Phe Asn		
100 105 110		
AAA ACG CAA GGG GCA AGC ATC GTG CCT AAT GGC TCT TTA GAG TTT ATG		440
Lys Thr Gln Gly Ala Ser Ile Val Pro Asn Gly Ser Leu Glu Phe Met		
115 120 125 130		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

```

TACTGAATTT ATCCAATCGC TAAAACCCTT AGAAGATTAA AGGAAAAGAG  ATG AAA      56
                                     Met Lys
                                     1

TTT TTA AAC GGA TTA GCA GGG AAT TTA CTG ATT GTG GTT ATT TTA TTG      104
Phe Leu Asn Gly Leu Ala Gly Asn Leu Leu Ile Val Val Ile Leu Leu
      5              10              15

TGT GTG GCC GTT TTT TTT ACG CTC AAA GCG ATC CAT ATC CAA AAA GAG      152
Cys Val Ala Val Phe Phe Thr Leu Lys Ala Ile His Ile Gln Lys Glu
      20              25              30

CAA GCC ACC AAT TAT TAC CGC TAT AAG GAT ATT AAC GCT TTA GAG ACA      200
Gln Ala Thr Asn Tyr Tyr Arg Tyr Lys Asp Ile Asn Ala Leu Glu Thr
      35              40              45              50

AAA AAC ACC CAA AAC CGG GCT AAC TAT GAA TTA GTC AAT CAA GGG AGT      248
Lys Asn Thr Gln Asn Arg Ala Asn Tyr Glu Leu Val Asn Gln Gly Ser
              55              60              65

AAA AAA TGAAATTCAC GACTTTAGAA AAAATTTTAG CTTTGATGGT AGTAGCGACC AT      306
Lys Lys

T                                                                 307

```

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

```

Met Lys Phe Leu Asn Gly Leu Ala Gly Asn Leu Leu Ile Val Val Ile
  1              5              10              15
Leu Leu Cys Val Ala Val Phe Phe Thr Leu Lys Ala Ile His Ile Gln
      20              25              30
Lys Glu Gln Ala Thr Asn Tyr Tyr Arg Tyr Lys Asp Ile Asn Ala Leu
      35              40              45
Glu Thr Lys Asn Thr Gln Asn Arg Ala Asn Tyr Glu Leu Val Asn Gln
      50              55              60
Gly Ser Lys Lys
65

```

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

```

Met Asp Phe Leu Asn Asp His Ile Asn Val Phe Gly Leu Ile Ala Ala
 1           5           10           15
Leu Val Ile Leu Val Leu Thr Ile Tyr Glu Ser Ser Ser Leu Ile Lys
           20           25           30
Glu Met Arg Asp Ser Lys Ser Gln Gly Glu Leu Val Glu Asn Gly His
           35           40           45
Leu Ile Asp Gly Ile Gly Glu Phe Ala Asn Asn Val Pro Val Gly Trp
           50           55           60
Ile Ala Ser Phe Met Cys Thr Ile Val Trp Ala Phe Trp Tyr Phe Phe
65           70           75           80
Phe Gly Tyr Pro Leu Asn Ser Phe Ser Gln Ile Gly Gln Tyr Asn Glu
           85           90           95
Glu Val Lys Ala His Asn Gln Lys Phe Glu Ala Lys Trp Lys His Leu
           100          105          110
Gly Gln Lys Glu Leu Val Asp Met Gly Gln Gly Ile Phe Leu Val His
           115          120          125
Cys Ser Gln Cys His Gly Ile Thr Ala Glu Gly Leu His Gly Ser Ala
           130          135          140
Gln Asn Leu Val Arg Trp Gly Lys Glu Glu Gly Ile Met Asp Thr Ile
145          150          155          160
Lys His Gly Ser Lys Gly Met Asp Tyr Leu Ala Gly Glu Met Pro Ala
           165          170          175
Met Glu Leu Asp Glu Lys Asp Ala Lys Ala Ile Ala Ser Tyr Val Met
           180          185          190
Ala Glu Leu Ser Ser Val Lys Lys Thr Lys Asn Pro Gln Leu Ile Asp
           195          200          205
Lys Gly Lys Glu Leu Phe Glu Ser Met Gly Cys Thr Gly Cys His Gly
           210          215          220
Asn Asp Gly Lys Gly Leu Gln Glu Asn Gln Val Phe Ala Ala Asp Leu
225          230          235          240
Thr Ala Tyr Gly Thr Glu Asn Phe Leu Arg Asn Ile Leu Thr His Gly
           245          250          255
Lys Lys Gly Asn Ile Gly His Met Pro Ser Phe Lys Tyr Lys Asn Phe
           260          265          270
Ser Asp Leu Gln Val Lys Ala Leu Leu Asn Leu Ser Asn Arg
           275          280          285

```

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...254
- (D) OTHER INFORMATION:

AAG GAA CTG GTG GAT ATG GGT CAA GGC ATC TTT TTA GTC CAT TGT TCG	440
Lys Glu Leu Val Asp Met Gly Gln Gly Ile Phe Leu Val His Cys Ser	
115 120 125 130	
CAA TGC CAT GGC ATC ACC GCT GAG GGC TTG CAT GGG AGC GCT CAA AAT	488
Gln Cys His Gly Ile Thr Ala Glu Gly Leu His Gly Ser Ala Gln Asn	
135 140 145	
CTG GTG CGC TGG GGT AAA GAA GAG GGT ATT ATG GAT ACC ATT AAG CAT	536
Leu Val Arg Trp Gly Lys Glu Glu Gly Ile Met Asp Thr Ile Lys His	
150 155 160	
GGC TCT AAG GGC ATG GAT TAT CTC GCT GGG GAA ATG CCC GCT ATG GAA	584
Gly Ser Lys Gly Met Asp Tyr Leu Ala Gly Glu Met Pro Ala Met Glu	
165 170 175	
TTG GAC GAA AAA GAC GCT AAA GCG ATC GCA AGC TAT GTG ATG GCA GAA	632
Leu Asp Glu Lys Asp Ala Lys Ala Ile Ala Ser Tyr Val Met Ala Glu	
180 185 190	
CTT TCT AGC GTT AAA AAA ACC AAA AAC CCT CAA CTC ATT GAT AAA GGC	680
Leu Ser Ser Val Lys Lys Thr Lys Asn Pro Gln Leu Ile Asp Lys Gly	
195 200 205 210	
AAG GAA TTG TTT GAA AGC ATG GGT TGC ACA GGC TGT CAT GGC AAT GAT	728
Lys Glu Leu Phe Glu Ser Met Gly Cys Thr Gly Cys His Gly Asn Asp	
215 220 225	
GGT AAG GGC TTG CAA GAA AAT CAA GTG TTT GCA GCC GAT TTG ACC GCT	776
Gly Lys Gly Leu Gln Glu Asn Gln Val Phe Ala Ala Asp Leu Thr Ala	
230 235 240	
TAC GGC ACA GAG AAT TTT TTG AGA AAT ATC TTA ACG CAT GGC AAA AAG	824
Tyr Gly Thr Glu Asn Phe Leu Arg Asn Ile Leu Thr His Gly Lys Lys	
245 250 255	
GGC AAT ATA GGG CAT ATG CCA TCA TTC AAG TAT AAA AAC TTT AGC GAT	872
Gly Asn Ile Gly His Met Pro Ser Phe Lys Tyr Lys Asn Phe Ser Asp	
260 265 270	
TTG CAA GTT AAA GCG TTA CTG AAT TTA TCC AAT CGC TAAAACCCTT AGAAGA	924
Leu Gln Val Lys Ala Leu Leu Asn Leu Ser Asn Arg	
275 280 285	
TTAAAGGAAA AGAGATGAAA TTTTAAACG GATTAGC	961

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:639:

(A) LENGTH: 961 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...908
(D) OTHER INFORMATION: .

TGA	ACCACGC	CATAAAAAAG	TTCATGATAA	TGGCATAAAG	GAAAGTTGAA		ATG	GAT								56
								Met	Asp							
								1								
TTT	TTA	AAC	GAC	CAT	ATA	AAT	GTT	TTT	GGC	TTG	ATT	GCA	GCG	CTT	GTG	104
Phe	Leu	Asn	Asp	His	Ile	Asn	Val	Phe	Gly	Leu	Ile	Ala	Ala	Leu	Val	
		5					10					15				
ATT	TTA	GTT	TTA	ACC	ATC	TAT	GAA	TCC	AGT	TCG	CTC	ATT	AAA	GAA	ATG	152
Ile	Leu	Val	Leu	Thr	Ile	Tyr	Glu	Ser	Ser	Ser	Leu	Ile	Lys	Glu	Met	
	20					25					30					
CGC	GAC	AGC	AAA	TCT	CAA	GGT	GAG	CTT	GTA	GAA	AAT	GGG	CAT	TTG	ATT	200
Arg	Asp	Ser	Lys	Ser	Gln	Gly	Glu	Leu	Val	Glu	Asn	Gly	His	Leu	Ile	
35				40						45					50	
GAT	GGG	ATA	GGG	GAG	TTT	GCC	AAT	AAT	GTG	CCA	GTA	GGC	TGG	ATC	GCA	248
Asp	Gly	Ile	Gly	Glu	Phe	Ala	Asn	Asn	Val	Pro	Val	Gly	Trp	Ile	Ala	
				55					60					65		
AGC	TTT	ATG	TGC	ACG	ATT	GTG	TGG	GCT	TTT	TGG	TAT	TTC	TTC	TTT	GGG	296
Ser	Phe	Met	Cys	Thr	Ile	Val	Trp	Ala	Phe	Trp	Tyr	Phe	Phe	Phe	Gly	
			70					75					80			
TAT	CCG	CTG	AAT	AGC	TTT	TCT	CAA	ATC	GGG	CAA	TAC	AAT	GAA	GAG	GTT	344
Tyr	Pro	Leu	Asn	Ser	Phe	Ser	Gln	Ile	Gly	Gln	Tyr	Asn	Glu	Glu	Val	
		85					90					95				
AAA	GCG	CAC	AAC	CAA	AAA	TTT	GAG	GCC	AAG	TGG	AAG	CAT	TTG	GGT	CAA	392
Lys	Ala	His	Asn	Gln	Lys	Phe	Glu	Ala	Lys	Trp	Lys	His	Leu	Gly	Gln	
	100--					105					110					

```

Ser Gly Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu
      100      105      110
Asp His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe
      115      120      125
Leu Glu Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala
      130      135      140
Ile Leu Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys
145      150      155      160
Leu Ile Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro
      165      170      175
Ile Ser Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser
      180      185      190
Ala Met Thr Gly Lys Ile Leu Phe Phe Val Ser Leu Leu Val Pro Phe
      195      200      205
Phe Ile Val Phe Leu Met Asp Gly Phe Lys Gly Ile Lys Glu Thr Phe
      210      215      220
Pro Ala Val Phe Ile Ala Ala Phe Ser Phe Ala Gly Ala Gln Phe Leu
225      230      235      240
Ser Ser Asn Tyr Leu Gly Pro Glu Leu Pro Gly Ile Ile Ser Ala Leu
      245      250      255
Val Ser Leu Val Ala Thr Ala Leu Phe Leu Lys Phe Trp Gln Pro Lys
      260      265      270
Ala Ile Phe Arg Ser Asp Gly Lys Ala Ala Ser Phe Thr Lys Ser Asn
      275      280      285
His His Ile Cys Lys Ile Tyr Val Ala Trp Ser Pro Phe Val Ile Leu
      290      295      300
Val Leu Val Ile Val Leu Trp Ile Gln Pro Phe Phe Lys Ala Leu Phe
305      310      315      320
Glu Lys Asp Gly Leu Leu Ala Phe Ser Asn Phe Tyr Phe Glu Phe Asn
      325      330      335
Asn Ile Ser Asn His Ile Phe Lys Ser Pro Pro Phe Val Glu Ala Asn
      340      345      350
Gln Ser Val Ser Phe Pro Val Val Phe Lys Phe Leu Leu Ile Asn Thr
      355      360      365
Val Gly Thr Ser Ile Phe Leu Ala Ala Leu Val Ser Met Leu Val Leu
      370      375      380
Arg Val Arg Val Ser Asp Ala Leu Ser Val Phe Gly Glu Thr Leu Lys
385      390      395      400
Glu Met Arg Tyr Pro Ile Leu Thr Ile Gly Leu Val Leu Ser Phe Ala
      405      410      415
Tyr Val Ser Asn Tyr Ser Gly Ile Ser Ser Thr Leu Ala Leu Ala Leu
      420      425      430
Thr His Thr Gly Leu Ala Phe Thr Phe Phe Ser Pro Leu Ile Gly Trp
      435      440      445
Val Gly Val Phe Leu Thr Gly Ser Asp Thr Ser Ser Asn Leu Leu Phe
      450      455      460
Gly Ser Leu Gln Gln Leu Thr Ala Gln Arg Leu His Leu Pro Glu Val
465      470      475      480
Leu Thr Leu Thr Ala Asn Thr Val Gly Gly Thr Leu Gly Lys Met Ile
      485      490      495
Ser Pro Gln Ser Ile Ala Ile Ala Cys Ala Ala Val Gly Leu Ala Gly
      500      505      510
Lys Glu Ser Asp Leu Phe Lys Phe Thr Val Lys Tyr Ser Leu Ile Phe
      515      520      525
Val Ala Ile Met Gly Val Val Ile Ser Ala Ile Ala Tyr Leu Ile Pro

```

GTG TTT TTA ACC GGG AGC GAT ACG AGT TCC AAT CTT TTG TTT GGC TCT 1448
 Val Phe Leu Thr Gly Ser Asp Thr Ser Ser Asn Leu Leu Phe Gly Ser
 455 460 465

TTA CAG CAA CTC ACC GCC CAA CGA TTG CAC CTC CCT GAG GTT TTA ACC 1496
 Leu Gln Gln Leu Thr Ala Gln Arg Leu His Leu Pro Glu Val Leu Thr
 470 475 480

CTA ACG GCT AAT ACC GTG GGT GGC ACT TTA GGC AAG ATG ATA AGC CCT 1544
 Leu Thr Ala Asn Thr Val Gly Gly Thr Leu Gly Lys Met Ile Ser Pro
 485 490 495

CAA AGC ATC GCT ATC GCT TGC GCG GCG GTG GGG TTA GCC GGG AAA GAG 1592
 Gln Ser Ile Ala Ile Ala Cys Ala Ala Val Gly Leu Ala Gly Lys Glu
 500 505 510

AGC GAT TTG TTC AAA TTC ACG GTT AAA TAC TCC CTT ATT TTT GTA GCG 1640
 Ser Asp Leu Phe Lys Phe Thr Val Lys Tyr Ser Leu Ile Phe Val Ala
 515 520 525 530

ATC ATG GGA GTT GTG ATC AGC GCG ATT GCG TAT TTG ATC CCT GAA GTG 1688
 Ile Met Gly Val Val Ile Ser Ala Ile Ala Tyr Leu Ile Pro Glu Val
 535 540 545

GTG CCT GCG ATA AAG TAGGGCCATT TTAGATTTAG CAGGGTTTAA CCCCCAAATA A 1744
 Val Pro Ala Ile Lys
 550

ATTTTTTTTGT TT 1756

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Val Leu Glu Phe His Gln Ile Tyr Asp Pro Leu Gly Asn Ile Trp Leu
 1 5 10 15
 Ser Ala Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu
 20 25 30
 Met Val Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala
 35 40 45
 Leu Ser Ala Val Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met
 50 55 60
 Val Gly Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile
 65 70 75 80
 Ala Trp Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys
 85 90 95

GTT TTT ATC GCG GCT TTT TCT TTC GCT GGT GCG CAA TTT TTA AGC TCT	776
Val Phe Ile Ala Ala Phe Ser Phe Ala Gly Ala Gln Phe Leu Ser Ser	
230 235 240	
AAT TAT TTA GGG CCA GAA TTG CCT GGT ATT ATT TCA GCC CTT GTT TCA	824
Asn Tyr Leu Gly Pro Glu Leu Pro Gly Ile Ile Ser Ala Leu Val Ser	
245 250 255	
CTC GTT GCA ACA GCG CTC TTT TTG AAA TTT TGG CAG CCT AAA GCG ATT	872
Leu Val Ala Thr Ala Leu Phe Leu Lys Phe Trp Gln Pro Lys Ala Ile	
260 265 270	
TTT AGA AGC GAC GGC AAA GCG GCT TCG TTC ACT AAG AGT AAC CAT CAT	920
Phe Arg Ser Asp Gly Lys Ala Ala Ser Phe Thr Lys Ser Asn His His	
275 280 285 290	
ATT TGT AAG ATC TAT GTC GCT TGG TCT CCT TTT GTG ATT TTA GTT TTA	968
Ile Cys Lys Ile Tyr Val Ala Trp Ser Pro Phe Val Ile Leu Val Leu	
295 300 305	
GTG ATT GTG CTA TGG ATA CAG CCT TTT TTT AAA GCC TTG TTT GAA AAA	1016
Val Ile Val Leu Trp Ile Gln Pro Phe Phe Lys Ala Leu Phe Glu Lys	
310 315 320	
GAC GGC TTG TTA GCT TTT TCT AAT TTT TAT TTT GAA TTC AAT AAC ATC	1064
Asp Gly Leu Leu Ala Phe Ser Asn Phe Tyr Phe Glu Phe Asn Asn Ile	
325 330 335	
AGT AAC CAC ATC TTT AAA AGC CCG CCT TTT GTA GAA GCC AAT CAA AGC	1112
Ser Asn His Ile Phe Lys Ser Pro Pro Phe Val Glu Ala Asn Gln Ser	
340 345 350	
GTG AGT TTT CCG GTG GTG TTT AAA TTT CTC TTA ATC AAC ACG GTT GGC	1160
Val Ser Phe Pro Val Val Phe Lys Phe Leu Leu Ile Asn Thr Val Gly	
355 360 365 370	
ACT TCC ATT TTT TTA GCC GCT CTT GTT AGC ATG CTC GTT TTA AGG GTG	1208
Thr Ser Ile Phe Leu Ala Ala Leu Val Ser Met Leu Val Leu Arg Val	
375 380 385	
CGA GTG AGC GAT GCG CTG AGC GTC TTT GGC GAG ACT TTA AAA GAA ATG	1256
Arg Val Ser Asp Ala Leu Ser Val Phe Gly Glu Thr Leu Lys Glu Met	
390 395 400	
CGT TAC CCC ATT CTC ACC ATT GGT TTA GTC TTA AGC TTT GCC TAT GTG	1304
Arg Tyr Pro Ile Leu Thr Ile Gly Leu Val Leu Ser Phe Ala Tyr Val	
405 410 415	
TCT AAT TAC AGC GGG ATT TCT TCC ACT CTA GCC TTA GCG CTC ACG CAT	1352
Ser Asn Tyr Ser Gly Ile Ser Ser Thr Leu Ala Leu Ala Leu Thr His	
420 425 430	
ACG GGT TTG GCT TTC ACC TTT TTC TCG CCC TTG ATC GGG TGG GTA GGC	1400
Thr Gly Leu Ala Phe Thr Phe Phe Ser Pro Leu Ile Gly Trp Val Gly	
435 440 445 450	

GAA TTT CAT CAA ATT TAT GAT CCT TTG GGT AAT ATT TGG CTG AGC GCT	104
Glu Phe His Gln Ile Tyr Asp Pro Leu Gly Asn Ile Trp Leu Ser Ala	
5 10 15	
CTT GTG GCC TTA TTG CCG ATT TTA TTG TTT TTC TTA TCT TTA ATG GTT	152
Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu Met Val	
20 25 30	
TTT AAA CTC AAA GGT TAT ACA GCG GCC TTT TTG AGC GTG GCC TTA TCA	200
Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala Leu Ser	
35 40 45 50	
GCC GTT ATT GCG GTT TTA GTG TAT AAA ATG CCT GTT AGC ATG GTG GGT	248
Ala Val Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met Val Gly	
55 60 65	
TCA AGC TTC CTT TAC GGC TTT CTT TAT GGC TTA TGG CCG ATC GCT TGG	296
Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala Trp	
70 75 80	
ATC ATT ATT GCG GCG ATT TTT TTA TAC AAA CTC AGC GTT AAA TCC GGC	344
Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys Ser Gly	
85 90 95	
TAT TTT GAA ATT TTA AAA GAA AGC GTC CAG TCC ATC ACT TTA GAT CAC	392
Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu Asp His	
100 105 110	
CGC ATT TTA GTG ATT TTG ATT GGC TTT TGT TTT GGC TCG TTT TTA GAA	440
Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu Glu	
115 120 125 130	
GGG GCG ATC GGC TTT GGA GGG CCT ATT GCC ATT ACC GCA GCG ATT TTA	488
Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala Ile Leu	
135 140 145	
GTG GGC TTA GGG TTA AGC CCT TTG TAT TCT GCC GGG TTA TGT TTG ATC	536
Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys Leu Ile	
150 155 160	
GCT AAT ACC GCT CCT GTA GCT TTT GGC GCG GTG GGT ATC CCT ATA AGT	584
Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro Ile Ser	
165 170 175	
GCT ATG GCG AGC GCG GTA GGG GTG CCA GCG ATT TTA ATT TCA GCC ATG	632
Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser Ala Met	
180 185 190	
ACG GGT AAA ATC CTC TTT TTT GTG AGC TTG TTA GTG CCG TTT TTC ATT	680
Thr Gly Lys Ile Leu Phe Phe Val Ser Leu Leu Val Pro Phe Phe Ile	
195 200 205 210	
GTG TTT TTA ATG GAT GGC TTT AAA GGG ATT AAA GAA ACT TTT CCG GCC	728
Val Phe Leu Met Asp Gly Phe Lys Gly Ile Lys Glu Thr Phe Pro Ala	
215 220 225	

GTAAAATCCT TAAACGCTTC AAAATTCAAA TTCAAATCTG T 388

(2) INFORMATION FOR SEO ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:636:

Met	Ser	Ala	Val	Arg	Leu	Gly	Pro	Pro	Ile	Arg	Ser	Met	Phe	Val	Gly
1				5					10					15	
Asn	Ala	Pro	Phe	Trp	Leu	Trp	Phe	Phe	Lys	Ala	Cys	Met	Pro	Ser	Leu
			20					25					30		
Lys	Leu	Arg	Thr	Met	Asp	Ser	Phe	Phe	Asn	Lys	Met	Met	Gln	Leu	Arg
			35				40					45			
Val	Met	Ser	Glu	Ser	Asn	Arg	Gly	Leu	Ala	Cys	Glu	Glu	Thr	Ala	Pro
	50					55					60				
Ile	Met	Pro	Lys	Leu	Glu	Ile	Pro	Gln	Thr	Pro	Cys	Asn	Lys	Ala	Val
65					70					75					80
Ser	Ile	Ser	Asn	Asn	Ser	Ser	Arg	Ile	Ala	Ser	Ile	Ser	Leu	Ser	
				85					90					95	

(2) INFORMATION FOR SEO ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1703
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

TTTTAAAGAG AACTAGCACT AAGAGAATAT TTTTAAAAAG GGATTTTTTTA GTG CTA 56
Val Leu
1

```

Asp Glu Val Lys Ser Phe Phe Glu Ile His Arg Ala Glu Gly Ser Leu
 290                295                300
Ala Ser Gly Val His Leu Glu Met Thr Gly Glu Asn Val Thr Glu Cys
305                310                315                320
Ile Gly Gly Ser Gln Ala Ile Thr Glu Glu Gly Leu Ser Cys His Tyr
                325                330                335
Tyr Thr Gln Cys Asp Pro Arg Leu Asn Ala Thr Gln Ala Leu Glu Leu
                340                345                350
Ala Phe Leu Ile Ala Asp Met Leu Lys Lys Gln His Ala
 355                360                365

```

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...335
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

```

TGATAGCGAC TTTTGTGAGGC CCATGCACCC CAAAAACGGT TTTTAATTCA  ATG TCA      56
                                     Met Ser
                                     1

GCT GTC CGG CTA GGC CCG CCA ATA AGG AGC ATG TTT GTG GGT AAT GCA      104
Ala Val Arg Leu Gly Pro Pro Ile Arg Ser Met Phe Val Gly Asn Ala
      5                10                15

CCG TTT TGG CTT TGG TTT TTT AAA GCT TGC ATG CCT TCA CTC AAA TTG      152
Pro Phe Trp Leu Trp Phe Phe Lys Ala Cys Met Pro Ser Leu Lys Leu
      20                25                30

CGC ACA ATG GAT TCT TTT TTC AAT AAG ATG ATG CAA TTA AGG GTG ATG      200
Arg Thr Met Asp Ser Phe Phe Asn Lys Met Met Gln Leu Arg Val Met
      35                40                45                50

AGC GAA AGC AAT CGC GGG CTT GCA TGC GAA GAG ACC GCC CCA ATC ATG      248
Ser Glu Ser Asn Arg Gly Leu Ala Cys Glu Glu Thr Ala Pro Ile Met
                55                60                65

CCC AAG CTT GAA ATC CCA CAA ACC CCA TGC AAT AAA GCC GTA TCA ATC      296
Pro Lys Leu Glu Ile Pro Gln Thr Pro Cys Asn Lys Ala Val Ser Ile
      70                75                80

```

TTA ATC GCT GAC ATG CTC AAA AAA CAG CAC GCT TAGTTAAAAA GAGATTAATC 1165
 Leu Ile Ala Asp Met Leu Lys Lys Gln His Ala
 355 360 365

TTTTTTTAAC TCTTTTACTT TATAATTATC GTT 1198

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

Met	Phe	Lys	Val	Met	Met	Gln	Met	Ala	Ile	Val	Leu	Thr	Phe	Ala	Gly
1				5				10						15	
Ser	Ile	Pro	Ile	Val	Lys	Val	Gly	Arg	Ile	Ala	Gly	Gln	Phe	Ala	Lys
		20						25					30		
Pro	Arg	Ser	Asn	Ala	Thr	Glu	Met	Leu	Asp	Asn	Glu	Glu	Val	Leu	Ser
		35					40					45			
Tyr	Arg	Gly	Asp	Ile	Ile	Asn	Gly	Ile	Ser	Lys	Lys	Glu	Arg	Glu	Pro
	50					55					60				
Asn	Pro	Glu	Arg	Met	Leu	Lys	Ala	Tyr	His	Gln	Ser	Val	Ala	Thr	Leu
65					70					75				80	
Asn	Leu	Ile	Arg	Ala	Phe	Ala	Gln	Gly	Gly	Leu	Ala	Asp	Leu	Glu	Gln
			85					90					95		
Val	His	Arg	Phe	Asn	Leu	Asp	Phe	Val	Lys	Asn	Asn	Asp	Phe	Gly	Gln
		100					105					110			
Lys	Tyr	Gln	Gln	Ile	Ala	Asp	Arg	Ile	Thr	Gln	Ala	Leu	Gly	Phe	Met
	115					120						125			
Arg	Ala	Cys	Gly	Val	Glu	Ile	Glu	Arg	Thr	Pro	Ile	Leu	Arg	Glu	Val
	130					135					140				
Glu	Phe	Tyr	Thr	Ser	His	Glu	Ala	Leu	Leu	Leu	His	Tyr	Glu	Glu	Pro
145				150						155				160	
Leu	Val	Arg	Lys	Asp	Ser	Leu	Thr	Asn	Gln	Phe	Tyr	Asp	Cys	Ser	Ala
			165					170					175		
His	Met	Leu	Trp	Ile	Gly	Glu	Arg	Thr	Arg	Asp	Pro	Lys	Gly	Ala	His
		180					185						190		
Val	Glu	Phe	Leu	Arg	Gly	Val	Cys	Asn	Pro	Ile	Gly	Val	Lys	Ile	Gly
	195					200						205			
Pro	Asn	Ala	Ser	Val	Ser	Glu	Val	Leu	Glu	Leu	Cys	Asp	Val	Leu	Asn
	210					215					220				
Pro	Arg	Asn	Ile	Lys	Gly	Arg	Leu	Asn	Leu	Ile	Val	Arg	Met	Gly	Ser
225				230						235				240	
Lys	Met	Ile	Lys	Glu	Arg	Leu	Pro	Lys	Leu	Leu	Gln	Gly	Val	Leu	Glu
			245						250				255		
Glu	Lys	Arg	His	Ile	Leu	Trp	Ser	Ile	Asp	Pro	Met	His	Gly	Asn	Thr
		260				265						270			
Val	Lys	Thr	Ser	Leu	Gly	Val	Lys	Thr	Arg	Ala	Phe	Asp	Ser	Val	Leu
	275					280						285			

TGC GGG GTG GAG ATA GAG CGA ACG CCT ATT CTT AGG GAA GTG GAA TTT	488
Cys Gly Val Glu Ile Glu Arg Thr Pro Ile Leu Arg Glu Val Glu Phe	
135 140 145	
TAC ACC AGC CAC GAA GCG TTA CTG CTC CAT TAT GAA GAG CCG TTG GTG	536
Tyr Thr Ser His Glu Ala Leu Leu His Tyr Glu Glu Pro Leu Val	
150 155 160	
CGT AAG GAT AGT CTG ACT AAC CAG TTT TAT GAT TGC TCC GCG CAC ATG	584
Arg Lys Asp Ser Leu Thr Asn Gln Phe Tyr Asp Cys Ser Ala His Met	
165 170 175	
CTA TGG ATT GGC GAA AGG ACA AGA GAC CCT AAG GGT GCG CAT GTG GAG	632
Leu Trp Ile Gly Glu Arg Thr Arg Asp Pro Lys Gly Ala His Val Glu	
180 185 190	
TTT TTA AGG GGG GTT TGT AAC CCT ATT GGC GTG AAA ATC GGG CCT AAT	680
Phe Leu Arg Gly Val Cys Asn Pro Ile Gly Val Lys Ile Gly Pro Asn	
195 200 205 210	
GCG AGC GTG AGC GAA GTG TTA GAA TTG TGC GAT GTT TTA AAC CCG CGC	728
Ala Ser Val Ser Glu Val Leu Glu Leu Cys Asp Val Leu Asn Pro Arg	
215 220 225	
AAC ATT AAG GGG CGT TTG AAT TTG ATC GTG CGC ATG GGT TCT AAG ATG	776
Asn Ile Lys Gly Arg Leu Asn Leu Ile Val Arg Met Gly Ser Lys Met	
230 235 240	
ATT AAA GAG CGT TTG CCT AAA CTT TTA CAA GGG GTG TTG GAA GAA AAA	824
Ile Lys Glu Arg Leu Pro Lys Leu Leu Gln Gly Val Leu Glu Glu Lys	
245 250 255	
CGC CAT ATT TTA TGG AGC ATT GAT CCC ATG CAT GGC AAC ACG GTT AAA	872
Arg His Ile Leu Trp Ser Ile Asp Pro Met His Gly Asn Thr Val Lys	
260 265 270	
ACC AGC TTG GGG GTT AAA ACA AGG GCT TTT GAT AGC GTG TTA GAT GAA	920
Thr Ser Leu Gly Val Lys Thr Arg Ala Phe Asp Ser Val Leu Asp Glu	
275 280 285 290	
GTG AAA AGC TTT TTT GAA ATC CAT AGG GCT GAA GGG AGT TTG GCT TCA	968
Val Lys Ser Phe Phe Glu Ile His Arg Ala Glu Gly Ser Leu Ala Ser	
295 300 305	
GGG GTT CAT TTG GAA ATG ACA GGT GAG AAT GTT ACA GAA TGT ATC GGT	1016
Gly Val His Leu Glu Met Thr Gly Glu Asn Val Thr Glu Cys Ile Gly	
310 315 320	
GGC TCG CAA GCG ATC ACC GAA GAG GGT TTG AGC TGC CAT TAC TAC ACG	1064
Gly Ser Gln Ala Ile Thr Glu Glu Gly Leu Ser Cys His Tyr Tyr Thr	
325 330 335	
CAA TGC GAT CCA AGA TTA AAC GCC ACC CAA GCC CTA GAA CTC GCC TTC	1112
Gln Cys Asp Pro Arg Leu Asn Ala Thr Gln Ala Leu Glu Leu Ala Phe	
340 345 350	

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1145
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GCGATTGTGC GGAGTCGTTT TCTCAATTTA GCGCCAATCG GATTAGAGAC	ATG TTT	56
	Met Phe	
	1	
AAA GTA ATG ATG CAA ATG GCG ATC GTT CTC ACT TTT GCT GGC TCT ATA		104
Lys Val Met Met Gln Met Ala Ile Val Leu Thr Phe Ala Gly Ser Ile		
5 10 15		
CCG ATC GTG AAA GTG GGG CGC ATT GCC GGG CAA TTT GCC AAG CCT CGC		152
Pro Ile Val Lys Val Gly Arg Ile Ala Gly Gln Phe Ala Lys Pro Arg		
20 25 30		
TCC AAT GCG ACT GAA ATG CTG GAT AAT GAA GAA GTG TTG AGT TAC AGA		200
Ser Asn Ala Thr Glu Met Leu Asp Asn Glu Glu Val Leu Ser Tyr Arg		
35 40 45 50		
GGG GAT ATT ATC AAT GGG ATT TCC AAA AAA GAA AGA GAG CCA AAT CCT		248
Gly Asp Ile Ile Asn Gly Ile Ser Lys Lys Glu Arg Glu Pro Asn Pro		
55 60 65		
GAA AGA ATG CTT AAG GCC TAC CAT CAA AGC GTA GCG ACT TTA AAC CTT		296
Glu Arg Met Leu Lys Ala Tyr His Gln Ser Val Ala Thr Leu Asn Leu		
70 75 80		
ATC AGA GCC TTT GCT CAA GGC GGG TTA GCG GAT TTG GAG CAA GTG CAT		344
Ile Arg Ala Phe Ala Gln Gly Gly Leu Ala Asp Leu Glu Gln Val His		
85 90 95		
CGT TTC AAT TTG GAT TTT GTC AAA AAC AAC GAC TTT GGG CAA AAA TAC		392
Arg Phe Asn Leu Asp Phe Val Lys Asn Asn Asp Phe Gly Gln Lys Tyr		
100 105 110		
CAG CAA ATC GCT GAC CGG ATC ACG CAA GCT TTA GGG TTT ATG CGA GCA		440
Gln Gln Ile Ala Asp Arg Ile Thr Gln Ala Leu Gly Phe Met Arg Ala		
115 120 125 130		

```

Ile Tyr Gly Ile Ala Phe Ala Thr Lys Glu Gly Leu Lys Asp Tyr Leu
      195                200                205
Phe Gln Ile Glu Glu Ala Lys Lys Arg Asp His Arg Lys Leu Gly Val
      210                215                220
Glu Leu Gly Leu Phe Ser Phe Asp Asp Glu Ile Gly Ala Gly Leu Pro
225                230                235                240
Leu Trp Leu Pro Lys Gly Ala Arg Leu Arg Lys Arg Ile Glu Asp Leu
      245                250                255
Leu Ser Gln Ala Leu Leu Leu Arg Gly Tyr Glu Pro Val Lys Gly Pro
      260                265                270
Glu Ile Leu Lys Ser Asp Val Trp Lys Ile Ser Gly His Tyr Asp Asn
      275                280                285
Tyr Lys Glu Asn Met Tyr Phe Thr Thr Ile Asp Glu Gln Glu Tyr Gly
      290                295                300
Ile Lys Pro Met Asn Cys Val Gly His Ile Lys Val Tyr Gln Ser Ala
305                310                315                320
Leu His Ser Tyr Arg Asp Leu Pro Leu Arg Phe Tyr Glu Tyr Gly Val
      325                330                335
Val His Arg His Glu Lys Ser Gly Val Leu His Gly Leu Leu Arg Val
      340                345                350
Arg Glu Phe Thr Gln Asp Asp Ala His Ile Phe Cys Ser Phe Glu Gln
      355                360                365
Ile Gln Ser Glu Val Ser Ala Ile Leu Asp Phe Thr His Lys Ile Met
      370                375                380
Gln Ala Phe Asp Phe Ser Tyr Glu Met Glu Leu Ser Thr Arg Pro Ala
385                390                395                400
Lys Ser Ile Gly Asp Asp Lys Val Trp Glu Lys Ala Thr Asn Ala Leu
      405                410                415
Lys Glu Ala Leu Lys Glu His Arg Ile Asp Tyr Lys Ile Asp Glu Gly
      420                425                430
Gly Gly Ala Phe Tyr Gly Pro Lys Ile Asp Ile Lys Ile Thr Asp Ala
      435                440                445
Leu Lys Arg Lys Trp Gln Cys Gly Thr Ile Gln Val Asp Met Asn Leu
      450                455                460
Pro Glu Arg Phe Lys Leu Ala Phe Thr Asn Glu Tyr Asn His Ala Glu
465                470                475                480
Gln Pro Val Met Ile His Arg Ala Ile Leu Gly Ser Phe Glu Arg Phe
      485                490                495
Ile Ala Ile Leu Ser Glu His Phe Gly Gly Asn Phe Pro Phe Phe Val
      500                505                510
Ala Pro Thr Gln Ile Ala Leu Ile Pro Ile Asn Glu Glu His His Val
      515                520                525
Phe Ala Leu Lys Leu Lys Glu Ala Leu Lys Lys Arg Asp Ile Phe Val
      530                535                540
Glu Val Leu Asp Lys Asn Asp Ser Leu Asn Lys Lys Val Arg Leu Ala
545                550                555                560
Glu Lys Gln Lys Ile Pro Met Ile Leu Val Leu Gly Asn Glu Glu Val
      565                570                575
Glu Thr Glu Ile Leu Ser Ile Arg Asp Arg Glu Lys Gln Asp Gln Tyr
      580                585                590
Lys Met Pro Leu Lys Glu Phe Leu Asn Met Val Glu Ser Lys Met Gln
      595                600                605
Glu Val Ser Phe
      610

```


CAA AAA ATC CCT ATG ATT TTA GTG TTA GGG AAT GAA GAA GTG GAG ACC 1784
 Gln Lys Ile Pro Met Ile Leu Val Leu Gly Asn Glu Glu Val Glu Thr
 565 570 575

GAA ATT TTA TCC ATT AGA GAC AGA GAA AAA CAA GAT CAA TAT AAA ATG 1832
 Glu Ile Leu Ser Ile Arg Asp Arg Glu Lys Gln Asp Gln Tyr Lys Met
 580 585 590

CCC TTA AAG GAG TTT TTA AAC ATG GTT GAA TCT AAG ATG CAA GAG GTT 1880
 Pro Leu Lys Glu Phe Leu Asn Met Val Glu Ser Lys Met Gln Glu Val
 595 600 605 610

AGT TTT TGAGTAGAAA CGAAGTGTTG TTAAACGGAG ACATTAATTT TAAAGAAGTG CG 1938
 Ser Phe

T 1939

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

Met Ser Ala Glu Leu Ile Ala Val Tyr Lys Asp Glu Gln Ile Ile Asp
 1 5 10 15
 Leu Glu Ser Ala Lys Val Leu Gly Leu Ser Asp Gly Ile Lys Ala Leu
 20 25 30
 Asn Gly Thr Glu Pro Ile Tyr Phe Asp Asp Ser Pro Leu Ala Leu Glu
 35 40 45
 Val Ile Arg His Ser Cys Ala His Leu Leu Ala Gln Ser Leu Lys Ala
 50 55 60
 Leu Tyr Pro Asp Ala Lys Phe Phe Val Gly Pro Val Val Glu Glu Gly
 65 70 75 80
 Phe Tyr Tyr Asp Phe Lys Thr Ser Ser Lys Ile Ser Glu Glu Asp Leu
 85 90 95
 Pro Lys Ile Glu Ala Lys Met Lys Glu Phe Ala Lys Leu Lys Leu Ala
 100 105 110
 Ile Thr Lys Glu Thr Leu Thr Arg Glu Gln Ala Leu Glu Arg Phe Lys
 115 120 125
 Gly Asp Glu Leu Lys His Ala Val Met Ser Lys Ile Gly Gly Asp Ala
 130 135 140
 Phe Gly Val Tyr Gln Gln Gly Glu Phe Glu Asp Leu Cys Lys Gly Pro
 145 150 155 160
 His Leu Pro Asn Thr Arg Phe Leu Asn His Phe Lys Leu Thr Lys Leu
 165 170 175
 Ala Gly Ala Tyr Leu Gly Gly Asp Glu Asn Asn Glu Met Leu Ile Arg
 180 185 190

CGG CAT GAA AAA AGC GGC GTG TTG CAT GGG CTT TTA AGG GTT AGG GAA	1112
Arg His Glu Lys Ser Gly Val Leu His Gly Leu Leu Arg Val Arg Glu	
340 345 350	
TTT ACC CAA GAT GAT GCA CAT ATT TTT TGC TCT TTT GAA CAG ATC CAA	1160
Phe Thr Gln Asp Asp Ala His Ile Phe Cys Ser Phe Glu Gln Ile Gln	
355 360 365 370	
AGC GAA GTG AGC GCG ATT TTA GAT TTT ACG CAC AAA ATC ATG CAA GCG	1208
Ser Glu Val Ser Ala Ile Leu Asp Phe Thr His Lys Ile Met Gln Ala	
375 380 385	
TTT GAT TTT AGC TAT GAA ATG GAA TTA TCC ACA AGG CCG GCT AAA TCC	1256
Phe Asp Phe Ser Tyr Glu Met Glu Leu Ser Thr Arg Pro Ala Lys Ser	
390 395 400	
ATA GGC GAT GAT AAA GTT TGG GAA AAG GCC ACT AAC GCT TTA AAA GAA	1304
Ile Gly Asp Asp Lys Val Trp Glu Lys Ala Thr Asn Ala Leu Lys Glu	
405 410 415	
GCC TTA AAA GAA CAC CGC ATT GAT TAC AAG ATT GAT GAA GGG GGA GGG	1352
Ala Leu Lys Glu His Arg Ile Asp Tyr Lys Ile Asp Glu Gly Gly Gly	
420 425 430	
GCT TTC TAT GGG CCT AAG ATT GAC ATT AAA ATC ACT GAC GCT TTA AAG	1400
Ala Phe Tyr Gly Pro Lys Ile Asp Ile Lys Ile Thr Asp Ala Leu Lys	
435 440 445 450	
CGT AAA TGG CAG TGT GGC ACG ATT CAA GTG GAT ATG AAT TTG CCT GAA	1448
Arg Lys Trp Gln Cys Gly Thr Ile Gln Val Asp Met Asn Leu Pro Glu	
455 460 465	
CGC TTC AAG CTC GCT TTC ACT AAT GAG TAT AAT CAC GCT GAG CAG CCG	1496
Arg Phe Lys Leu Ala Phe Thr Asn Glu Tyr Asn His Ala Glu Gln Pro	
470 475 480	
GTG ATG ATC CAC AGA GCG ATT TTA GGC TCG TTT GAA AGG TTT ATT GCG	1544
Val Met Ile His Arg Ala Ile Leu Gly Ser Phe Glu Arg Phe Ile Ala	
485 490 495	
ATT TTG AGC GAA CAT TTT GGG GGG AAT TTC CCT TTC TTT GTC GCG CCC	1592
Ile Leu Ser Glu His Phe Phe Gly Gly Asn Phe Pro Phe Phe Val Ala Pro	
500 505 510	
ACT CAA ATC GCT CTC ATC CCT ATT AAT GAA GAG CAT CAT GTT TTT GCT	1640
Thr Gln Ile Ala Leu Ile Pro Ile Asn Glu Glu His His Val Phe Ala	
515 520 525 530	
TTG AAA TTA AAA GAG GCG CTA AAA AAG CGC GAT ATT TTT GTA GAA GTG	1688
Leu Lys Leu Lys Glu Ala Leu Lys Lys Arg Asp Ile Phe Val Glu Val	
535 540 545	
TTA GAT AAA AAC GAC AGC TTG AAT AAA AAG GTG CGA TTA GCC GAA AAG	1736
Leu Asp Lys Asn Asp Ser Leu Asn Lys Lys Val Arg Leu Ala Glu Lys	
550 555 560	

AAA GAG ACT TTA ACC AGA GAG CAA GCT TTG GAG CGT TTT AAG GGC GAT	440
Lys Glu Thr Leu Thr Arg Glu Gln Ala Leu Glu Arg Phe Lys Gly Asp	
115 120 125 130	
GAA TTA AAG CAT GCG GTG ATG AGT AAA ATC GGT GGC GAT GCC TTT GGC	488
Glu Leu Lys His Ala Val Met Ser Lys Ile Gly Gly Asp Ala Phe Gly	
135 140 145	
GTG TAT CAA CAA GGC GAG TTT GAA GAT TTG TGT AAG GGG CCG CAT CTC	536
Val Tyr Gln Gln Gly Glu Phe Glu Asp Leu Cys Lys Gly Pro His Leu	
150 155 160	
CCA AAC ACC CGT TTT TTA AAC CAT TTT AAG CTC ACT AAA CTG GCT GGG	584
Pro Asn Thr Arg Phe Leu Asn His Phe Lys Leu Thr Lys Leu Ala Gly	
165 170 175	
GCT TAT TTG GGC GGC GAT GAA AAC AAT GAA ATG CTC ATT AGA ATC TAT	632
Ala Tyr Leu Gly Gly Asp Glu Asn Asn Glu Met Leu Ile Arg Ile Tyr	
180 185 190	
GGA ATC GCT TTT GCC ACC AAA GAG GGT TTA AAA GAC TAT CTT TTC CAA	680
Gly Ile Ala Phe Ala Thr Lys Glu Gly Leu Lys Asp Tyr Leu Phe Gln	
195 200 205 210	
ATA GAA GAA GCG AAA AAA CGA GAT CAC AGA AAG CTA GGC GTG GAG CTA	728
Ile Glu Glu Ala Lys Lys Arg Asp His Arg Lys Leu Gly Val Glu Leu	
215 220 225	
GGG CTT TTT AGC TTT GAT GAT GAG ATA GGG GCG GGC TTA CCT TTA TGG	776
Gly Leu Phe Ser Phe Asp Asp Glu Ile Gly Ala Gly Leu Pro Leu Trp	
230 235 240	
CTG CCT AAA GGG GCA AGG CTT AGG AAG CGC ATT GAA GAT TTA TTG AGT	824
Leu Pro Lys Gly Ala Arg Leu Arg Lys Arg Ile Glu Asp Leu Leu Ser	
245 250 255	
CAA GCG TTA CTT TTA AGA GGC TAT GAG CCG GTT AAA GGT CCT GAG ATT	872
Gln Ala Leu Leu Leu Arg Gly Tyr Glu Pro Val Lys Gly Pro Glu Ile	
260 265 270	
TTA AAG AGC GAT GTG TGG AAA ATC AGC GGG CAT TAT GAC AAC TAT AAA	920
Leu Lys Ser Asp Val Trp Lys Ile Ser Gly His Tyr Asp Asn Tyr Lys	
275 280 285 290	
GAA AAC ATG TAT TTC ACC ACG ATT GAT GAG CAA GAA TAT GGC ATA AAG	968
Glu Asn Met Tyr Phe Thr Thr Ile Asp Glu Gln Glu Tyr Gly Ile Lys	
295 300 305	
CCT ATG AAC TGC GTG GGG CAT ATT AAA GTC TAT CAA AGC GCT TTG CAC	1016
Pro Met Asn Cys Val Gly His Ile Lys Val Tyr Gln Ser Ala Leu His	
310 315 320	
AGC TAC AGA GAT TTG CCC TTA AGG TTT TAT GAA TAC GGC GTG GTG CAT	1064
Ser Tyr Arg Asp Leu Pro Leu Arg Phe Tyr Glu Tyr Gly Val Val His	
325 330 335	

```

          370          375          380
Lys Lys Ala Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met
385          390          395

```

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1886
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

```

AAGATTGCTA AATTTTAAGG TTTGAAGAAA GGAAACATAA GTTTTAAAGA  ATG AGT      56
                                     Met Ser
                                     1

GCG GAA CTG ATT GCT GTT TAT AAA GAC GAG CAA ATA ATA GAT TTA GAG      104
Ala Glu Leu Ile Ala Val Tyr Lys Asp Glu Gln Ile Ile Asp Leu Glu
          5          10          15

AGC GCG AAA GTC TTA GGG CTG AGC GAT GGG ATT AAA GCG TTA AAC GGG      152
Ser Ala Lys Val Leu Gly Leu Ser Asp Gly Ile Lys Ala Leu Asn Gly
          20          25          30

ACA GAG CCG ATA TAT TTT GAT GAT TCG CCT TTG GCT TTA GAG GTG ATT      200
Thr Glu Pro Ile Tyr Phe Asp Asp Ser Pro Leu Ala Leu Glu Val Ile
          35          40          45          50

AGG CAT TCA TGC GCG CAT TTG CTT GCG CAA AGC TTG AAA GCC CTT TAT      248
Arg His Ser Cys Ala His Leu Leu Ala Gln Ser Leu Lys Ala Leu Tyr
          55          60          65

CCG GAC GCG AAA TTT TTT GTA GGC CCT GTG GTA GAA GAG GGG TTT TAT      296
Pro Asp Ala Lys Phe Phe Val Gly Pro Val Val Glu Glu Gly Phe Tyr
          70          75          80

TAC GAT TTC AAG ACT TCT TCA AAA ATC AGC GAA GAG GAT TTG CCT AAA      344
Tyr Asp Phe Lys Thr Ser Ser Lys Ile Ser Glu Glu Asp Leu Pro Lys
          85          90          95

ATT GAA GCG AAA ATG AAA GAG TTT GCG AAG TTG AAA CTC GCT ATC ACT      392
Ile Glu Ala Lys Met Lys Glu Phe Ala Lys Leu Lys Leu Ala Ile Thr
          100          105          110

```

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

```

Met Glu Ser Val Lys Thr Gly Lys Thr Asn Lys Val Gly Lys Asn Thr
 1           5           10           15
Glu Met Ala Asn Thr Lys Ala Asn Lys Glu Thr His Phe Lys Gln Val
          20           25           30
Ser Ala Ile Thr Asn Ile Ile Arg Ser Val Gly Gly Phe Phe Thr Lys
          35           40           45
Ile Ala Lys Arg Val Arg Gly Leu Val Lys Lys His Pro Lys Lys Ser
          50           55           60
Ser Ala Ala Leu Val Val Leu Thr His Ile Ala Cys Lys Lys Ala Lys
          65           70           75           80
Glu Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu
          85           90           95
Asn Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Ala Ser
          100          105          110
Leu Leu Leu Ala Ala Cys Ser Ala Gly Asp Thr Asp Lys Gln Ile Glu
          115          120          125
Leu Glu Gln Glu Lys Lys Glu Ala Glu Asn Ala Arg Asp Arg Ala Asn
          130          135          140
Lys Ser Gly Ile Glu Leu Glu Gln Glu Arg Gln Lys Thr Asn Lys Ser
          145          150          155          160
Gly Ile Glu Leu Ala Asn Ser Gln Ile Lys Ala Glu Gln Glu Arg Gln
          165          170          175
Lys Thr Glu Gln Glu Lys Gln Lys Ala Asn Lys Ser Ala Ile Glu Leu
          180          185          190
Glu Gln Gln Lys Gln Lys Thr Ile Asn Thr Gln Arg Asp Leu Ile Lys
          195          200          205
Glu Gln Lys Asp Phe Ile Lys Glu Thr Glu Gln Asn Cys Gln Glu Asn
          210          215          220
His Asn Gln Phe Phe Ile Lys Lys Leu Gly Ile Lys Gly Gly Ile Ala
          225          230          235          240
Ile Glu Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn
          245          250          255
Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro His
          260          265          270
Ser Gln Arg Gly Ser Lys Ala Gln Glu Phe Ile Ala Tyr Leu Gln Lys
          275          280          285
Glu Leu Glu Phe Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val
          290          295          300
Asn Phe Tyr Lys Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro Arg
          305          310          315          320
Asp Phe Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg
          325          330          335
Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Asp Leu Lys Pro Asp
          340          345          350
Pro Gln Ala His Leu Pro Thr Ser Gln Ser Leu Leu Phe Val Gln Lys
          355          360          365
Ile Phe Ala Asp Val Asn Lys Glu Ile Glu Ala Val Ala Asn Thr Glu

```

GAA CAA AAT TGC CAA GAA AAT CAT AAT CAA TTC TTT ATT AAA AAA TTA	785
Glu Gln Asn Cys Gln Glu Asn His Asn Gln Phe Phe Ile Lys Lys Leu	
220 225 230	
GGA ATT AAG GGT GGC ATT GCT ATA GAA GTA GAA GCT GAA TGC AAA ACC	833
Gly Ile Lys Gly Gly Ile Ala Ile Glu Val Glu Ala Glu Cys Lys Thr	
235 240 245	
CCT AAA CCT GCA AAA ACC AAT CAA ACC CCT ATC CAG CCA AAA CAC CTC	881
Pro Lys Pro Ala Lys Thr Asn Gln Thr Pro Ile Gln Pro Lys His Leu	
250 255 260 265	
CCA AAC TCT AAA CAA CCT CAT TCT CAA AGA GGA TCA AAA GCG CAA GAG	929
Pro Asn Ser Lys Gln Pro His Ser Gln Arg Gly Ser Lys Ala Gln Glu	
270 275 280	
TTT ATC GCT TAT TTG CAA AAA GAG CTA GAA TTT CTG CCC TAT TCG CAA	977
Phe Ile Ala Tyr Leu Gln Lys Glu Leu Glu Phe Leu Pro Tyr Ser Gln	
285 290 295	
AAA GCT ATC GCT AAA CAA GTG AAT TTC TAT AAA CCA AGT TCT ATC GCT	1025
Lys Ala Ile Ala Lys Gln Val Asn Phe Tyr Lys Pro Ser Ser Ile Ala	
300 305 310	
TAT TTA GAA CTA GAT CCT AGA GAT TTT AAG GTT ACA GAA GAA TGG CAA	1073
Tyr Leu Glu Leu Asp Pro Arg Asp Phe Lys Val Thr Glu Glu Trp Gln	
315 320 325	
AAA GAA AAT CTA AAA ATA CGC TCT AAA GCT CAA GCT AAA ATG CTT GAA	1121
Lys Glu Asn Leu Lys Ile Arg Ser Lys Ala Gln Ala Lys Met Leu Glu	
330 335 340 345	
ATG AGG GAT TTA AAA CCA GAC CCA CAA GCC CAC CTT CCA ACC TCT CAA	1169
Met Arg Asp Leu Lys Pro Asp Pro Gln Ala His Leu Pro Thr Ser Gln	
350 355 360	
AGC CTT TTG TTC GTT CAA AAA ATA TTT GCT GAT GTT AAT AAA GAA ATA	1217
Ser Leu Leu Phe Val Gln Lys Ile Phe Ala Asp Val Asn Lys Glu Ile	
365 370 375	
GAA GCA GTT GCT AAT ACT GAA AAG AAA GCA GAA AAA GCG GGT TAT GGT	1265
Glu Ala Val Ala Asn Thr Glu Lys Lys Ala Glu Lys Ala Gly Tyr Gly	
380 385 390	
TAT AGT AAA AGG ATG TAGGCATAAG AAAATAAGAA CACCATAAAA TCGTTTTTTAG C	1321
Tyr Ser Lys Arg Met	
395	
TTCTAGGAGA CATCAGTCAG TTTCTTGCC	1350

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

																Met	Glu	Ser	Val	Lys	Thr	Gly	Lys	Thr			
																1											
																				5							
AAT	AAG	GTT	GGC	AAG	AAT	ACA	GAG	ATG	GCT	AAT	ACA	AAG	GCA	AAT	AAA						161						
Asn	Lys	Val	Gly	Lys	Asn	Thr	Glu	Met	Ala	Asn	Thr	Lys	Ala	Asn	Lys												
10					15					20					25												
GAG	ACT	CAT	TTT	AAA	CAA	GTG	AGC	GCC	ATT	ACA	AAT	ATA	ATC	AGA	TCA						209						
Glu	Thr	His	Phe	Lys	Gln	Val	Ser	Ala	Ile	Thr	Asn	Ile	Ile	Arg	Ser												
				30					35					40													
GTT	GGT	GGG	TTT	TTT	ACA	AAA	ATT	GCA	AAG	AGA	GTT	AGA	GGA	CTT	GTA						257						
Val	Gly	Gly	Phe	Phe	Thr	Lys	Ile	Ala	Lys	Arg	Val	Arg	Gly	Leu	Val												
			45					50					55														
AAA	AAA	CAC	CCC	AAG	AAA	AGC	AGT	GCG	GCA	TTA	GTA	GTA	TTG	ACC	CAT						305						
Lys	Lys	His	Pro	Lys	Lys	Ser	Ser	Ala	Ala	Leu	Val	Val	Leu	Thr	His												
		60					65					70															
ATT	GCG	TGC	AAG	AAA	GCG	AAA	GAA	TTA	GAC	GAT	AAA	GTC	CAA	GAT	AAA						353						
Ile	Ala	Cys	Lys	Lys	Ala	Lys	Glu	Leu	Asp	Asp	Lys	Val	Gln	Asp	Lys												
	75					80					85																
TCC	AAA	CAA	GCT	GAA	AAA	GAA	AAT	CAA	ATC	AAT	TGG	TGG	AAA	TAT	TCA						401						
Ser	Lys	Gln	Ala	Glu	Lys	Glu	Asn	Gln	Ile	Asn	Trp	Trp	Lys	Tyr	Ser												
90					95					100					105												
GGA	TTA	ACA	ATA	GCG	GCA	AGT	TTA	TTA	TTA	GCC	GCT	TGT	AGC	GCT	GGT						449						
Gly	Leu	Thr	Ile	Ala	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Cys	Ser	Ala	Gly												
				110					115					120													
GAT	ACT	GAT	AAA	CAG	ATA	GAA	CTA	GAA	CAA	GAA	AAA	AAG	GAA	GCT	GAA						497						
Asp	Thr	Asp	Lys	Gln	Ile	Glu	Leu	Glu	Gln	Glu	Lys	Lys	Glu	Ala	Glu												
			125					130					135														
AAC	GCT	AGG	GAT	AGA	GCG	AAC	AAG	AGT	GGG	ATA	GAA	CTA	GAA	CAA	GAA						545						
Asn	Ala	Arg	Asp	Arg	Ala	Asn	Lys	Ser	Gly	Ile	Glu	Leu	Glu	Gln	Glu												
		140					145					150															
AGA	CAG	AAA	ACA	AAC	AAG	AGT	GGG	ATA	GAA	CTC	GCT	AAT	AGT	CAA	ATA						593						
Arg	Gln	Lys	Thr	Asn	Lys	Ser	Gly	Ile	Glu	Leu	Ala	Asn	Ser	Gln	Ile												
	155					160					165																
AAA	GCA	GAA	CAA	GAA	AGA	CAA	AAG	ACA	GAA	CAA	GAA	AAA	CAA	AAA	GCA						641						
Lys	Ala	Glu	Gln	Glu	Arg	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Ala												
170					175					180					185												
AAT	AAG	AGT	GCG	ATA	GAG	TTA	GAA	CAG	CAA	AAA	CAA	AAG	ACC	ATT	AAT						689						
Asn	Lys	Ser	Ala	Ile	Glu	Leu	Glu	Gln	Gln	Lys	Gln	Lys	Thr	Ile	Asn												
			190					195					200														
ACA	CAA	AGA	GAT	TTG	ATT	AAA	GAA	CAG	AAA	GAT	TTC	ATT	AAA	GAA	ACA						737						
Thr	Gln	Arg	Asp	Leu	Ile	Lys	Glu	Gln	Lys	Asp	Phe	Ile	Lys	Glu	Thr												
			205					210					215														

```

Gln Asn Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile
65              70              75              80
Thr Ala Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile
85              90              95
Gln Ser Ile Lys Pro Phe Leu Lys Gly Val Lys Thr Leu Ile Leu Ser
100            105            110
Asn Gly Ser Leu Phe Tyr Glu Pro Lys Val Gln Gln Ala Leu Lys Glu
115            120            125
Phe Asp Ile Val Lys Phe Ser Leu Asp Ala Ile Asp Leu Lys Ala Phe
130            135            140
Glu Arg Val Asp Lys Pro Tyr Ser Lys Asp Ile Asn Lys Ile Leu Glu
145            150            155            160
Gly Ile Leu Arg Phe Ser Gln Ile Tyr Gln Gly Gln Leu Val Ala Glu
165            170            175
Val Leu Leu Ile Lys Gly Val Asn Asp Ser Ala Asn Asn Leu Lys Leu
180            185            190
Ile Ala Ala Phe Leu Lys Gln Ile Asn Ile Ala Arg Val Asp Leu Ser
195            200            205
Thr Ile Asp Arg Pro Ser Ser Phe Lys Ala Pro Lys Leu Ser Glu Asp
210            215            220
Glu Leu Leu Lys Cys Ser Leu Phe Phe Glu Gly Leu Cys Val Ser Leu
225            230            235            240
Pro Lys Arg Ser Ile Thr Gln Ala Lys Lys Leu Ile Ser Cys Gly Ile
245            250            255
Asp Glu Leu Leu Ala Leu Ile Ser Arg Arg Pro Leu Ser Ala Glu Glu
260            265            270
Ala Pro Leu Ile Leu Asp Ser Asn Ala Phe Lys His Leu Glu Thr Leu
275            280            285
Leu Asn His Lys Gln Ile Thr Ile Lys Lys Val Gly Ser Leu Glu Phe
290            295            300
Tyr Cys Ala Phe
305

```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 87...1280
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

```

ATCAATCTAA CTTGAGTGGA TTTTCGTAT TAGTTTCCAT GATATAATTT TGAAAAGTAA      60
GATTGTTTTT TAAAAAAGG TTGGTA ATG GAA TCA GTA AAA ACA GGA AAA ACA      113

```



```

GCC TTT TTA AAA CAA ATC AAT ATA GCC AGA GTG GAT TTA AGC ACC ATA      680
Ala Phe Leu Lys Gln Ile Asn Ile Ala Arg Val Asp Leu Ser Thr Ile
195                               200                               205                               210

GAC AGA CCC TCA AGC TTT AAA GCC CCT AAA TTA AGC GAA GAT GAA TTG      728
Asp Arg Pro Ser Ser Phe Lys Ala Pro Lys Leu Ser Glu Asp Glu Leu
215                               220                               225

TTA AAA TGC TCT TTA TTT TTT GAA GGG CTT TGC GTG AGT TTG CCT AAA      776
Leu Lys Cys Ser Leu Phe Phe Glu Gly Leu Cys Val Ser Leu Pro Lys
230                               235                               240

CGA TCC ATT ACT CAA GCT AAA AAA TTG ATT TCT TGC GGT ATA GAC GAA      824
Arg Ser Ile Thr Gln Ala Lys Lys Leu Ile Ser Cys Gly Ile Asp Glu
245                               250                               255

TTG CTC GCT TTA ATT TCC AGG CGC CCT TTA AGC GCA GAA GAA GCC CCC      872
Leu Leu Ala Leu Ile Ser Arg Arg Pro Leu Ser Ala Glu Glu Ala Pro
260                               265                               270

CTA ATT CTA GAT TCT AAC GCT TTT AAG CAT TTA GAA ACT TTG TTA AAC      920
Leu Ile Leu Asp Ser Asn Ala Phe Lys His Leu Glu Thr Leu Leu Asn
275                               280                               285                               290

CAT AAG CAA ATT ACG ATT AAA AAA GTC GGC TCT TTG GAG TTT TAT TGC      968
His Lys Gln Ile Thr Ile Lys Lys Val Gly Ser Leu Glu Phe Tyr Cys
295                               300                               305

GCG TTT TAACCTCCAT TTGTAAGTTT TACCTTACTT TAGGGATAGC TTAAGCTTTT AA 1026
Ala Phe

A                                                                 1027

```

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

```

Met Ala Lys Glu Asn Pro Pro Ile Val Phe Gly Pro Val Leu Ser Arg
 1             5             10             15
Arg Phe Gly Lys Ser Leu Gly Val Asp Leu Ser Pro Ser Lys Lys Gln
20             25             30
Cys Asn Tyr Asn Cys Ile Tyr Cys Glu Leu Gly Lys Ala Lys Pro Ile
35             40             45
Glu Arg Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile
50             55             60

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GGCGCATGAA TGCATTAAAT GTAAAGAACG CGTGTTTTTA GAGGAAGATA	ATG GCT	56
	Met Ala	
	1	
AAA GAA AAT CCG CCT ATC GTT TTT GGG CCT GTT TTA TCC AGG CGT TTT		104
Lys Glu Asn Pro Pro Ile Val Phe Gly Pro Val Leu Ser Arg Arg Phe		
5 10 15		
GGG AAG TCT TTG GGC GTG GAT CTA TCG CCC TCT AAA AAA CAA TGC AAT		152
Gly Lys Ser Leu Gly Val Asp Leu Ser Pro Ser Lys Lys Gln Cys Asn		
20 25 30		
TAC AAT TGC ATT TAT TGC GAG TTG GGT AAA GCC AAG CCC ATT GAA CGC		200
Tyr Asn Cys Ile Tyr Cys Glu Leu Gly Lys Ala Lys Pro Ile Glu Arg		
35 40 45 50		
ATG GAA GAA GTG ATC AAA GTG GAA ACC TTG ATT AAC GCC ATT CAA AAC		248
Met Glu Glu Val Ile Lys Val Glu Thr Leu Ile Asn Ala Ile Gln Asn		
55 60 65		
GCC CTA AAC AAC CTC ACC ACC CCC ATT GAT GTT TTA ACC ATT ACC GCT		296
Ala Leu Asn Asn Leu Thr Thr Pro Ile Asp Val Leu Thr Ile Thr Ala		
70 75 80		
AAT GGC GAA CCC ACG CTA TAC CCT CAT TTA TTA GAG CTT ATC CAA AGC		344
Asn Gly Glu Pro Thr Leu Tyr Pro His Leu Leu Glu Leu Ile Gln Ser		
85 90 95		
ATC AAG CCT TTT TTA AAG GGC GTT AAA ACT TTG ATT TTA AGC AAT GGC		392
Ile Lys Pro Phe Leu Lys Gly Val Lys Thr Leu Ile Leu Ser Asn Gly		
100 105 110		
TCG CTC TTT TAT GAG CCA AAA GTC CAG CAA GCC TTA AAG GAA TTT GAC		440
Ser Leu Phe Tyr Glu Pro Lys Val Gln Gln Ala Leu Lys Glu Phe Asp		
115 120 125 130		
ATC GTT AAA TTT TCT TTA GAC GCT ATT GAT TTG AAA GCC TTT GAA AGA		488
Ile Val Lys Phe Ser Leu Asp Ala Ile Asp Leu Lys Ala Phe Glu Arg		
135 140 145		
GTG GAT AAA CCC TAT TCT AAA GAC ATT AAT AAG ATT TTA GAG GGG ATT		536
Val Asp Lys Pro Tyr Ser Lys Asp Ile Asn Lys Ile Leu Glu Gly Ile		
150 155 160		
TTG CGC TTT TCT CAA ATT TAT CAA GGG CAA TTG GTG GCT GAA GTG TTG		584
Leu Arg Phe Ser Gln Ile Tyr Gln Gly Gln Leu Val Ala Glu Val Leu		
165 170 175		
TTA ATT AAG GGC GTG AAT GAT AGC GCG AAC AAC TTA AAA CTC ATC GCT		632
Leu Ile Lys Gly Val Asn Asp Ser Ala Asn Asn Leu Lys Leu Ile Ala		
180 185 190		

	80	85	90	
AAG GAG TGG GTG AAA ATA GAA TCC CAT TTT GAG GTA AAA TCC CAA AAG				579
Lys Glu Trp Val Lys Ile Glu Ser His Phe Glu Val Lys Ser Gln Lys				
	95	100	105	
TAT AAC GCT TAAAGTGGCT TAAAAAAGG CTTTATTGGT GGTTTAAATC TTTGATTTT				637
Tyr Asn Ala				
	110			
AGATCGGAT				646

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Met	Ala	Lys	Arg	Val	Pro	Asn	Met	Glu	Leu	Phe	Val	Phe	Cys	Glu	Asp
1				5					10					15	
Leu	Glu	Phe	Thr	Gln	Asn	Leu	Asp	Leu	Gly	Tyr	Pro	Phe	Met	Asp	Met
			20					25					30		
Thr	Thr	Arg	Asp	Lys	Glu	Glu	Glu	Ala	Tyr	Trp	Asp	Met	Leu	Leu	Met
		35				40						45			
Gln	Ser	Cys	Gln	His	Gly	Ile	Ile	Ala	Asn	Ser	Thr	Tyr	Ser	Trp	Trp
	50					55					60				
Ala	Ala	Tyr	Leu	Ile	Glu	Asn	Pro	Glu	Lys	Ile	Ile	Ile	Gly	Pro	Lys
65					70				75					80	
His	Trp	Leu	Phe	Gly	His	Glu	Asn	Ile	Leu	Cys	Lys	Glu	Trp	Val	Lys
			85					90					95		
Ile	Glu	Ser	His	Phe	Glu	Val	Lys	Ser	Gln	Lys	Tyr	Asn	Ala		
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...974
- (D) OTHER INFORMATION:

```

Gly Ser Ser Thr Thr Gly Ile Ala Ala Asn Leu Leu Lys Arg Glu Phe
225                               230                               235                               240
Ile Gly Ile Glu Lys Glu Ser Glu Phe Ile Lys Ile Ser Met Asp Arg
                               245                               250                               255
Lys Ile Glu Leu Asp Ala Arg Tyr Lys Glu Ile Arg Ser Lys Ile Lys
                               260                               265                               270
Asp Leu Asn His Gln
                               275

```

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 259...588
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

```

CTTGACTTAT TTTTGTGGCT ATTTCCAAGA TCCACGATAC TTTGATGCTA TATCCCCTTT      60
AATCAAGCAA ACCTTCACTC TACCCCCCCC CCCCCCGAAA ATAATAAGAA TAATAATAAA      120
AAAGAGGAAG AATATCAGTG CAAGCTTTCT TTGATTTTAG CCGCTAAAAA CAGCGTGTTT      180
GTGCATATAA GAAGAGGGGA TTATGTGGGG ATTGGCTGTC AGCTTGGTAT TGACTATCAA      240
AAAAAGGCGC TTGAGTAT ATG GCA AAG CGC GTG CCA AAC ATG GAG CTT TTT      291
                Met Ala Lys Arg Val Pro Asn Met Glu Leu Phe
                  1             5             10

GTG TTT TGC GAA GAC TTA GAA TTC ACG CAA AAT CTT GAT CTT GGC TAC      339
Val Phe Cys Glu Asp Leu Glu Phe Thr Gln Asn Leu Asp Leu Gly Tyr
              15             20             25

CCT TTT ATG GAC ATG ACC ACT AGG GAT AAA GAA GAA GAG GCG TAT TGG      387
Pro Phe Met Asp Met Thr Thr Arg Asp Lys Glu Glu Ala Tyr Trp
              30             35             40

GAC ATG CTG CTC ATG CAA TCT TGT CAG CAT GGC ATT ATC GCT AAT AGC      435
Asp Met Leu Leu Met Gln Ser Cys Gln His Gly Ile Ile Ala Asn Ser
              45             50             55

ACT TAT AGC TGG TGG GCG GCC TAT TTG ATA GAA AAT CCA GAA AAA ATC      483
Thr Tyr Ser Trp Trp Ala Ala Tyr Leu Ile Glu Asn Pro Glu Lys Ile
              60             65             70             75

ATT ATT GGC CCC AAA CAC TGG CTT TTT GGG CAT GAG AAT ATC CTT TGT      531
Ile Ile Gly Pro Lys His Trp Leu Phe Gly His Glu Asn Ile Leu Cys

```

ATA GAA AAA GAA AGC GAG TTT ATC AAA ATA TCC ATG GAT AGA AAA ATA 824
 Ile Glu Lys Glu Ser Glu Phe Ile Lys Ile Ser Met Asp Arg Lys Ile
 245 250 255

 GAA TTA GAC GCT CGC TAT AAA GAA ATC CGA TCT AAA ATC AAA GAT TTA 872
 Glu Leu Asp Ala Arg Tyr Lys Glu Ile Arg Ser Lys Ile Lys Asp Leu
 260 265 270

 AAC CAC CAA TAAAGCCTTT TTTTAAGCCA CTTTAAGCGT TATACTTTTG GGATTTTAC 930
 Asn His Gln
 275

 CTCA 934

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

Met Val Ile Ala His Ser Asn Glu Ile Ala Arg Pro Ile Phe Lys Ser
 1 5 10 15
 Gln Asp Gln Leu Phe Thr Leu Tyr Gln Gly Asp Cys Asn Glu Val Leu
 20 25 30
 Pro Gln Phe Glu Asn Gln Phe Asp Leu Ile Phe Ala Asp Pro Pro Tyr
 35 40 45
 Phe Leu Ser Asn Asp Gly Leu Ser Ile Gln Ser Gly Lys Ile Val Ser
 50 55 60
 Val Asn Lys Gly Asp Trp Asp Lys Glu Asp Gly Ile Asn Gly Ile Asp
 65 70 75 80
 Glu Phe Asn Tyr Gln Trp Ile Asn Asn Ala Lys Lys Ala Leu Lys Asp
 85 90 95
 Thr Gly Ser Leu Ile Ser Gly Thr Tyr His Asn Ile Phe Ser Leu
 100 105 110
 Gly Cys Val Leu Gln Lys Leu Asp Phe Lys Ile Leu Asn Leu Ile Thr
 115 120 125
 Trp Gln Lys Thr Asn Pro Pro Pro Asn Phe Ser Cys Arg Tyr Leu Thr
 130 135 140
 His Ser Ala Glu Gln Ile Ile Trp Ala Arg Lys Ser Arg Lys His Lys
 145 150 155 160
 His Val Phe Asn Tyr Glu Val Leu Lys Lys Ile Asn Asn Asp Lys Gln
 165 170 175
 Met Arg Asp Val Trp Ser Phe Pro Ala Ile Ala Pro Trp Glu Lys Val
 180 185 190
 Asn Gly Lys His Pro Thr Gln Lys Pro Leu Ala Leu Leu Val Arg Leu
 195 200 205
 Leu Leu Met Ala Ser Asp Glu Asn Ser Leu Ile Gly Asp Pro Phe Ser
 210 215 220

Gln	Leu	Phe	Thr	Leu	Tyr	Gln	Gly	Asp	Cys	Asn	Glu	Val	Leu	Pro	Gln	
20						25					30					
TTT	GAA	AAC	CAG	TTT	GAT	TTG	ATT	TTT	GCT	GAT	CCG	CCT	TAT	TTC	CTC	200
Phe	Glu	Asn	Gln	Phe	Asp	Leu	Ile	Phe	Ala	Asp	Pro	Pro	Tyr	Phe	Leu	
35					40					45					50	
TCT	AAT	GAC	GGC	TTA	AGC	ATA	CAG	AGC	GGT	AAA	ATC	GTG	AGC	GTC	AAT	248
Ser	Asn	Asp	Gly	Leu	Ser	Ile	Gln	Ser	Gly	Lys	Ile	Val	Ser	Val	Asn	
				55					60					65		
AAA	GGC	GAT	TGG	GAT	AAA	GAA	GAT	GGG	ATT	AAT	GGT	ATT	GAT	GAG	TTT	296
Lys	Gly	Asp	Trp	Asp	Lys	Glu	Asp	Gly	Ile	Asn	Gly	Ile	Asp	Glu	Phe	
			70					75					80			
AAT	TAC	CAG	TGG	ATA	AAC	AAC	GCT	AAA	AAG	GCT	TTA	AAA	GAC	ACA	GGA	344
Asn	Tyr	Gln	Trp	Ile	Asn	Asn	Ala	Lys	Lys	Ala	Leu	Lys	Asp	Thr	Gly	
		85					90					95				
AGC	CTT	TTA	ATC	AGC	GGG	ACT	TAC	CAC	AAC	ATC	TTT	TCT	TTG	GGG	TGT	392
Ser	Leu	Leu	Ile	Ser	Gly	Thr	Tyr	His	Asn	Ile	Phe	Ser	Leu	Gly	Cys	
	100					105					110					
GTT	TTA	CAA	AAA	TTG	GAT	TTT	AAG	ATT	TTA	AAC	CTC	ATC	ACC	TGG	CAA	440
Val	Leu	Gln	Lys	Leu	Asp	Phe	Lys	Ile	Leu	Asn	Leu	Ile	Thr	Trp	Gln	
115					120					125					130	
AAA	ACC	AAC	CCT	CCT	CCC	AAT	TTC	AGC	TGC	CGT	TAT	TTG	ACG	CAT	TCA	488
Lys	Thr	Asn	Pro	Pro	Pro	Asn	Phe	Ser	Cys	Arg	Tyr	Leu	Thr	His	Ser	
			135						140					145		
GCT	GAG	CAA	ATC	ATT	TGG	GCG	AGA	AAA	AGC	CGC	AAA	CAC	AAG	CAT	GTT	536
Ala	Glu	Gln	Ile	Ile	Trp	Ala	Arg	Lys	Ser	Arg	Lys	His	Lys	His	Val	
			150					155					160			
TTT	AAC	TAT	GAG	GTT	TTA	AAA	AAG	ATC	AAT	AAC	GAC	AAG	CAA	ATG	CGC	584
Phe	Asn	Tyr	Glu	Val	Leu	Lys	Lys	Ile	Asn	Asn	Asp	Lys	Gln	Met	Arg	
		165					170					175				
GAT	GTG	TGG	AGC	TTC	CCA	GCG	ATC	GCT	CCT	TGG	GAA	AAA	GTT	AAT	GGC	632
Asp	Val	Trp	Ser	Phe	Pro	Ala	Ile	Ala	Pro	Trp	Glu	Lys	Val	Asn	Gly	
	180					185					190					
AAG	CAC	CCC	ACT	CAA	AAA	CCC	CTC	GCT	TTA	TTA	GTG	CGC	TTG	CTT	TTA	680
Lys	His	Pro	Thr	Gln	Lys	Pro	Leu	Ala	Leu	Leu	Val	Arg	Leu	Leu	Leu	
195					200					205					210	
ATG	GCG	AGC	GAT	GAA	AAT	TCT	CTC	ATT	GGC	GAT	CCT	TTT	AGC	GGG	AGC	728
Met	Ala	Ser	Asp	Glu	Asn	Ser	Leu	Ile	Gly	Asp	Pro	Phe	Ser	Gly	Ser	
				215					220					225		
TCT	ACC	ACA	GGC	ATT	GCG	GCT	AAT	CTT	TTG	AAG	AGG	GAA	TTT	ATT	GGC	776
Ser	Thr	Thr	Gly	Ile	Ala	Ala	Asn	Leu	Leu	Lys	Arg	Glu	Phe	Ile	Gly	
			230					235					240			

370		375		380
Lys Glu Phe Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe				
385		390		395
Arg Ile Lys Arg Tyr Leu Ser Lys Tyr Thr Ile Asn Pro Ala Ile Ala				400
	405		410	
His Gly Ile Ser Glu Tyr Val Gly Ser Val Glu Val Gly Lys Val Ala				415
	420		425	
Asp Leu Val Leu Trp Ser Pro Ala Phe Phe Gly Val Lys Pro Asn Met				430
	435		440	
Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn				445
	450		455	
Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala				460
465		470		475
His His Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln				480
	485		490	
Ala Ala Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln				495
	500		505	
Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln				510
	515		520	
Phe Asn Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His				525
	530		535	
Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val				540
545		550		555
Ser Leu Ala Gln Leu Phe Ser Ile Phe				560
	565			

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...881
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GAGATCTACA ATTTGAGCAA TGTAATGAT TTTATATCAA AGGCACAAAA	ATG GTA	56
	Met Val	
	1	
ATC GCG CAT TCT AAT GAA ATC GCA CGC CCC ATT TTT AAA AGC CAA GAC		104
Ile Ala His Ser Asn Glu Ile Ala Arg Pro Ile Phe Lys Ser Gln Asp		
5	10	15
CAG CTT TTC ACT CTT TAT CAA GGG GAT TGT AAT GAG GTT TTG CCC CAA		152

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

```

Met Lys Lys Ile Ser Arg Lys Glu Tyr Val Ser Met Tyr Gly Pro Thr
 1           5           10           15
Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Ile Ala Glu Val
      20           25           30
Glu His Asp Tyr Thr Ile Tyr Gly Glu Glu Leu Lys Phe Gly Gly Gly
      35           40           45
Lys Thr Leu Arg Glu Gly Met Ser Gln Ser Asn Asn Pro Ser Lys Glu
      50           55           60
Glu Leu Asp Leu Ile Ile Thr Asn Ala Leu Ile Val Asp Tyr Thr Gly
65           70           75           80
Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile
      85           90           95
Gly Lys Gly Gly Asn Lys Asp Met Gln Asp Gly Val Lys Asn Asn Leu
      100           105           110
Ser Val Gly Pro Ala Thr Glu Ala Leu Ala Gly Glu Gly Leu Ile Val
      115           120           125
Thr Ala Gly Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln
      130           135           140
Ile Pro Thr Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly
145           150           155           160
Thr Gly Pro Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg
      165           170           175
Arg Asn Leu Lys Trp Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn
      180           185           190
Leu Gly Phe Leu Ala Lys Gly Asn Ala Ser Asn Asp Ala Ser Leu Ala
      195           200           205
Asp Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp
      210           215           220
Gly Thr Thr Pro Ser Ala Ile Asn His Ala Leu Asp Val Ala Asp Lys
225           230           235           240
Tyr Asp Val Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly
      245           250           255
Cys Val Glu Asp Thr Met Ala Ala Ile Ala Gly Arg Thr Met His Thr
      260           265           270
Phe His Thr Glu Gly Ala Gly Gly His Ala Pro Asp Ile Ile Lys
      275           280           285
Val Ala Gly Glu His Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile
      290           295           300
Pro Phe Thr Val Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val
305           310           315           320
Cys His His Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp
      325           330           335
Ser Arg Ile Arg Pro Gln Thr Ile Ala Ala Glu Asp Thr Leu His Asp
      340           345           350
Met Gly Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg
      355           360           365
Val Gly Glu Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys

```


TTT GGC CGC TTG AAA GAA GAA AAA GGC GAT AAC GAC AAC TTC AGG ATC	1256
Phe Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe Arg Ile	
390 395 400	
AAA CGC TAC TTG TCT AAA TAC ACC ATT AAC CCA GCG ATC GCT CAT GGG	1304
Lys Arg Tyr Leu Ser Lys Tyr Thr Ile Asn Pro Ala Ile Ala His Gly	
405 410 415	
ATT AGC GAG TAT GTA GGT TCT GTA GAA GTG GGC AAA GTG GCT GAC TTG	1352
Ile Ser Glu Tyr Val Gly Ser Val Glu Val Gly Lys Val Ala Asp Leu	
420 425 430	
GTA TTG TGG AGT CCC GCA TTC TTT GGC GTA AAA CCC AAC ATG ATC ATC	1400
Val Leu Trp Ser Pro Ala Phe Phe Gly Val Lys Pro Asn Met Ile Ile	
435 440 445 450	
AAA GGC GGG TTC ATT GCG TTG AGT CAA ATG GGT GAC GCG AAC GCT TCT	1448
Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn Ala Ser	
455 460 465	
ATC CCT ACC CCA CAA CCA GTT TAT TAC AGA GAA ATG TTC GCT CAT CAT	1496
Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Ala His His	
470 475 480	
GGT AAA GCC AAA TAC GAT GCA AAC ATC ACT TTT GTG TCT CAA GCG GCT	1544
Gly Lys Ala Lys Tyr Asp Ala Asn Ile Thr Phe Val Ser Gln Ala Ala	
485 490 495	
TAT GAC AAA GGC ATT AAA GAA GAA TTA GGG CTT GAA AGA CAA GTG TTG	1592
Tyr Asp Lys Gly Ile Lys Glu Glu Leu Gly Leu Glu Arg Gln Val Leu	
500 505 510	
CCG GTA AAA AAT TGC AGA AAC ATC ACT AAA AAA GAC ATG CAA TTC AAC	1640
Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Met Gln Phe Asn	
515 520 525 530	
GAC ACT ACC GCT CAC ATT GAA GTC AAT CCT GAA ACT TAC CAT GTG TTC	1688
Asp Thr Thr Ala His Ile Glu Val Asn Pro Glu Thr Tyr His Val Phe	
535 540 545	
GTG GAT GGC AAA GAA GTA ACT TCT AAA CCA GCC AAT AAA GTG AGC TTG	1736
Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys Val Ser Leu	
550 555 560	
GCG CAA CTC TTT AGC ATT TTC TAGGATTTTT TAGGAGCAAC GCTCCTTAAA TCCT	1791
Ala Gln Leu Phe Ser Ile Phe	
565	
TAGTTTTTAG CTCTCTGATT TTTT	1815

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569 amino acids

(B) TYPE: amino acid

CCT GCT GAT GGC ACT AAT GCG ACT ACT ATC ACT CCA GGC AGA AGA AAT	584
Pro Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg Arg Asn	
165 170 175	
TTA AAA TGG ATG CTC AGA GCG GCT GAA GAA TAT TCT ATG AAC TTA GGT	632
Leu Lys Trp Met Leu Arg Ala Glu Glu Tyr Ser Met Asn Leu Gly	
180 185 190	
TTC TTG GCT AAA GGT AAC GCT TCT AAC GAC GCG AGC TTA GCC GAT CAA	680
Phe Leu Ala Lys Gly Asn Ala Ser Asn Asp Ala Ser Leu Ala Asp Gln	
195 200 205 210	
ATT GAA GCT GGT GCG ATT GGC TTT AAA ATC CAC GAA GAC TGG GGC ACC	728
Ile Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp Gly Thr	
215 220 225	
ACT CCT TCT GCA ATC AAT CAT GCG TTA GAT GTT GCA GAC AAA TAC GAT	776
Thr Pro Ser Ala Ile Asn His Ala Leu Asp Val Ala Asp Lys Tyr Asp	
230 235 240	
GTG CAA GTC GCT ATC CAC ACA GAC ACT TTG AAT GAA GCC GGT TGC GTG	824
Val Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly Cys Val	
245 250 255	
GAA GAC ACT ATG GCA GCT ATT GCC GGA CGC ACT ATG CAC ACT TTC CAC	872
Glu Asp Thr Met Ala Ala Ile Ala Gly Arg Thr Met His Thr Phe His	
260 265 270	
ACT GAA GGT GCT GGC GGC GGA CAC GCT CCT GAT ATT ATT AAA GTA GCT	920
Thr Glu Gly Ala Gly Gly Gly His Ala Pro Asp Ile Ile Lys Val Ala	
275 280 285 290	
GGT GAA CAC AAC ATT CTT CCC GCT TCC ACT AAC CCC ACT ATC CCT TTC	968
Gly Glu His Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile Pro Phe	
295 300 305	
ACT GTG AAT ACA GAA GCA GAA CAC ATG GAC ATG CTT ATG GTG TGC CAC	1016
Thr Val Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val Cys His	
310 315 320	
CAC TTG GAT AAA AGC ATT AAA GAA GAT GTT CAG TTC GCT GAT TCA AGG	1064
His Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp Ser Arg	
325 330 335	
ATC CGC CCT CAA ACC ATT GCG GCT GAA GAC ACT TTG CAT GAC ATG GGG	1112
Ile Arg Pro Gln Thr Ile Ala Ala Glu Asp Thr Leu His Asp Met Gly	
340 345 350	
ATT TTC TCA ATC ACC AGC TCT GAC TCT CAA GCT ATG GGT CGT GTG GGT	1160
Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Val Gly	
355 360 365 370	
GAA GTT ATC ACT AGA ACT TGG CAA ACA GCT GAC AAA AAC AAA AAA GAA	1208
Glu Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys Glu	
375 380 385	

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...1757

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

ATGGCGCTAA AAGCGATGAC AACTATGTAA AAACAATTAA GGAGTAAGAA	ATG AAA	56
	Met Lys	
	1	
AAG ATT AGC AGA AAA GAA TAT GTT TCT ATG TAT GGC CCT ACT ACA GGC		104
Lys Ile Ser Arg Lys Glu Tyr Val Ser Met Tyr Gly Pro Thr Thr Gly		
5 10 15		
GAT AAA GTG AGA TTG GGC GAT ACA GAC TTG ATC GCT GAA GTA GAA CAT		152
Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Ile Ala Glu Val Glu His		
20 25 30		
GAC TAC ACC ATT TAT GGC GAA GAG CTT AAA TTC GGT GGC GGT AAA ACC		200
Asp Tyr Thr Ile Tyr Gly Glu Glu Leu Lys Phe Gly Gly Gly Lys Thr		
35 40 45 50		
CTG AGA GAA GGC ATG AGC CAA TCC AAC AAC CCT AGC AAA GAA GAA TTG		248
Leu Arg Glu Gly Met Ser Gln Ser Asn Asn Pro Ser Lys Glu Glu Leu		
55 60 65		
GAT CTA ATC ATC ACT AAC GCT TTA ATC GTG GAT TAC ACC GGT ATT TAT		296
Asp Leu Ile Ile Thr Asn Ala Leu Ile Val Asp Tyr Thr Gly Ile Tyr		
70 75 80		
AAA GCG GAT ATT GGT ATT AAA GAT GGC AAA ATC GCT GGC ATT GGT AAA		344
Lys Ala Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile Gly Lys		
85 90 95		
GGC GGT AAC AAA GAC ATG CAA GAT GGC GTT AAA AAC AAT CTT AGC GTA		392
Gly Gly Asn Lys Asp Met Gln Asp Gly Val Lys Asn Asn Leu Ser Val		
100 105 110		
GGT CCT GCT ACT GAA GCC TTA GCC GGT GAA GGT TTG ATC GTA ACT GCT		440
Gly Pro Ala Thr Glu Ala Leu Ala Gly Glu Gly Leu Ile Val Thr Ala		
115 120 125 130		
GGT GGT ATT GAC ACA CAC ATC CAC TTC ATT TCA CCC CAA CAA ATC CCT		488
Gly Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln Ile Pro		
135 140 145		
ACA GCT TTT GCA AGC GGT GTA ACA ACC ATG ATT GGT GGC GGA ACT GGT		536
Thr Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly Thr Gly		
150 155 160		

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

```

Met Asn Thr Tyr Ala Gln Glu Ser Lys Leu Arg Leu Lys Thr Lys Ile
 1             5             10             15
Gly Ala Asp Gly Arg Cys Val Ile Glu Asp Asn Phe Phe Thr Pro Pro
      20             25             30
Phe Lys Leu Met Ala Pro Phe Tyr Pro Lys Asp Asp Leu Ala Glu Ile
      35             40             45
Met Leu Leu Ala Val Ser Pro Gly Met Met Arg Gly Asp Ala Gln Asp
 50             55             60
Val Gln Leu Asn Ile Gly Pro Asn Cys Lys Leu Arg Ile Thr Ser Gln
 65             70             75             80
Ser Phe Glu Lys Ile His Asn Thr Glu Asp Gly Phe Ala Ser Arg Asp
      85             90             95
Met His Ile Val Val Gly Glu Asn Ala Phe Leu Asp Phe Ala Pro Phe
      100            105            110
Pro Leu Ile Pro Phe Glu Asn Ala His Phe Lys Gly Asn Thr Thr Ile
      115            120            125
Ser Leu Arg Ser Ser Ser Gln Leu Leu Tyr Ser Glu Ile Ile Val Ala
 130            135            140
Gly Arg Val Ala Arg Asn Glu Leu Phe Lys Phe Asn Arg Leu His Thr
 145            150            155            160
Lys Ile Ser Ile Leu Gln Asp Glu Lys Pro Ile Tyr Tyr Asp Asn Thr
      165            170            175
Ile Leu Asp Pro Lys Thr Thr Asp Leu Asn Asn Met Cys Met Phe Asp
      180            185            190
Gly Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn Cys Pro Ile Glu
 195            200            205
Leu Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu Gly Val Asp Gly
 210            215            220
Ala Val Ser Glu Thr Ala Ser Ser His Leu Cys Val Lys Ala Leu Ala
 225            230            235            240
Lys Gly Ser Glu Pro Leu Leu His Leu Arg Glu Lys Ile Ala Arg Leu
      245            250            255
Val Thr Gln Thr Thr Gln Lys Val
      260            265

```

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50	55	60	65	
CAA TTA AAC ATC GGT CCA AAT TGC AAG TTA AGG ATC ACT TCG CAA TCC				300
Gln Leu Asn Ile Gly Pro Asn Cys Lys Leu Arg Ile Thr Ser Gln Ser				
70		75	80	
TTT GAA AAA ATC CAT AAC ACT GAA GAT GGG TTT GCC AGC AGA GAC ATG				348
Phe Glu Lys Ile His Asn Thr Glu Asp Gly Phe Ala Ser Arg Asp Met				
85		90	95	
CAT ATT GTT GTG GGG GAA AAC GCT TTT TTA GAT TTT GCG CCT TTC CCG				396
His Ile Val Val Gly Glu Asn Ala Phe Leu Asp Phe Ala Pro Phe Pro				
100		105	110	
TTA ATC CCC TTT GAA AAC GCG CAT TTT AAG GGC AAC ACC ACG ATT TCT				444
Leu Ile Pro Phe Glu Asn Ala His Phe Lys Gly Asn Thr Thr Ile Ser				
115		120	125	
TTG CGC TCT AGC TCT CAA TTG CTC TAT AGT GAA ATC ATT GTC GCA GGG				492
Leu Arg Ser Ser Ser Gln Leu Leu Tyr Ser Glu Ile Ile Val Ala Gly				
130		135	140	145
CGA GTG GCG CGC AAT GAG TTG TTT AAA TTC AAC CGC TTG CAC ACC AAA				540
Arg Val Ala Arg Asn Glu Leu Phe Lys Phe Asn Arg Leu His Thr Lys				
150		155	160	
ATC TCT ATT TTA CAA GAT GAG AAA CCC ATC TAT TAT GAC AAC ACG ATT				588
Ile Ser Ile Leu Gln Asp Glu Lys Pro Ile Tyr Tyr Asp Asn Thr Ile				
165		170	175	
TTA GAT CCC AAA ACC ACC GAC TTA AAT AAC ATG TGC ATG TTT GAT GGC				636
Leu Asp Pro Lys Thr Thr Asp Leu Asn Asn Met Cys Met Phe Asp Gly				
180		185	190	
TAT ACG CAT TAT TTG AAT TTG GTG CTT GTC AAT TGC CCC ATA GAG CTC				684
Tyr Thr His Tyr Leu Asn Leu Val Leu Val Asn Cys Pro Ile Glu Leu				
195		200	205	
TCT GGT GTG CGA GAA TGC ATT GAA GAA AGC GAA GGG GTG GAT GGG GCA				732
Ser Gly Val Arg Glu Cys Ile Glu Glu Ser Glu Gly Val Asp Gly Ala				
210		215	220	225
GTG AGT GAA ACC GCT AGT TCT CAT TTA TGC GTG AAA GCT TTA GCG AAA				780
Val Ser Glu Thr Ala Ser Ser His Leu Cys Val Lys Ala Leu Ala Lys				
230		235	240	
GGC TCA GAA CCC TTA TTG CAT TTA AGA GAA AAA ATC GCT CGC TTG GTT				828
Gly Ser Glu Pro Leu Leu His Leu Arg Glu Lys Ile Ala Arg Leu Val				
245		250	255	
ACG CAA ACC ACC ACG CAA AAG GTT TGAAAGCACT TCAAAAAGAT TAAAGTCCTT				882
Thr Gln Thr Thr Thr Gln Lys Val				
260		265		
TAGTCTTTTT ACTCCCCCT TTTTTTGACC CTATAAGCTG AAAGGCCTGA ATTCAGTA				940

```

Lys Pro Ser Ala His Glu Ile Phe Ser Leu Cys Lys Glu Leu Lys Asn
65          70          75          80
Ser Ile Trp Asp Arg Lys Leu Val Val Ala Leu Val Glu Ala Leu Glu
          85          90          95
Gly Phe Lys Asp Trp Asn Leu Ser Leu Lys Ile Glu Asp Lys Arg Ser
          100         105         110
Asn Ser Leu Gly Asn Gly Thr Lys Leu Leu Thr Asn Ala Asp Leu
          115         120         125
Gly Ser Asp Tyr Lys Thr Ile Val Ile Asp Ser Met Lys Thr Tyr His
          130         135         140
Gln Ser Gln Gln Glu Lys Tyr Lys Arg Glu Arg Gly Glu Thr Leu Glu
145          150         155         160
Val Arg Pro Thr Thr Pro Pro Ser Tyr Gly Gly Gly Ser Ile Arg Ile
          165         170         175
Ser Gly Asp Lys Lys Pro Asp Phe Asp Glu Glu Asn Phe
          180         185

```

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...852
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

```

AGAAGGCTTA GACGATGTGA TCGCTTGGAT CAAGCGCAAC GCTTTATTGG AAGATTG ATG      60
                                         Met
                                         1

AAC ACT TAC GCT CAA GAA TCC AAG CTC AGG TTA AAA ACC AAA ATA GGG      108
Asn Thr Tyr Ala Gln Glu Ser Lys Leu Arg Leu Lys Thr Lys Ile Gly
          5          10          15

GCT GAT GGG CGG TGC GTG ATT GAA GAC AAT TTT TTC ACG CCC CCC TTT      156
Ala Asp Gly Arg Cys Val Ile Glu Asp Asn Phe Phe Thr Pro Pro Phe
          20          25          30

AAG CTC ATG GCG CCC TTT TAC CCT AAA GAC GAT TTA GCG GAA ATC ATG      204
Lys Leu Met Ala Pro Phe Tyr Pro Lys Asp Asp Leu Ala Glu Ile Met
          35          40          45

CTT TTA GCG GTA AGC CCT GGC ATG ATG AGG GGC GAT GCG CAA GAT GTG      252
Leu Leu Ala Val Ser Pro Gly Met Met Arg Gly Asp Ala Gln Asp Val

```

Ala	His	Glu	Ile	Phe	Ser	Leu	Cys	Lys	Glu	Leu	Lys	Asn	Ser	Ile	Trp		
	70						75					80					
GAC	AGG	AAG	CTT	GTG	GTA	GCG	CTA	GTG	GAG	GCT	TTA	GAG	GGG	TTT	AAG	403	
Asp	Arg	Lys	Leu	Val	Val	Ala	Leu	Val	Glu	Ala	Leu	Glu	Gly	Phe	Lys		
	85					90					95						
GAT	TGG	AAT	TTG	TCG	CTT	AAA	ATA	GAA	GAC	AAG	CGT	TCT	AAC	AGC	TTG	451	
Asp	Trp	Asn	Leu	Ser	Leu	Lys	Ile	Glu	Asp	Lys	Arg	Ser	Asn	Ser	Leu		
100					105					110					115		
GGT	AAT	GGC	ACC	AAA	AAA	TTG	CTC	ACC	AAC	GCT	GAT	TTA	GGG	AGC	GAC	499	
Gly	Asn	Gly	Thr	Lys	Lys	Leu	Leu	Thr	Asn	Ala	Asp	Leu	Gly	Ser	Asp		
				120					125					130			
TAT	AAA	ACA	ATC	GTG	ATA	GAC	AGC	ATG	AAA	ACA	TAC	CAC	CAA	AGC	CAG	547	
Tyr	Lys	Thr	Ile	Val	Ile	Asp	Ser	Met	Lys	Thr	Tyr	His	Gln	Ser	Gln		
			135					140					145				
CAA	GAA	AAA	TAT	AAA	AGA	GAA	AGA	GGC	GAA	ACG	CTA	GAG	GTT	CGC	CCC	595	
Gln	Glu	Lys	Tyr	Lys	Arg	Glu	Arg	Gly	Glu	Thr	Leu	Glu	Val	Arg	Pro		
		150					155					160					
ACA	ACA	CCC	CCT	AGC	TAT	GGG	GGT	GGA	AGC	ATT	AGA	ATC	AGC	GGC	GAT	643	
Thr	Thr	Pro	Pro	Ser	Tyr	Gly	Gly	Gly	Ser	Ile	Arg	Ile	Ser	Gly	Asp		
		165				170					175						
AAA	AAG	CCT	GAT	TTT	GAT	GAA	GAA	AAT	TTT	TAAAAGAAAG	GACAACCGAT	GAG				696	
Lys	Lys	Pro	Asp	Phe	Asp	Glu	Glu	Asn	Phe								
180					185												
CAGAGTGCAA	ATGGATACCG	AAGAGGTCAG	GGAATTTGTA	GGGCATTTAG	AACGCTTTAA								756				
AGAGTTACTA	AGAGAGGAAG	TGAACAGCTT	GAGTAATCAT	TTCCATAATT	TAGA								810				

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

Met	Met	Thr	Lys	Asn	Ala	Tyr	Ala	Phe	Val	Val	Ile	Glu	Glu	Ser	Val		
1				5				10						15			
Met	Val	Phe	Lys	Arg	Thr	Lys	Asp	Glu	Gly	Leu	Met	Pro	Ile	Phe	Glu		
			20					25					30				
Gly	Phe	Val	Pro	Leu	Lys	Glu	Gly	Phe	Leu	Lys	Ser	Phe	Lys	Glu	Arg		
		35				40					45						
Cys	Asn	Leu	Glu	Phe	Leu	Glu	Asn	Leu	Asp	Leu	Leu	Phe	Leu	Tyr	Asp		
	50					55					60						

```

Ser Glu Lys Leu Asn Thr Phe Asn Arg Val Arg Tyr Leu Lys Ser Asp
105          1110          1115          1120
Leu Asp Leu Leu His Glu Gln Ala Ser Ala Leu Gly Met Val Leu Ala
          1125          1130          1135
Thr Ala Lys Pro Cys Leu Asn Gly Arg Phe Glu Leu Leu Tyr Tyr His
          1140          1145          1150
Leu Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly
          1155          1160          1165
Ser Arg Val Leu Arg Gln Pro Thr Cys His Lys Ser Cys Cys Ala Glu
          1170          1175          1180
Lys
185

```

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 107...673
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

```

AGCATGAAGA AGTGGATGTG AAGGTGTGCA GTATAGATTC ACAAAGCATT AAAGTGGGGC      60
TGTTTAAAGA TAACCAATTA ATCTATGAAA GCGAGGCAGA AAAATT ATG ATG ACT      115
                               Met Met Thr
                               1

AAG AAC GCG TAT GCG TTT GTT GTG ATT GAA GAA AGC GTT ATG GTG TTT      163
Lys Asn Ala Tyr Ala Phe Val Val Ile Glu Glu Ser Val Met Val Phe
    5              10              15

AAA CGC ACC AAA GAT GAG GGG TTA ATG CCT ATC TTT GAA GGC TTT GTG      211
Lys Arg Thr Lys Asp Glu Gly Leu Met Pro Ile Phe Glu Gly Phe Val
    20              25              30              35

CCT TTA AAA GAG GGC TTT TTG AAA AGT TTT AAA GAG CGT TGC AAT TTG      259
Pro Leu Lys Glu Gly Phe Leu Lys Ser Phe Lys Glu Arg Cys Asn Leu
          40              45              50

GAA TTT TTA GAA AAT TTA GAC CTT TTG TTT TTG TAT GAC AAA CCA TCC      307
Glu Phe Leu Glu Asn Leu Asp Leu Leu Phe Leu Tyr Asp Lys Pro Ser
          55              60              65

GCA CAC GAG ATC TTT TCC TTG TGC AAG GAG CTG AAA AAT TCC ATC TGG      355

```


Ser	Val	Thr	Gly	Tyr	Lys	Leu	Cys	Glu	Cys	Phe	Trp	Asp	Ala	Gly	Val
		675					680					685			
Pro	Arg	Asp	Ala	Leu	Ile	Tyr	Leu	Pro	Ser	Lys	Gly	Ser	Asp	Ile	Ser
	690					695					700				
Glu	His	Leu	Leu	Arg	Asp	Glu	Ser	Ile	Gln	Phe	Ala	Ile	Leu	Thr	Gly
705					710					715					720
Gly	Glu	Asp	Thr	Ala	Tyr	Lys	Met	Leu	Lys	Ala	Asn	Pro	Thr	Leu	Ala
				725					730					735	
Leu	Ser	Ala	Glu	Thr	Gly	Gly	Lys	Asn	Ala	Thr	Ile	Val	Ser	Lys	Met
			740				745					750			
Ala	Asp	Arg	Asp	Gln	Ala	Ile	Lys	Asn	Val	Ile	His	Ser	Ala	Phe	Ser
	755						760					765			
Asn	Ser	Gly	Gln	Lys	Cys	Ser	Ala	Thr	Ser	Leu	Leu	Val	Leu	Glu	Lys
	770					775					780				
Glu	Val	Tyr	Glu	Asp	Glu	Asn	Phe	Lys	Lys	Thr	Leu	Ile	Asp	Ala	Thr
785					790					795					800
Leu	Ser	Leu	Ser	Val	Gly	Asp	Pro	Phe	Asp	Phe	Lys	Asn	Lys	Ile	Gly
				805					810					815	
Ala	Leu	Ala	Asp	Lys	Pro	Asn	Glu	Lys	Val	Ile	Lys	Ala	Ile	Asp	Glu
			820					825					830		
Leu	Lys	Ser	Tyr	Glu	Asn	Tyr	Glu	Ile	Pro	Val	Ser	Phe	Val	Asn	Asp
		835					840					845			
Asn	Pro	Tyr	Leu	Met	Lys	Pro	Ser	Ile	Lys	Tyr	Gly	Thr	Lys	Lys	Gly
	850					855					860				
Asp	Phe	Thr	His	Gln	Thr	Glu	Leu	Phe	Thr	Pro	Ile	Leu	Ser	Val	Met
865					870					875					880
Glu	Ala	Lys	Asp	Leu	Asp	Glu	Ala	Ile	Glu	Ile	Ala	Asn	Ser	Thr	Gly
			885						890					895	
Tyr	Gly	Leu	Thr	Ser	Ala	Leu	Glu	Ser	Leu	Asp	Glu	Arg	Glu	Trp	Glu
			900					905					910		
Tyr	Tyr	Leu	Glu	Arg	Ile	Glu	Ala	Gly	Asn	Ile	Tyr	Ile	Asn	Lys	Pro
	915					920						925			
Thr	Thr	Gly	Ala	Ile	Val	Leu	Arg	Gln	Pro	Phe	Gly	Gly	Val	Lys	Lys
	930					935					940				
Ser	Ala	Val	Gly	Phe	Gly	Arg	Lys	Val	Gly	Ile	Phe	Asn	Tyr	Ile	Thr
945					950					955					960
Gln	Phe	Val	Asn	Ile	Cys	Gln	Glu	Glu	Glu	Asp	Glu	Asn	Ala	Leu	Lys
			965						970					975	
Asn	Pro	Leu	Ser	Glu	Ala	Leu	Glu	Asn	Leu	Thr	Gln	Lys	Gly	Tyr	Asp
		980					985					990			
Glu	His	Thr	His	Glu	Leu	Lys	Arg	Ala	Ile	Phe	Met	Ala	Lys	Ser	Tyr
	995					1000					1005				
Ala	Tyr	His	Tyr	Lys	His	Glu	Phe	Ser	Gln	Thr	Lys	Asp	Tyr	Val	Lys
	1010														

```

Met Glu Glu Phe Arg Asp Leu Glu Leu Thr Val Glu Ser Phe Met Glu
225                230                235                240
Ser Ile Ala Lys Phe Asp Leu Asn Ala Gly Ile Val Leu Gln Ala Tyr
                245                250                255
Ile Pro Asp Ser Tyr Glu Tyr Leu Lys Lys Leu His Ala Phe Ser Lys
                260                265                270
Glu Arg Val Leu Lys Gly Leu Lys Pro Ile Lys Ile Arg Phe Val Lys
                275                280                285
Gly Ala Asn Met Glu Ser Glu Glu Thr Ile Ala Ser Val Lys Asp Trp
                290                295                300
Ala Leu Pro Thr Phe Ser Asn Lys Gln Asp Thr Asp Ser Asn Tyr Asn
305                310                315                320
Lys Met Leu Asp Phe Val Leu Glu Gly Asp Asn Tyr Lys Tyr Ile His
                325                330                335
Ile Gly Ala Ala Ser His Asn Ile Phe Glu Ile Ala Tyr Val Tyr Thr
                340                345                350
Arg Ile His Ala Ile Asn Asp Pro Val Val Leu Glu His Phe Ser Phe
                355                360                365
Glu Met Leu Glu Gly Met Ser Leu Gln Ala Ser Gln Glu Leu Lys Glu
370                375                380
Met His Lys Leu Ile Leu Tyr Ala Pro Val Cys Asp Glu Ala His Phe
385                390                395                400
Asn Asn Ala Ile Ala Tyr Leu Val Arg Arg Leu Asp Glu Asn Thr Ser
                405                410                415
Ser Asp Asn Phe Met Lys Ala Phe Phe Asn Leu Lys Val Gly Thr Ser
                420                425                430
Glu Trp Lys Asp Gln Glu Gln Arg Phe Leu Asn Ser Leu Lys Gly Ile
435                440                445
Ala Thr Leu Asp Asn Ala Thr His Arg Thr Gln Asp Arg Asn Ala Lys
450                455                460
Gln Ser Gly His Thr Thr Tyr Pro Asn His Ser Phe Lys Asn Glu Ser
465                470                475                480
Asp Thr Asp Phe Ile Leu Lys Ala Asn Arg Glu Trp Ala Lys Lys Val
                485                490                495
Arg Glu Lys Met Arg Asn Ala Pro Ile Leu Glu Leu Tyr Pro Glu Met
500                505                510
Asp Gly Arg Phe Glu Asp Pro Asn Leu Thr Pro Leu Glu Val Phe Asp
515                520                525
Arg Ile His His Lys Lys Ile Ala Ser Val His Leu Ala Asp Lys Glu
530                535                540
Ala Ile Leu Lys Ala Leu Glu Val Ala Lys Ser Asp Lys Ser Arg Phe
545                550                555                560
Ser Gln Lys Ser Phe Thr Glu Ile His Ala Leu Met Ser Gln Thr Ala
                565                570                575
Gln Leu Phe Arg Glu Arg Arg Gly Asp Leu Ile Gly Ile Ser Ala Leu
580                585                590
Glu Val Gly Lys Thr Phe Ala Glu Thr Asp Ala Glu Val Ser Glu Ala
595                600                605
Ile Asp Phe Leu Glu Phe Tyr Pro Tyr Ser Leu Arg Val Leu Gln Glu
610                615                620
Gln Asn Thr Lys Thr Gln Phe Thr Pro Lys Gly Val Gly Val Val Ile
625                630                635                640
Ala Pro Trp Asn Phe Pro Val Gly Ile Ser Val Gly Thr Ile Ala Ala
                645                650                655
Pro Leu-Ala Thr Gly Asn Arg Val Ile Tyr Lys Pro Ser Ser Leu Ser

```

```

GCT AAA CCA TGC CTA AAT GGG CGT TTT GAA TTG CTG TAT TAC CAC TTA      3512
Ala Lys Pro Cys Leu Asn Gly Arg Phe Glu Leu Leu Tyr Tyr His Leu
      1140                      1145                      1150

GAG CGA TCG GTT AGC ATC TCT TAT CAC CGT TAT GGG AAT TTA GGC TCA      3560
Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly Ser
      1155                      1160                      1165

AGG GTT TTA AGG CAA CCC ACT TGC CAC AAA TCA TGC TGT GCT GAA AAA T      3609
Arg Val Leu Arg Gln Pro Thr Cys His Lys Ser Cys Cys Ala Glu Lys
1170                      1175                      1180                      1185

AAATATTGTA TTAAATAAGG AGATCAAAAT GGGACATGTT GTTTTAAGTA CCCCTAT      3666

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

Met Gln Lys Ile Ile Asp Asp Ser Leu Glu Leu Ala Lys Lys Leu Gln
 1           5           10           15
Asp Ser Ile Ser Asn His Leu Ser Asp Gln Glu Lys Ala Phe His Ser
      20           25           30
Lys Met Gln Lys Leu Leu Asn Asn Pro Glu Asn Lys Val Met Leu Ile
      35           40           45
Glu Leu Met Asp Arg Ser Phe Arg Cys Leu Asp Asn Lys Ala Arg Phe
      50           55           60
Glu Met Ile Glu His Val Leu Asp Lys Tyr Lys Ser Arg Glu Ile Phe
      65           70           75           80
Ser Pro Phe Glu Lys Val Leu Leu Met Gly Phe Leu Ser Phe Gly Lys
      85           90           95
Met Leu Pro Asp Met Ser Val Pro Phe Phe Val Asn Lys Ile Arg Ser
      100          105          110
Asp Thr Lys Ala Met Val Leu Asp Gln Glu Glu Ser Gln Leu Lys Glu
      115          120          125
Arg Ile Leu Lys Arg Lys Asn Glu Lys Ile Ile Leu Asn Val Asn Phe
      130          135          140
Ile Gly Glu Glu Val Leu Gly Glu Glu Glu Ala Asn Ala Arg Phe Glu
      145          150          155          160
Lys Tyr Ser Gln Ala Leu Lys Ser Asn Tyr Ile Gln Tyr Ile Ser Ile
      165          170          175
Lys Ile Thr Thr Ile Phe Ser Gln Ile Asn Ile Leu Asp Phe Glu Tyr
      180          185          190
Ser Lys Lys Glu Ile Val Lys Arg Leu Asp Ala Leu Tyr Ala Leu Ala
      195          200          205
Leu Glu Glu Glu Lys Lys Gln Gly Met Pro Lys Phe Ile Asn Leu Asp
      210          215          220

```

TAT TTA GAA CGC ATT GAA GCC GGT AAT ATC TAT ATC AAC AAG CCC ACC	2840
Tyr Leu Glu Arg Ile Glu Ala Gly Asn Ile Tyr Ile Asn Lys Pro Thr	
915 920 925	
ACA GGA GCG ATT GTC TTG CGC CAG CCT TTT GGG GGG GTT AAA AAA TCC	2888
Thr Gly Ala Ile Val Leu Arg Gln Pro Phe Gly Gly Val Lys Lys Ser	
930 935 940 945	
GCT GTG GGG TTT GGG AGG AAA GTA GGC ATT TTC AAC TAT ATC ACG CAA	2936
Ala Val Gly Phe Gly Arg Lys Val Gly Ile Phe Asn Tyr Ile Thr Gln	
950 955 960	
TTT GTG AAT ATC TGC CAA GAA GAA GAA GAC GAA AAC GCC TTA AAA AAC	2984
Phe Val Asn Ile Cys Gln Glu Glu Glu Asp Glu Asn Ala Leu Lys Asn	
965 970 975	
CCC TTA AGC GAA GCC TTA GAA AAC TTA ACT CAA AAA GGC TAT GAT GAG	3032
Pro Leu Ser Glu Ala Leu Glu Asn Leu Thr Gln Lys Gly Tyr Asp Glu	
980 985 990	
CAT ACG CAT GAG TTG AAG CGC GCG ATT TTT ATG GCA AAA AGC TAC GCT	3080
His Thr His Glu Leu Lys Arg Ala Ile Phe Met Ala Lys Ser Tyr Ala	
995 1000 1005	
TAT CAT TAC AAA CAT GAA TTC AGC CAA ACT AAA GAC TAT GTC AAA ATC	3128
Tyr His Tyr Lys His Glu Phe Ser Gln Thr Lys Asp Tyr Val Lys Ile	
1010 1015 1020 1025	
AGA GGC GAA GAC AAC CTT TTT TCC TAC ACT AAA GTT AAA AGC GTG GGC	3176
Arg Gly Glu Asp Asn Leu Phe Ser Tyr Thr Lys Val Lys Ser Val Gly	
1030 1035 1040	
TAT CGC ATC ACC GAA AAG GAC ACT TTA AGC GAC ATG TTA GGC GTT GCT	3224
Tyr Arg Ile Thr Glu Lys Asp Thr Leu Ser Asp Met Leu Gly Val Ala	
1045 1050 1055	
TTA GCA TGT TTA ATT TCT CAA ATC CCT TTA ACG CTC AGC ATA GAA AAC	3272
Leu Ala Cys Leu Ile Ser Gln Ile Pro Leu Thr Leu Ser Ile Glu Asn	
1060 1065 1070	
GAA CGA ACG AAC AAA GAT TTA ACC TTT TTC TTA GAA TGC TTA AAA GCG	3320
Glu Arg Thr Asn Lys Asp Leu Thr Phe Phe Leu Glu Cys Leu Lys Ala	
1075 1080 1085	
CTC CAA GCA AGC GCC CCT ATT GTT TAT GAA AGC TTG CAA AAA TTT AGC	3368
Leu Gln Ala Ser Ala Pro Ile Val Tyr Glu Ser Leu Gln Lys Phe Ser	
1090 1095 1100 1105	
GAG AAA TTG AAT ACT TTC AAT CGT GTC CGT TAT CTC AAA AGC GAT TTG	3416
Glu Lys Leu Asn Thr Phe Asn Arg Val Arg Tyr Leu Lys Ser Asp Leu	
1110 1115 1120	
GAT TTA TTG CAC GAA CAA GCG AGC GCT TTA GGG ATG GTT TTA GCC ACG	3464
Asp Leu Leu His Glu Gln Ala Ser Ala Leu Gly Met Val Leu Ala Thr	
1125 1130 1135	

AGA GAT GCG CTC ATT TAC TTG CCC TCT AAA GGG AGC GAT ATT AGC GAA	2168
Arg Asp Ala Leu Ile Tyr Leu Pro Ser Lys Gly Ser Asp Ile Ser Glu	
690 695 700 705	
CAT CTT TTA AGA GAT GAA AGC ATC CAG TTT GCC ATT TTA ACC GGG GGC	2216
His Leu Leu Arg Asp Glu Ser Ile Gln Phe Ala Ile Leu Thr Gly Gly	
710 715 720	
GAA GAC ACC GCT TAT AAA ATG TTA AAA GCT AAC CCC ACT TTA GCC TTG	2264
Glu Asp Thr Ala Tyr Lys Met Leu Lys Ala Asn Pro Thr Leu Ala Leu	
725 730 735	
AGC GCT GAA ACA GGC GGT AAA AAC GCC ACC ATT GTG AGC AAA ATG GCA	2312
Ser Ala Glu Thr Gly Gly Lys Asn Ala Thr Ile Val Ser Lys Met Ala	
740 745 750	
GAC AGA GAC CAG GCG ATT AAG AAT GTT ATC CAT TCA GCT TTT AGC AAT	2360
Asp Arg Asp Gln Ala Ile Lys Asn Val Ile His Ser Ala Phe Ser Asn	
755 760 765	
TCG GGG CAA AAA TGC TCC GCC ACT TCG CTT TTA GTA TTA GAA AAA GAA	2408
Ser Gly Gln Lys Cys Ser Ala Thr Ser Leu Leu Val Leu Glu Lys Glu	
770 775 780 785	
GTC TAT GAA GAT GAG AAC TTT AAA AAG ACT CTA ATA GAT GCG ACT CTA	2456
Val Tyr Glu Asp Glu Asn Phe Lys Lys Thr Leu Ile Asp Ala Thr Leu	
790 795 800	
AGC CTT AGC GTG GGC GAT CCT TTT GAT TTC AAA AAC AAA ATC GGC GCT	2504
Ser Leu Ser Val Gly Asp Pro Phe Asp Phe Lys Asn Lys Ile Gly Ala	
805 810 815	
CTA GCG GAC AAG CCT AAT GAA AAG GTC ATC AAA GCC ATA GAT GAA TTA	2552
Leu Ala Asp Lys Pro Asn Glu Lys Val Ile Lys Ala Ile Asp Glu Leu	
820 825 830	
AAA AGC TAT GAA AAT TAC GAA ATC CCG GTA AGC TTT GTC AAT GAT AAC	2600
Lys Ser Tyr Glu Asn Tyr Glu Ile Pro Val Ser Phe Val Asn Asp Asn	
835 840 845	
CCC TAT TTG ATG AAG CCA AGC ATC AAA TAC GGC ACT AAA AAA GGC GAT	2648
Pro Tyr Leu Met Lys Pro Ser Ile Lys Tyr Gly Thr Lys Lys Gly Asp	
850 855 860 865	
TTC ACG CAC CAA ACT GAG CTT TTT ACG CCC ATT TTA TCC GTG ATG GAA	2696
Phe Thr His Gln Thr Glu Leu Phe Thr Pro Ile Leu Ser Val Met Glu	
870 875 880	
GCA AAA GAT TTA GAC GAA GCG ATA GAA ATA GCC AAT TCT ACC GGT TAC	2744
Ala Lys Asp Leu Asp Glu Ala Ile Glu Ile Ala Asn Ser Thr Gly Tyr	
885 890 895	
GGG CTG ACT AGC GCG TTA GAG TCG TTG GAC GAA AGG GAG TGG GAA TAT	2792
Gly Leu Thr Ser Ala Leu Glu Ser Leu Asp Glu Arg Glu Trp Glu Tyr	
900 905 910	

AGC GGG CAT ACC ACT TAC CCA AAC CAC TCC TTT AAA AAC GAA AGC GAT	1496
Ser Gly His Thr Thr Tyr Pro Asn His Ser Phe Lys Asn Glu Ser Asp	
470 475 480	
ACC GAT TTT ATT TTA AAA GCC AAC CGA GAA TGG GCT AAA AAA GTG CGC	1544
Thr Asp Phe Ile Leu Lys Ala Asn Arg Glu Trp Ala Lys Lys Val Arg	
485 490 495	
GAG AAA ATG CGT AAC GCT CCT ATT TTA GAG CTT TAC CCA GAG ATG GAT	1592
Glu Lys Met Arg Asn Ala Pro Ile Leu Glu Leu Tyr Pro Glu Met Asp	
500 505 510	
GGG AGG TTT GAA GAT CCT AAT CTA ACC CCT TTA GAA GTC TTT GAT AGA	1640
Gly Arg Phe Glu Asp Pro Asn Leu Thr Pro Leu Glu Val Phe Asp Arg	
515 520 525	
ATC CAT CAT AAA AAA ATC GCT AGC GTG CAT TTA GCG GAT AAG GAA GCG	1688
Ile His His Lys Lys Ile Ala Ser Val His Leu Ala Asp Lys Glu Ala	
530 535 540 545	
ATT TTA AAA GCC CTA GAA GTG GCT AAA AGC GAT AAG AGC CGT TTC AGT	1736
Ile Leu Lys Ala Leu Glu Val Ala Lys Ser Asp Lys Ser Arg Phe Ser	
550 555 560	
CAA AAA AGC TTT ACA GAA ATC CAT GCC TTA ATG AGT CAA ACC GCC CAG	1784
Gln Lys Ser Phe Thr Glu Ile His Ala Leu Met Ser Gln Thr Ala Gln	
565 570 575	
CTT TTT AGA GAA AGA AGA GGC GAT TTG ATA GGG ATT TCC GCT TTA GAA	1832
Leu Phe Arg Glu Arg Arg Gly Asp Leu Ile Gly Ile Ser Ala Leu Glu	
580 585 590	
GTG GGT AAG ACT TTC GCT GAA ACG GAC GCT GAA GTG AGC GAA GCC ATT	1880
Val Gly Lys Thr Phe Ala Glu Thr Asp Ala Glu Val Ser Glu Ala Ile	
595 600 605	
GAC TTT TTA GAG TTT TAC CCT TAC AGC TTA AGG GTG TTG CAA GAG CAA	1928
Asp Phe Leu Glu Phe Tyr Pro Tyr Ser Leu Arg Val Leu Gln Glu Gln	
610 615 620 625	
AAC ACA AAA ACG CAA TTC ACC CCT AAA GGC GTG GGC GTG GTC ATT GCC	1976
Asn Thr Lys Thr Gln Phe Thr Pro Lys Gly Val Gly Val Val Ile Ala	
630 635 640	
CCA TGG AAT TTC CCT GTG GGC ATT TCT GTA GGC ACT ATC GCT GCC CCC	2024
Pro Trp Asn Phe Pro Val Gly Ile Ser Val Gly Thr Ile Ala Ala Pro	
645 650 655	
CTA GCT ACG GGC AAT CGG GTG ATT TAC AAG CCC TCA AGT TTG TCT AGC	2072
Leu Ala Thr Gly Asn Arg Val Ile Tyr Lys Pro Ser Ser Leu Ser Ser	
660 665 670	
GTA ACG GGC TAT AAG CTT TGT GAG TGC TTT TGG GAT GCG GGC GTG CCT	2120
Val Thr Gly Tyr Lys Leu Cys Glu Cys Phe Trp Asp Ala Gly Val Pro	
675 680 685	

ATC GCT AAA TTT GAT TTG AAC GCT GGT ATT GTG CTG CAA GCC TAT ATT	824
Ile Ala Lys Phe Asp Leu Asn Ala Gly Ile Val Leu Gln Ala Tyr Ile	
245 250 255	
CCG GAT TCT TAT GAA TAT TTG AAA AAA CTG CAC GCT TTT TCT AAA GAA	872
Pro Asp Ser Tyr Glu Tyr Leu Lys Lys Leu His Ala Phe Ser Lys Glu	
260 265 270	
AGG GTT TTA AAA GGG TTG AAG CCC ATT AAA ATC CGC TTT GTT AAG GGA	920
Arg Val Leu Lys Gly Leu Lys Pro Ile Lys Ile Arg Phe Val Lys Gly	
275 280 285	
GCG AAC ATG GAG AGC GAA GAA ACT ATC GCT TCC GTG AAA GAT TGG GCG	968
Ala Asn Met Glu Ser Glu Glu Thr Ile Ala Ser Val Lys Asp Trp Ala	
290 295 300 305	
TTA CCC ACA TTT TCC AAT AAG CAA GAC ACC GAT TCT AAT TAC AAT AAA	1016
Leu Pro Thr Phe Ser Asn Lys Gln Asp Thr Asp Ser Asn Tyr Asn Lys	
310 315 320	
ATG TTG GAT TTT GTT TTA GAG GGC GAT AAT TAT AAA TAC ATT CAT ATT	1064
Met Leu Asp Phe Val Leu Glu Gly Asp Asn Tyr Lys Tyr Ile His Ile	
325 330 335	
GGC GCA GCG AGT CAT AAT ATT TTT GAA ATC GCT TAT GTC TAT ACG CGT	1112
Gly Ala Ala Ser His Asn Ile Phe Glu Ile Ala Tyr Val Tyr Thr Arg	
340 345 350	
ATC CAT GCC ATT AAT GAT CCT GTT GTG TTA GAG CAT TTC AGC TTT GAA	1160
Ile His Ala Ile Asn Asp Pro Val Val Leu Glu His Phe Ser Phe Glu	
355 360 365	
ATG CTA GAG GGC ATG AGT TTG CAA GCG AGC CAG GAA CTA AAA GAG ATG	1208
Met Leu Glu Gly Met Ser Leu Gln Ala Ser Gln Glu Leu Lys Glu Met	
370 375 380 385	
CAC AAG CTC ATT CTT TAT GCG CCG GTG TGC GAT GAA GCG CAT TTT AAC	1256
His Lys Leu Ile Leu Tyr Ala Pro Val Cys Asp Glu Ala His Phe Asn	
390 395 400	
AAT GCG ATC GCT TAC TTG GTG AGG AGG TTA GAC GAA AAC ACC TCA AGC	1304
Asn Ala Ile Ala Tyr Leu Val Arg Arg Leu Asp Glu Asn Thr Ser Ser	
405 410 415	
GAT AAT TTC ATG AAG GCT TTC TTT AAC CTC AAA GTA GGC ACG AGC GAA	1352
Asp Asn Phe Met Lys Ala Phe Phe Asn Leu Lys Val Gly Thr Ser Glu	
420 425 430	
TGG AAA GAT CAA GAA CAA CGC TTT TTA AAC AGC CTT AAA GGA ATT GCC	1400
Trp Lys Asp Gln Glu Gln Arg Phe Leu Asn Ser Leu Lys Gly Ile Ala	
435 440 445	
ACT TTA GAC AAT GCC ACC CAT AGG ACT CAA GAT AGG AAC GCC AAA CAA	1448
Thr Leu Asp Asn Ala Thr His Arg Thr Gln Asp Arg Asn Ala Lys Gln	
450 455 460 465	

Ser	Ile	Ser	Asn	His	Leu	Ser	Asp	Gln	Glu	Lys	Ala	Phe	His	Ser	Lys		
		20					25					30					
ATG	CAA	AAG	CTT	TTA	AAC	AAC	CCT	GAA	AAC	AAA	GTC	ATG	CTC	ATA	GAG		200
Met	Gln	Lys	Leu	Leu	Asn	Asn	Pro	Glu	Asn	Lys	Val	Met	Leu	Ile	Glu		
		35				40				45							
CTT	ATG	GAT	CGG	AGT	TTC	AGG	TGC	TTG	GAC	AAT	AAA	GCC	CGC	TTT	GAA		248
Leu	Met	Asp	Arg	Ser	Phe	Arg	Cys	Leu	Asp	Asn	Lys	Ala	Arg	Phe	Glu		
50					55				60					65			
ATG	ATT	GAG	CAT	GTT	TTA	GAC	AAA	TAC	AAA	AGC	CGT	GAG	ATT	TTT	TCT		296
Met	Ile	Glu	His	Val	Leu	Asp	Lys	Tyr	Lys	Ser	Arg	Glu	Ile	Phe	Ser		
				70				75						80			
CCG	TTT	GAA	AAA	GTG	CTT	TTA	ATG	GGG	TTT	TTA	AGC	TTT	GGG	AAA	ATG		344
Pro	Phe	Glu	Lys	Val	Leu	Leu	Met	Gly	Phe	Leu	Ser	Phe	Gly	Lys	Met		
			85					90					95				
CTC	CCT	GAT	ATG	AGC	GTG	CCT	TTC	TTT	GTC	AAT	AAA	ATC	AGA	AGC	GAC		392
Leu	Pro	Asp	Met	Ser	Val	Pro	Phe	Phe	Val	Asn	Lys	Ile	Arg	Ser	Asp		
		100					105					110					
ACG	AAA	GCG	ATG	GTC	TTG	GAT	CAA	GAA	GAG	AGC	CAG	TTA	AAA	GAG	CGG		440
Thr	Lys	Ala	Met	Val	Leu	Asp	Gln	Glu	Glu	Ser	Gln	Leu	Lys	Glu	Arg		
		115				120					125						
ATT	TTA	AAA	AGA	AAA	AAT	GAA	AAA	ATC	ATT	TTG	AAT	GTG	AAT	TTT	ATT		488
Ile	Leu	Lys	Arg	Lys	Asn	Glu	Lys	Ile	Ile	Leu	Asn	Val	Asn	Phe	Ile		
130					135					140					145		
GGC	GAA	GAG	GTT	TTA	GGC	GAA	GAA	GAA	GCT	AAT	GCG	CGT	TTT	GAA	AAA		536
Gly	Glu	Glu	Val	Leu	Gly	Glu	Glu	Glu	Ala	Asn	Ala	Arg	Phe	Glu	Lys		
				150					155					160			
TAC	TCT	CAA	GCC	CTA	AAA	TCC	AAC	TAC	ATC	CAA	TAC	ATT	TCC	ATT	AAA		584
Tyr	Ser	Gln	Ala	Leu	Lys	Ser	Asn	Tyr	Ile	Gln	Tyr	Ile	Ser	Ile	Lys		
			165					170					175				
ATC	ACG	ACG	ATT	TTT	TCT	CAA	ATC	AAT	ATC	CTT	GAT	TTT	GAA	TAC	TCT		632
Ile	Thr	Thr	Ile	Phe	Ser	Gln	Ile	Asn	Ile	Leu	Asp	Phe	Glu	Tyr	Ser		
			180					185					190				
AAA	AAA	GAG	ATT	GTC	AAA	CGC	CTA	GAC	GCT	CTT	TAC	GCC	CTG	GCT	TTA		680
Lys	Lys	Glu	Ile	Val	Lys	Arg	Leu	Asp	Ala	Leu	Tyr	Ala	Leu	Ala	Leu		
		195				200					205						
GAA	GAA	GAA	AAA	AAA	CAA	GGC	ATG	CCT	AAA	TTC	ATC	AAT	TTG	GAT	ATG		728
Glu	Glu	Glu	Lys	Lys	Gln	Gly	Met	Pro	Lys	Phe	Ile	Asn	Leu	Asp	Met		
210					215					220				225			
GAA	GAA	TTT	AGG	GAT	TTA	GAG	CTA	ACA	GTG	GAG	TCG	TTT	ATG	GAA	TCC		776
Glu	Glu	Phe	Arg	Asp	Leu	Glu	Leu	Thr	Val	Glu	Ser	Phe	Met	Glu	Ser		
				230				235						240			


```

625          630          635          640
Pro Leu Asn Leu Ser Ile Lys Gln Lys Pro Ser Tyr Ile Phe Asp Lys
          645          650          655
Gln Leu Pro Tyr Trp Val Ile Tyr Arg Asn Ala Phe Phe Asp Lys Val
          660          665          670
Phe His Ser Met Gln Phe Gly Leu Phe Glu Val Phe Arg Asp Arg Gln
          675          680          685
Ile Thr Asn Ser Val Leu Val Lys Asn Gly Ile Arg Val Ile Lys Ser
          690          695          700
Arg Asn Ile Asp Glu Asn Gly Lys Ile Ile Ser Ile Glu Asn Tyr Asp
705          710          715          720
Ser Tyr Ile Gln Lys Glu Val Leu Ser Pro Phe Lys Ile Ala Ser Phe
          725          730          735
Leu Asp Arg Asp Asp Val Tyr Leu Thr Pro Asn Met Thr Tyr Lys Pro
          740          745          750
Arg Ile Leu Lys Lys Glu Lys Gly Tyr Val Val Asn Gly Ser Val Ala
          755          760          765
Ile Leu Ile Pro Lys Asn Pro Ile Ser Leu Ser Lys Lys Gln Cys Asp
          770          775          780
Tyr Ile Ser Ser Val Glu Phe Arg Asp Phe Tyr Lys Ile Ala Arg Asn
785          790          795          800
Tyr Gln Thr Arg Thr Leu Asn Ile Asp Ser Met Ser Cys Phe Trp Phe
          805          810          815
Gly Ile Leu Arg Ser Ser Leu
          820

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 54...3608
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

CCCGCTTAAA ACATGCTACA ATCAAGTCAA ATTCTTAAAT AAAAGGTAAG CTC ATG      56
                                     Met
                                     1

CAA AAA ATC ATT GAC GAT TCG CTA GAA TTA GCT AAA AAA CTG CAA GAT      104
Gln Lys Ile Ile Asp Asp Ser Leu Glu Leu Ala Lys Lys Leu Gln Asp
          5          10          15

AGT ATC AGT AAC CAT TTG AGC GAT CAG GAA AAA GCG TTC CAC TCT AAA      152

```

Cys Lys Glu Phe Lys Asp Phe Ile Ser Ala Leu Glu Phe Phe Pro Asp
 195 200 205
 Phe Lys Gln Glu Lys Thr Leu Lys Glu Val Ile Gly Ser Leu Lys Pro
 210 215 220
 Leu Ala Trp Gly Glu Tyr Asp Asn Thr Asp Phe Tyr His Ser Phe Arg
 225 230 235 240
 Thr Tyr Pro Lys His Met Gln Glu Trp Ile Lys Asp Leu Lys Glu Gly
 245 250 255
 Gln Ser Ala Phe Glu Asn Thr Glu Leu Asn Lys Lys Pro His Arg Ile
 260 265 270
 Val Gly Ser Lys Ile Val Leu Asn Val Ser Lys Asn Gly Asp Lys Tyr
 275 280 285
 Lys Arg Gln Lys Tyr His Ser Val Ala Pro Cys Ile His Thr Arg Asn
 290 295 300
 Asp Gln Met Ala Ser Gln Asn Thr Ile His Pro Lys Asp Asp Arg Val
 305 310 315 320
 Phe Ser Ile Arg Glu Leu Met Leu Leu Met Asn Ile Pro Ser Arg Phe
 325 330 335
 Lys Trp Leu Asp Leu Glu Leu Gln Glu Leu Asn Ala Leu Asn Gln Gln
 340 345 350
 Glu Lys Glu Lys Ile Ser Lys Gln Asn Glu Met Asn Ile Arg Gln Ser
 355 360 365
 Ile Gly Glu Ala Val Pro Thr Ile Ile Phe Lys Gln Ile Ala Ile Lys
 370 375 380
 Ile Lys Asn Phe Met Ser Gln Thr His Leu Glu Pro Lys Glu Ile Ile
 385 390 395 400
 Arg Leu Ile Asp Val His His Leu Leu Glu Pro Gln Asn Leu Lys Arg
 405 410 415
 Phe Ile Leu Glu Asn Gln Asn Lys Ile Ala Arg Ala Ser Leu Val Ser
 420 425 430
 Leu Ala Glu Met Ser Asn Ser Lys Arg Ile Glu Lys Ser Ala Tyr Phe
 435 440 445
 Thr Asn Pro Phe Ile Ile Asn Glu Ile Ala Lys Leu Leu Pro Ser Phe
 450 455 460
 Lys Gln Glu Ser Val Thr Ile Ile Glu Pro Ser Ala Gly Cys Gly Asn
 465 470 475 480
 Phe Leu Ser Ala Leu Phe Lys Lys Tyr Thr Ser Val Lys Lys Val Tyr
 485 490 495
 Leu Lys Cys Ile Asp Ile Asp Lys Asn Ser Leu Glu Ile Leu Glu Ile
 500 505 510
 Leu Tyr Lys Asp Cys Ile Pro Asn Asn Phe Glu Met Glu Leu Ile Cys
 515 520 525
 Lys Asp Phe Leu Ala Tyr Glu Cys Gly Lys Val Asp Leu Ile Val Gly
 530 535 540
 Asn Pro Pro Phe Gly Lys Thr His Glu Arg Phe Lys Asp Tyr Ser Leu
 545 550 555 560
 Arg Leu Thr His Leu Ala Gly Ile Phe Leu Glu Lys Ser Leu Lys Leu
 565 570 575
 Ala Asn Phe Thr Ala Met Val Met Pro Lys Asn Leu Leu Asn Thr Lys
 580 585 590
 Glu Tyr Ala Glu Thr Arg Thr Lys Leu Glu Lys Lys Gly Val Gly Ala
 595 600 605
 Ile Leu Asp Phe Gly Glu Leu Gly Phe Lys Gly Val Leu Val Glu Thr
 610 615 620
 Ile Ala Ile Val Thr Gln Lys Ser Lys Glu Val Leu Ala Arg Ser Leu

```

TAT GTG GTT AAT GGC TCT GTG GCT ATT TTA ATC CCT AAA AAC CCC ATA      2417
Tyr Val Val Asn Gly Ser Val Ala Ile Leu Ile Pro Lys Asn Pro Ile
              765                      770                      775

TCT TTA AGC AAG AAA CAA TGC GAT TAT ATC TCT AGC GTT GAA TTT AGA      2465
Ser Leu Ser Lys Lys Gln Cys Asp Tyr Ile Ser Ser Val Glu Phe Arg
              780                      785                      790

GAT TTT TAT AAA ATC GCT AGG AAT TAT CAA ACG CGC ACC TTA AAT ATT      2513
Asp Phe Tyr Lys Ile Ala Arg Asn Tyr Gln Thr Arg Thr Leu Asn Ile
              795                      800                      805

GAT AGC ATG AGT TGT TTT TGG TTT GGA ATT TTA AGG AGT AGC TTA TGAAA    2563
Asp Ser Met Ser Cys Phe Trp Phe Gly Ile Leu Arg Ser Ser Leu
              810                      815                      820

GAGCAATCAA TGATTGATTT TTAAAACTT AGAGATTATG ACATTAG                  2610

```

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```

Met Leu Phe Asp Gln Thr Leu Thr Tyr Ile Ser Leu Phe Ser Gly Ala
 1             5             10             15
Gly Val Gly Cys Tyr Gly Leu Leu Glu Glu Gly Phe Glu Cys Val Ala
              20             25             30
Thr Asn Glu Ile Leu Glu Lys Arg Leu Asn Ile Gln Arg Ile Asn Arg
              35             40             45
Lys Cys Lys Leu Asp Glu Ser Tyr Ile Ser Gly Asp Ile Lys Lys Pro
              50             55             60
Glu Thr Lys Glu Lys Ile Leu Lys Gln Ile Glu Phe Tyr Ser Lys Lys
65             70             75             80
Phe Gly Asn Asp Arg Val Asp Leu Val Val Ala Thr Pro Pro Cys Gln
              85             90             95
Gly Met Ser Val Ala Asn His Lys Lys Lys Asn Asp Glu Ile Lys Arg
              100            105            110
Asn Ser Leu Val Val Glu Ser Ile Asp Leu Ile Lys Gln Ile Lys Pro
              115            120            125
Arg Phe Phe Ile Leu Glu Asn Val Pro Ser Phe Tyr Lys Thr Gly Cys
              130            135            140
Ile Asp Lys Asn Asp Asn Leu Leu Glu Ile Gly Ser Met Ile Glu Gln
145            150            155            160
Asn Leu Ser Gly Asp Tyr Met Leu Tyr Asp Glu Val Ile Asn Phe Lys
              165            170            175
Asn Phe Gly Ala Asn Ser Ser Arg Thr Arg Thr Leu Val Ile Gly Val
              180            185            190

```

GGC AAA GTG GAT TTA ATT GTG GGC AAT CCG CCT TTT GGC AAA ACG CAT	1745
Gly Lys Val Asp Leu Ile Val Gly Asn Pro Pro Phe Gly Lys Thr His	
540 545 550	
GAA AGA TTC AAA GAT TAT AGT TTA AGA CTC ACT CAT TTA GCA GGG ATT	1793
Glu Arg Phe Lys Asp Tyr Ser Leu Arg Leu Thr His Leu Ala Gly Ile	
555 560 565	
TTT TTA GAA AAG TCT TTA AAA CTA GCC AAC TTT ACA GCG ATG GTT ATG	1841
Phe Leu Glu Lys Ser Leu Lys Leu Ala Asn Phe Thr Ala Met Val Met	
570 575 580	
CCT AAA AAC CTT TTA AAC ACT AAA GAG TAT GCA GAA ACT AGA ACT AAG	1889
Pro Lys Asn Leu Leu Asn Thr Lys Glu Tyr Ala Glu Thr Arg Thr Lys	
585 590 595 600	
CTT GAA AAA AAG GGA GTA GGA GCG ATT TTA GAC TTT GGC GAG CTT GGT	1937
Leu Glu Lys Lys Gly Val Gly Ala Ile Leu Asp Phe Gly Glu Leu Gly	
605 610 615	
TTT AAG GGT GTT TTG GTA GAA ACA ATT GCT ATT GTT ACA CAA AAA TCA	1985
Phe Lys Gly Val Leu Val Glu Thr Ile Ala Ile Val Thr Gln Lys Ser	
620 625 630	
AAA GAA GTT TTA GCG CGT TCG TTA CCC CTA AAT CTA AGC ATC AAG CAA	2033
Lys Glu Val Leu Ala Arg Ser Leu Pro Leu Asn Leu Ser Ile Lys Gln	
635 640 645	
AAG CCA AGC TAT ATT TTT GAC AAA CAA TTG CCC TAT TGG GTT ATC TAT	2081
Lys Pro Ser Tyr Ile Phe Asp Lys Gln Leu Pro Tyr Trp Val Ile Tyr	
650 655 660	
CGC AAC GCT TTT TTT GAT AAG GTG TTT CAT TCC ATG CAG TTT GGT CTT	2129
Arg Asn Ala Phe Phe Asp Lys Val Phe His Ser Met Gln Phe Gly Leu	
665 670 675 680	
TTT GAA GTG TTT AGA GAC AGA CAA ATC ACT AAT TCT GTG TTG GTT AAA	2177
Phe Glu Val Phe Arg Asp Arg Gln Ile Thr Asn Ser Val Leu Val Lys	
685 690 695	
AAT GGT ATT CGT GTG ATT AAA TCT CGC AAT ATT GAT GAA AAC GGA AAG	2225
Asn Gly Ile Arg Val Ile Lys Ser Arg Asn Ile Asp Glu Asn Gly Lys	
700 705 710	
ATT ATT AGC ATT GAA AAT TAC GAT AGC TAC ATT CAA AAA GAG GTT TTA	2273
Ile Ile Ser Ile Glu Asn Tyr Asp Ser Tyr Ile Gln Lys Glu Val Leu	
715 720 725	
AGT CCG TTT AAG ATA GCT TCA TTT TTA GAC AGA GAT GAT GTC TAT TTA	2321
Ser Pro Phe Lys Ile Ala Ser Phe Leu Asp Arg Asp Asp Val Tyr Leu	
730 735 740	
ACC CCC AAC ATG ACC TAT AAG CCA AGG ATT TTA AAA AAA GAA AAA GGC	2369
Thr Pro Asn Met Thr Tyr Lys Pro Arg Ile Leu Lys Lys Glu Lys Gly	
745 750 755 760	

Ile	His	Pro	Lys	Asp	Asp	Arg	Val	Phe	Ser	Ile	Arg	Glu	Leu	Met	Leu		
		315					320					325					
TTA	ATG	AAT	ATC	CCT	AGC	CGT	TTT	AAG	TGG	TTA	GAT	TTA	GAA	TTA	CAA	1121	
Leu	Met	Asn	Ile	Pro	Ser	Arg	Phe	Lys	Trp	Leu	Asp	Leu	Glu	Leu	Gln		
		330				335					340						
GAA	TTA	AAC	GCC	CTT	AAC	CAA	CAA	GAA	AAA	GAA	AAA	ATC	TCC	AAA	CAA	1169	
Glu	Leu	Asn	Ala	Leu	Asn	Gln	Gln	Glu	Lys	Glu	Lys	Ile	Ser	Lys	Gln		
		345			350					355					360		
AAC	GAA	ATG	AAT	ATA	AGA	CAA	AGC	ATC	GGT	GAA	GCT	GTT	CCA	ACG	ATT	1217	
Asn	Glu	Met	Asn	Ile	Arg	Gln	Ser	Ile	Gly	Glu	Ala	Val	Pro	Thr	Ile		
				365					370						375		
ATT	TTT	AAG	CAA	ATT	GCC	ATA	AAG	ATA	AAA	AAT	TTC	ATG	TCT	CAA	ACC	1265	
Ile	Phe	Lys	Gln	Ile	Ala	Ile	Lys	Ile	Lys	Asn	Phe	Met	Ser	Gln	Thr		
			380					385					390				
CAC	TTA	GAG	CCT	AAA	GAA	ATC	ATT	AGG	CTT	ATT	GAT	GTG	CAC	CAT	TTA	1313	
His	Leu	Glu	Pro	Lys	Glu	Ile	Ile	Arg	Leu	Ile	Asp	Val	His	His	Leu		
		395						400				405					
TTA	GAG	CCA	CAA	AAT	TTG	AAG	CGA	TTT	ATT	TTA	GAA	AAT	CAA	AAC	AAG	1361	
Leu	Glu	Pro	Gln	Asn	Leu	Lys	Arg	Phe	Ile	Leu	Glu	Asn	Gln	Asn	Lys		
		410				415					420						
ATT	GCA	AGA	GCG	AGT	TTA	GTG	AGT	TTG	GCA	GAA	ATG	TCT	AAT	TCT	AAA	1409	
Ile	Ala	Arg	Ala	Ser	Leu	Val	Ser	Leu	Ala	Glu	Met	Ser	Asn	Ser	Lys		
					430					435					440		
CGC	ATA	GAA	AAA	AGC	GCG	TAT	TTT	ACA	AAC	CCT	TTT	ATT	ATT	AAT	GAA	1457	
Arg	Ile	Glu	Lys	Ser	Ala	Tyr	Phe	Thr	Asn	Pro	Phe	Ile	Ile	Asn	Glu		
				445					450					455			
ATA	GCG	AAG	TTA	TTG	CCA	AGC	TTT	AAA	CAA	GAG	AGT	GTT	ACT	ATT	ATA	1505	
Ile	Ala	Lys	Leu	Leu	Pro	Ser	Phe	Lys	Gln	Glu	Ser	Val	Thr	Ile	Ile		
			460				465						470				
GAG	CCA	AGT	GCA	GGG	TGT	GGG	AAT	TTC	TTA	AGT	GCT	CTT	TTT	AAA	AAA	1553	
Glu	Pro	Ser	Ala	Gly	Cys	Gly	Asn	Phe	Leu	Ser	Ala	Leu	Phe	Lys	Lys		
		475					480					485					
TAC	ACT	TCT	GTT	AAA	AAA	GTT	TAT	TTA	AAG	TGT	ATA	GAT	ATT	GAT	AAA	1601	
Tyr	Thr	Ser	Val	Lys	Lys	Val	Tyr	Leu	Lys	Cys	Ile	Asp	Ile	Asp	Lys		
		490				495					500						
AAT	AGT	TTA	GAA	ATT	TTA	GAG	ATT	TTA	TAT	AAA	GAT	TGC	ATT	CCT	AAC	1649	
Asn	Ser	Leu	Glu	Ile	Leu	Glu	Ile	Leu	Tyr	Lys	Asp	Cys	Ile	Pro	Asn		
		505			510					515					520		
AAT	TTT	GAG	ATG	GAA	TTG	ATT	TGC	AAA	GAT	TTT	CTA	GCC	TAT	GAA	TGC	1697	
Asn	Phe	Glu	Met	Glu	Leu	Ile	Cys	Lys	Asp	Phe	Leu	Ala	Tyr	Glu	Cys		
				525					530					535			

90	95	100	
AAG AAA AAC GAT GAG ATC AAA CGG AAT TCT TTG GTG GTT GAA AGC ATT			449
Lys Lys Asn Asp Glu Ile Lys Arg Asn Ser Leu Val Val Glu Ser Ile			
105	110	115	120
GAT TTG ATC AAA CAA ATC AAA CCC AGA TTT TTT ATT TTA GAA AAT GTC			497
Asp Leu Ile Lys Gln Ile Lys Pro Arg Phe Phe Ile Leu Glu Asn Val			
	125	130	135
CCT AGT TTT TAT AAA ACA GGT TGT ATA GAC AAA AAT GAT AAT TTG CTA			545
Pro Ser Phe Tyr Lys Thr Gly Cys Ile Asp Lys Asn Asp Asn Leu Leu			
	140	145	150
GAA ATA GGA TCT ATG ATA GAG CAA AAT TTG AGT GGC GAT TAT ATG CTC			593
Glu Ile Gly Ser Met Ile Glu Gln Asn Leu Ser Gly Asp Tyr Met Leu			
	155	160	165
TAT GAT GAG GTA ATC AAT TTT AAA AAT TTT GGA GCT AAT TCA AGC CGA			641
Tyr Asp Glu Val Ile Asn Phe Lys Asn Phe Gly Ala Asn Ser Ser Arg			
	170	175	180
ACA AGA ACT TTA GTG ATA GGG GTT TGT AAA GAG TTT AAA GAT TTT ATA			689
Thr Arg Thr Leu Val Ile Gly Val Cys Lys Glu Phe Lys Asp Phe Ile			
	185	190	195
AGC GCG TTA GAA TTT TTT CCT GAT TTC AAA CAA GAA AAA ACC TTA AAA			737
Ser Ala Leu Glu Phe Phe Pro Asp Phe Lys Gln Glu Lys Thr Leu Lys			
	205	210	215
GAA GTG ATA GGA TCG TTA AAA CCA CTT GCT TGG GGC GAG TAT GAC AAC			785
Glu Val Ile Gly Ser Leu Lys Pro Leu Ala Trp Gly Glu Tyr Asp Asn			
	220	225	230
ACG GAT TTT TAT CAT AGT TTT AGA ACT TAT CCA AAG CAT ATG CAA GAA			833
Thr Asp Phe Tyr His Ser Phe Arg Thr Tyr Pro Lys His Met Gln Glu			
	235	240	245
TGG ATT AAG GAT TTA AAA GAA GGA CAA AGC GCG TTT GAG AAT ACA GAA			881
Trp Ile Lys Asp Leu Lys Glu Gly Gln Ser Ala Phe Glu Asn Thr Glu			
	250	255	260
TTA AAC AAA AAA CCT CAT AGA ATT GTT GGC AGT AAG ATT GTC TTA AAT			929
Leu Asn Lys Lys Pro His Arg Ile Val Gly Ser Lys Ile Val Leu Asn			
	265	270	275
GTT TCT AAA AAT GGC GAT AAA TAT AAA AGA CAA AAA TAT CAT AGC GTT			977
Val Ser Lys Asn Gly Asp Lys Tyr Lys Arg Gln Lys Tyr His Ser Val			
	285	290	295
GCC CCT TGC ATT CAT ACA AGA AAC GAC CAA ATG GCT AGC CAA AAC ACG			1025
Ala Pro Cys Ile His Thr Arg Asn Asp Gln Met Ala Ser Gln Asn Thr			
	300	305	310
ATC CAC CCC AAA GAT GAT AGA GTG TTT TCC ATT AGA GAG CTG ATG CTT			1073

```

      370              375              380
Leu Lys Val Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp
385              390              395              400
Pro Ser Trp Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys
      405              410              415
Leu Lys Phe

```

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 90...2558
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

```

TAAAGAGGCT TTTGAAACCA TGCTTAAAGA AATTGAGAGC TTGAAACATT AATGCTTCAA      60
ATGAATTTGG TTTAATCCTT AATCCCCCTT ATG CTC TTT GAT CAA ACC TTA ACC      113
                               Met Leu Phe Asp Gln Thr Leu Thr
                               1              5

TAT ATT TCT TTA TTT TCT GGG GCA GGA GTG GGG TGC TAT GGG CTT TTA      161
Tyr Ile Ser Leu Phe Ser Gly Ala Gly Val Gly Cys Tyr Gly Leu Leu
10              15              20

GAA GAG GGG TTT GAA TGC GTT GCT ACC AAT GAA ATT TTA GAA AAA CGC      209
Glu Glu Gly Phe Glu Cys Val Ala Thr Asn Glu Ile Leu Glu Lys Arg
25              30              35              40

TTG AAT ATC CAA AGG ATT AAT CGC AAA TGC AAA TTA GAT GAA AGC TAC      257
Leu Asn Ile Gln Arg Ile Asn Arg Lys Cys Lys Leu Asp Glu Ser Tyr
45              50              55

ATT AGT GGG GAC ATT AAA AAG CCA GAA ACA AAA GAA AAA ATT TTA AAG      305
Ile Ser Gly Asp Ile Lys Lys Pro Glu Thr Lys Glu Lys Ile Leu Lys
60              65              70

CAA ATT GAA TTT TAT TCT AAA AAA TTT GGT AAT GAT AGG GTT GAT TTA      353
Gln Ile Glu Phe Tyr Ser Lys Lys Phe Gly Asn Asp Arg Val Asp Leu
75              80              85

GTG GTA GCA ACC CCA CCT TGT CAA GGC ATG AGC GTA GCC AAT CAT AAG      401
Val Val Ala Thr Pro Pro Cys Gln Gly Met Ser Val Ala Asn His Lys

```

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

```

Met Lys Glu Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp
 1           5           10           15
Ile Arg Lys Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro
          20           25           30
Asp Val Leu Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys
          35           40           45
Asn Ile Gly Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr
          50           55           60
Thr Asn Glu Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser
          65           70           75           80
Asp Phe Ser Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys
          85           90           95
Leu Leu Ala Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg
          100          105          110
Asn Ile Tyr Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln
          115          120          125
Arg Glu Thr Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val
          130          135          140
Leu Met Asp Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys
          145          150          155          160
Gln Asp Thr Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe
          165          170          175
Thr Ile Asn Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile
          180          185          190
Phe Thr Lys Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly
          195          200          205
Thr Arg Lys Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu
          210          215          220
Asn Tyr Asn Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr
          225          230          235          240
Thr Arg Gln Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser
          245          250          255
Asn Tyr Leu Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp
          260          265          270
Arg Phe Asn Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser
          275          280          285
Gln Ala Thr Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile
          290          295          300
Ile Ala Asn Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His
          305          310          315          320
Phe Ile Tyr Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp
          325          330          335
Phe Gln Tyr Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp
          340          345          350
Thr Gln Gly Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met
          355          360          365
Gly Leu Lys Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu

```


CGT ATC AAT TGG CGA GAT ATA GGA AAA GAT AAA AAT ACC ACC AGA CAA	777
Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr Thr Arg Gln	
230 235 240	
GAA TAC GAT CTT ATA AAC TCT AAA AGG ATT GCT AAT TCT AAC TAT CTT	825
Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser Asn Tyr Leu	
245 250 255	
ATT TCA AAA GCT AAG AAA GTG GTG AAA CGA TAT AAT GAT AGA TTT AAT	873
Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp Arg Phe Asn	
260 265 270 275	
AAT TCT CTC TCT GAA GTA AAA CAA GAA AAA GAA GAG TCG CAA GCC ACA	921
Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser Gln Ala Thr	
280 285 290	
CAA ATA CAC CAT ATT TTT CCC ATC CAA GAC TTT CCC ATT ATT GCT AAC	969
Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile Ile Ala Asn	
295 300 305	
TAT ATA GAG AAT CTT ATC GCA CTC ACT CCT AAT CAA CAT TTT ATT TAC	1017
Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His Phe Ile Tyr	
310 315 320	
GCC CAC CCT AAT AAT CAA ACC CGC TTG ATT GAT AAA GAT TTT CAA TAT	1065
Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp Phe Gln Tyr	
325 330 335	
ATC TGC TTA TTA GCT AAA ACG ACC ACA ATT CTT AAT GAC ACT CAA GGC	1113
Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp Thr Gln Gly	
340 345 350 355	
GTA TAT GAT TGG AAT GAT TAT ATT GTT GTG TTG AAT ATG GGC CTC AAA	1161
Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met Gly Leu Lys	
360 365 370	
ACA ACT ATC TTT TCT CAA GTC AAG AAC GAA TGG GAA TTA TTA AAA GTA	1209
Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu Leu Lys Val	
375 380 385	
ATA GAT GCT TTT TAT TTT GAT TTT AAC AAG AGC AAA GAT CCA AGT TGG	1257
Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp Pro Ser Trp	
390 395 400	
TCA TAC TTG CTA GAT AAA AAC GAT TTA AGA GCT TTC AAG CTA AAA TTT T	1306
Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys Leu Lys Phe	
405 410 415	
AATAAGTTTT ATTGAACTG GCTATAAAAA CCCGCTTGAC TTATCTTATC CTTTT	1361

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 amino acids

(B) TYPE: amino acid

CAA TCA ATG ATT GAT TTT TTA AAA CTT AGA GAT TAT GAC ATT AGA AAA Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp Ile Arg Lys 5 10 15	105
ACA CAA AAT GCG CGA TGG ATA GAT CAA AAA TGC ACC CCT GAT GTG TTG Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro Asp Val Leu 20 25 30 35	153
TCT CTT GTT GCT GAT TGT ATT TTA GAG TTT ACG CAA TGT AAT ATT GGA Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys Asn Ile Gly 40 45 50	201
AAA TCA TTT TCT ATT AGG GAT ATT TGG GAT AGC CCT TAC ACC AAT GAA Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr Thr Asn Glu 55 60 65	249
AAT GTT AAA ATG ATT TTT TCT AAA CCT GAT TTA AAT TCT GAC TTT TCC Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser Asp Phe Ser 70 75 80	297
ATG CAT GAA TAC GAT AAG TTT TTT TCT CAG CCT ATT AAA TTA TTA GCC Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys Leu Leu Ala 85 90 95	345
TAT AGC GGT ATT TTA TTT GAA ACA AAA ACT GGC AAT AGA AAT ATT TAT Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg Asn Ile Tyr 100 105 110 115	393
ACC ATA CAA AAC ATA GAG CTA TTA GAA TAT CTC ATG CAA AGA GAA ACA Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln Arg Glu Thr 120 125 130	441
AAC GCT TTG AAA TTC CTT ATT TTA TAT ATT CAA AAG GTA TTA ATG GAT Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val Leu Met Asp 135 140 145	489
AGT GGG ATT TAT CCT TTA TTT GAC AAC TTT TTA CAA AAA CAA GAC ACA Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys Gln Asp Thr 150 155 160	537
GAA AGT TTT AAG CAA CTA AAA GAT GGT TTC ACT CAT TTT ACT ATC AAT Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe Thr Ile Asn 165 170 175	585
AAC ACA GCA ATC AAT AAC GCT ACG GAA TGT TTT AGG ATT TTT ACT AAA Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile Phe Thr Lys 180 185 190 195	633
ATT ATC AAT CCT TTA GCT TTT TAT TAT GGT AAA AAA GGC ACA AGA AAA Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly Thr Arg Lys 200 205 210	681
GGG TAT TTG TCC AAC ACT ATA ATT ACA AAA GAT GAG CTT AAT TAT AAT Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu Asn Tyr Asn 215 220 225	729

```

Ala Lys Gly Tyr Phe Leu Glu Glu Ile Lys Glu Arg Leu Asn Ala Leu
 130                      135                      140
Gly Tyr Gln Leu Ser Tyr Gln Ile Leu Asn Ala Lys Asp Tyr Gly Val
 145                      150                      155                      160
Pro Gln Asn Arg Glu Arg Ala Phe Ile Val Gly Ala Ser Arg Phe Ser
                      165                      170                      175
Phe Asp Phe Asn Leu Leu Glu Pro Ser Gln Ser Val Asn Val Gln Asp
                      180                      185                      190
Ala Ile Ser Asp Leu Ala Tyr Leu Cys Ser Asn Glu Gly Ala Phe Glu
                      195                      200                      205
Ser Asp Tyr Leu Asn Pro Ile Gln Ser Ser Tyr Gln Ala Leu Met Arg
                      210                      215                      220
Lys Asp Ser Pro Lys Leu Tyr Asn His Gln Ala Thr Asn His Ser Gln
 225                      230                      235                      240
Ala Ala Leu Glu Lys Leu Lys Leu Ile Asn Lys Glu Gln Gly Lys Glu
                      245                      250                      255
Cys Leu Pro Lys Asn Leu His Gly Lys Gln Gln Phe Lys Ser Thr Trp
                      260                      265                      270
Gly Arg Leu Asn Trp Asn Lys Ile Ser Pro Thr Ile Asp Thr Arg Phe
                      275                      280                      285
Asp Thr Pro Ser Asn Gly Thr Asn Ser His Pro Glu Leu His Arg Ser
                      290                      295                      300
Ile Thr Pro Arg Glu Ala Ala Arg Ile Gln Ser Phe Ser Asp Asn Tyr
 305                      310                      315                      320
Ile Phe Tyr Gly Asn Lys Thr Ser Val Cys Lys Gln Ile Gly Asn Ala
                      325                      330                      335
Val Pro Pro Leu Leu Ala Leu Ala Leu Gly Lys Ala Ile Leu Lys Ser
                      340                      345                      350
Leu Arg Lys
                      355

```

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1305
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

TATTGATAGC ATGAGTTGTT TTTGGTTTGG AATTTTAAGG AGTAGCTT ATG AAA GAG
Met Lys Glu

57

1

```

Gly Arg Leu Asn Trp Asn Lys Ile Ser Pro Thr Ile Asp Thr Arg Phe
    275                                280                                285

GAC ACT CCC AGC AAT GGC ACC AAC TCC CAC CCC GAA TTG CAC CGC TCT      971
Asp Thr Pro Ser Asn Gly Thr Asn Ser His Pro Glu Leu His Arg Ser
    290                                295                                300

ATC ACG CCT AGA GAA GCC GCT AGG ATA CAA AGT TTT AGC GAT AAT TAT      1019
Ile Thr Pro Arg Glu Ala Ala Arg Ile Gln Ser Phe Ser Asp Asn Tyr
    305                                310                                315                                320

ATC TTT TAT GGC AAT AAA ACG AGC GTT TGT AAG CAA ATC GGT AAC GCT      1067
Ile Phe Tyr Gly Asn Lys Thr Ser Val Cys Lys Gln Ile Gly Asn Ala
    325                                330                                335

GTG CCT CCT CTT CTA GCC CTA GCC TTA GGC AAA GCG ATC TTA AAA AGC      1115
Val Pro Pro Leu Leu Ala Leu Ala Leu Gly Lys Ala Ile Leu Lys Ser
    340                                345                                350

TTA AGA AAA TGATACAAAT TTATCACGCT GACGCTTTTG AAATCATCAA AGACTTTTAC      1174
Leu Arg Lys
    355

CAGCAAAA                                                                1181

```

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

```

Met Asn Tyr Lys Ile Leu Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser
  1          5          10          15
Ala Gly Leu Glu Cys Leu Glu Glu Phe Asp Ala Leu Ile Gly Leu Asp
    20          25          30
Cys Asp Lys Gln Ala Leu Ile Thr Phe Glu Asn Asn His Lys Asn Ala
    35          40          45
Ile Gly Val Cys Gly Asp Ile Thr Gln Thr Glu Ile Lys Glu Lys Val
    50          55          60
Ile Lys Leu Ala Lys Lys Leu Glu Ile Asn Met Ile Ile Gly Gly Pro
    65          70          75          80
Pro Cys Gln Gly Phe Ser Asn Lys Gly Lys Asn Leu Gly Leu Lys Asp
    85          90          95
Pro Arg Asn Phe Leu Phe Leu Glu Tyr Ile Glu Ile Val Lys Ala Ile
    100         105         110
Lys Pro Glu Ile Phe Ile Ile Glu Asn Val Lys Asn Leu Ile Ser Cys
    115         120         125

```

50	55	60	
ATC AAA CTA GCT AAA AAA TTA GAA ATC AAC ATG ATC ATT GGC GGG CCT Ile Lys Leu Ala Lys Lys Leu Glu Ile Asn Met Ile Ile Gly Gly Pro 65 70 75 80			299
CCA TGT CAA GGC TTT TCT AAT AAA GGG AAA AAT TTA GGG CTA AAA GAC Pro Cys Gln Gly Phe Ser Asn Lys Gly Lys Asn Leu Gly Leu Lys Asp 85 90 95			347
CCT AGG AAT TTT TTA TTC TTA GAA TAT ATA GAA ATA GTC AAA GCC ATA Pro Arg Asn Phe Leu Phe Leu Glu Tyr Ile Glu Ile Val Lys Ala Ile 100 105 110			395
AAG CCA GAA ATT TTT ATC ATT GAA AAC GTG AAA AAC CTC ATC TCT TGC Lys Pro Glu Ile Phe Ile Ile Glu Asn Val Lys Asn Leu Ile Ser Cys 115 120 125			443
GCT AAA GGC TAT TTT TTA GAA GAA ATT AAA GAA AGG TTG AAC GCT TTA Ala Lys Gly Tyr Phe Leu Glu Glu Ile Lys Glu Arg Leu Asn Ala Leu 130 135 140			491
GGG TAT CAA TTG AGC TAT CAA ATC CTA AAC GCT AAA GAT TAT GGC GTG Gly Tyr Gln Leu Ser Tyr Gln Ile Leu Asn Ala Lys Asp Tyr Gly Val 145 150 155 160			539
CCT CAA AAC AGA GAG AGA GCC TTT ATT GTA GGG GCT AGT CGT TTC AGT Pro Gln Asn Arg Glu Arg Ala Phe Ile Val Gly Ala Ser Arg Phe Ser 165 170 175			587
TTT GAT TTC AAT CTT TTA GAG CCT TCT CAA AGC GTG AAT GTT CAA GAT Phe Asp Phe Asn Leu Leu Glu Pro Ser Gln Ser Val Asn Val Gln Asp 180 185 190			635
GCC ATA AGC GAT TTA GCC TAT CTT TGT TCT AAT GAG GGG GCG TTT GAG Ala Ile Ser Asp Leu Ala Tyr Leu Cys Ser Asn Glu Gly Ala Phe Glu 195 200 205			683
AGC GAT TAT TTA AAC CCT ATC CAA TCA AGC TAT CAA GCT TTA ATG CGA Ser Asp Tyr Leu Asn Pro Ile Gln Ser Ser Tyr Gln Ala Leu Met Arg 210 215 220			731
AAA GAT AGC CCT AAA TTA TAC AAC CAT CAA GCC ACC AAC CAC TCG CAA Lys Asp Ser Pro Lys Leu Tyr Asn His Gln Ala Thr Asn His Ser Gln 225 230 235 240			779
GCC GCT TTA GAG AAA TTA AAA CTC ATT AAC AAA GAA CAA GGC AAA GAA Ala Ala Leu Glu Lys Leu Lys Leu Ile Asn Lys Glu Gln Gly Lys Glu 245 250 255			827
TGC TTG CCT AAA AAC TTG CAT GGC AAA CAG CAA TTC AAA AGC ACA TGG Cys Leu Pro Lys Asn Leu His Gly Lys Gln Gln Phe Lys Ser Thr Trp 260 265 270			875
GGG CGC CTG AAT TGG AAT AAA ATC AGC CCC ACC ATA GAC ACA CGA TTT			923

		100						105					110				
Pro	Met	Pro	Arg	Asn	Ile	His	Arg	Arg	Tyr	Val	Gln	Asp	Thr	Glu	Phe		
		115						120					125				
Ala	Leu	Trp	Ala	Val	Lys	Lys	Lys	Ala	Lys	Trp	Val	Phe	Asn	Lys	Pro		
		130						135					140				
Lys	Asn	Glu	Lys	Tyr	Leu	Arg	Pro	Leu	Ile	Leu	Lys	Ser	Pro	Val	Val		
		145				150					155				160		
Ser	Gly	Leu	Glu	Lys	Thr	Lys	His	Pro	Thr	Gln	Lys	Ser	Leu	Ala	Leu		
				165					170						175		
Met	Glu	Lys	Ile	Ile	Ser	Ile	His	Thr	Asn	Pro	Asn	Asp	Ile	Val	Leu		
			180					185					190				
Asp	Pro	Phe	Met	Gly	Ser	Gly	Thr	Thr	Gly	Leu	Ala	Cys	Lys	Asn	Leu		
		195					200					205					
Glu	Arg	Asn	Phe	Ile	Gly	Ile	Glu	Ser	Glu	Lys	Glu	Tyr	Phe	Gln	Thr		
		210				215					220						
Ala	Lys	Lys	Arg	Leu	Asn	Leu	Phe										
		225				230											

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...1124
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

TTGCGTTTTG AAACCGATGA TTTTCAACG CTTATTGATC GTATTTGTGA AAGCTTGAA	59
ATG AAT TAT AAA ATT TTA GAT TTA TTT TGT GGG GCT GGG GGT TTT AGC	107
Met Asn Tyr Lys Ile Leu Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser	
1 5 10 15	
GCT GGG TTA GAG TGT TTA GAA GAG TTT GAC GCT TTA ATA GGG CTA GAT	155
Ala Gly Leu Glu Cys Leu Glu Glu Phe Asp Ala Leu Ile Gly Leu Asp	
20 25 30	
TGC GAT AAA CAA GCC CTA ATC ACT TTT GAA AAC AAC CAT AAA AAC GCC	203
Cys Asp Lys Gln Ala Leu Ile Thr Phe Glu Asn Asn His Lys Asn Ala	
35 40 45	
ATA GGC GTT TGT GGG GAC ATC ACT CAA ACC GAA ATT AAA GAA AAA GTC	251
Ile Gly Val Cys Gly Asp Ile Thr Gln Thr Glu Ile Lys Glu Lys Val	

Phe	Ala	Leu	Trp	Ala	Val	Lys	Lys	Lys	Ala	Lys	Trp	Val	Phe	Asn	Lys		
		130					135					140					
CCC	AAA	AAT	GAA	AAA	TAT	TTA	CGG	CCT	TTG	ATT	TTA	AAA	AGC	CCT	GTG	599	
Pro	Lys	Asn	Glu	Lys	Tyr	Leu	Arg	Pro	Leu	Ile	Leu	Lys	Ser	Pro	Val		
	145					150					155						
GTA	AGC	GGG	CTT	GAA	AAA	ACC	AAA	CAC	CCC	ACG	CAA	AAA	AGC	CTG	GCC	647	
Val	Ser	Gly	Leu	Glu	Lys	Thr	Lys	His	Pro	Thr	Gln	Lys	Ser	Leu	Ala		
160					165					170					175		
TTA	ATG	GAA	AAA	ATC	ATT	TCC	ATC	CAC	ACA	AAC	CCT	AAT	GAC	ATC	GTG	695	
Leu	Met	Glu	Lys	Ile	Ile	Ser	Ile	His	Thr	Asn	Pro	Asn	Asp	Ile	Val		
				180				185						190			
CTA	GAT	CCT	TTC	ATG	GGG	AGC	GGC	ACC	ACC	GGC	TTA	GCG	TGC	AAA	AAT	743	
Leu	Asp	Pro	Phe	Met	Gly	Ser	Gly	Thr	Thr	Gly	Leu	Ala	Cys	Lys	Asn		
			195					200					205				
TTA	GAA	CGG	AAT	TTT	ATC	GGC	ATA	GAA	TCA	GAA	AAA	GAA	TAT	TTT	CAA	791	
Leu	Glu	Arg	Asn	Phe	Ile	Gly	Ile	Glu	Ser	Glu	Lys	Glu	Tyr	Phe	Gln		
	210					215					220						
ACC	GCT	AAA	AAG	CGT	TTG	AAT	CTG	TTT	TAAAAACGCT	ATTTGAATGA	GATTGTG	845					
Thr	Ala	Lys	Lys	Arg	Leu	Asn	Leu	Phe									
	225				230												
TTATAGTTAT	TTAAAAGGAT	ATTTTGA														872	

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

Met	Ile	Gln	Ile	Tyr	His	Ala	Asp	Ala	Phe	Glu	Ile	Ile	Lys	Asp	Phe		
1				5					10					15			
Tyr	Gln	Gln	Asn	Leu	Lys	Val	Asp	Ala	Ile	Ile	Thr	Asp	Pro	Pro	Tyr		
		20						25					30				
Asn	Ile	Ser	Val	Lys	Asn	Asn	Phe	Pro	Thr	Leu	Lys	Ser	Ala	Lys	Arg		
		35					40					45					
Gln	Gly	Ile	Asp	Phe	Gly	Glu	Trp	Asp	Lys	Asn	Phe	Lys	Leu	Leu	Glu		
	50					55					60						
Trp	Ile	Ala	Arg	Tyr	Ala	Pro	Leu	Val	Asn	Pro	Asn	Gly	Cys	Met	Val		
65				70					75					80			
Ile	Phe	Cys	Ser	Tyr	Arg	Phe	Ile	Ser	Tyr	Ile	Ala	Asp	Phe	Leu	Glu		
			85					90						95			
Glu	Asn	Gly	Phe	Val	Val	Lys	Asp	Phe	Ile	Gln	Trp	Val	Lys	Asn	Asn		

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 123...818
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```

AGTTTTAGCG ATAATTATAT CTTTTATGGC AATAAAACGA GCGTTTGTA GCAAATCGGT      60
AACGCTGTGC CTCCTCTTCT AGCCCTAGCC TTAGGCAAAG CGATCTTAAA AAGCTTAAGA      120
AA ATG ATA CAA ATT TAT CAC GCT GAC GCT TTT GAA ATC ATC AAA GAC      167
  Met Ile Gln Ile Tyr His Ala Asp Ala Phe Glu Ile Ile Lys Asp
    1             5             10             15

TTT TAC CAG CAA AAT TTA AAA GTG GAT GCG ATC ATC ACG GAC CCT CCT      215
Phe Tyr Gln Gln Asn Leu Lys Val Asp Ala Ile Ile Thr Asp Pro Pro
           20             25             30

TAT AAC ATT TCG GTT AAA AAC AAT TTT CCC ACC CTA AAG AGC GCT AAA      263
Tyr Asn Ile Ser Val Lys Asn Asn Phe Pro Thr Leu Lys Ser Ala Lys
           35             40             45

AGG CAA GGC ATA GAT TTT GGG GAA TGG GAT AAA AAT TTC AAG CTT TTA      311
Arg Gln Gly Ile Asp Phe Gly Glu Trp Asp Lys Asn Phe Lys Leu Leu
           50             55             60

GAA TGG ATC GCA CGC TAC GCC CCC TTA GTC AAT CCA AAC GGC TGC ATG      359
Glu Trp Ile Ala Arg Tyr Ala Pro Leu Val Asn Pro Asn Gly Cys Met
           65             70             75

GTT ATT TTT TGC TCT TAC AGG TTT ATA AGC TAT ATC GCT GAT TTT TTA      407
Val Ile Phe Cys Ser Tyr Arg Phe Ile Ser Tyr Ile Ala Asp Phe Leu
           80             85             90             95

GAA GAA AAC GGC TTT GTG GTC AAA GAC TTT ATC CAA TGG GTT AAA AAT      455
Glu Glu Asn Gly Phe Val Val Lys Asp Phe Ile Gln Trp Val Lys Asn
           100            105            110

AAT CCC ATG CCA AGA AAC ATT CAC CGG CGT TAT GTC CAA GAC ACG GAA      503
Asn Pro Met Pro Arg Asn Ile His Arg Arg Tyr Val Gln Asp Thr Glu
           115            120            125

TTT GCT CTG TGG GCG GTT AAA AAG AAA GCC AAG TGG GTG TTT AAC AAA      551

```


1	5	10	15	
GAT CAT GGC GAA AGT TTG GGC GAA GAA GCG TTC TAT TTG CAT GGC ATT				338
Asp His Gly Glu Ser Leu Gly Glu Glu Ala Phe Tyr Leu His Gly Ile	20	25	30	
CCT AAA AGC ATC GCC CCC AAA GAA CAA TAC GAG ATC CCC TTT ATC GTT				386
Pro Lys Ser Ile Ala Pro Lys Glu Gln Tyr Glu Ile Pro Phe Ile Val	35	40	45	
TAT GCT AAT GAG CCT TTC AAA GAA AAG CAT TCC ATC ATT CAA ACC CAA				434
Tyr Ala Asn Glu Pro Phe Lys Glu Lys His Ser Ile Ile Gln Thr Gln	50	55	60	
ACC CCC ATT AAT CAA AAT GTG ATT TTC CAT AGC GTT TTA GGG GTG TTT				482
Thr Pro Ile Asn Gln Asn Val Ile Phe His Ser Val Leu Gly Val Phe	65	70	75	
TTG GAT TTT AAA AAC CCA AGC GTT GTT TAT CGC CCT TCT TTA GAT CTG				530
Leu Asp Phe Lys Asn Pro Ser Val Val Tyr Arg Pro Ser Leu Asp Leu	80	85	90	95
CTT AAA CAC AAA AAA GAG TAAAATAACA CGCATGAAAA AATTCTTATT TAAACAAA				586
Leu Lys His Lys Lys Glu	100			
AATTTTGTGA AAGCCTGCCC AAA				609

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Met	Leu	Glu	Asn	Ala	Lys	Gln	Pro	Ala	Leu	Met	Ile	Tyr	Leu	Ser	Asp
1				5					10					15	
His	Gly	Glu	Ser	Leu	Gly	Glu	Glu	Ala	Phe	Tyr	Leu	His	Gly	Ile	Pro
	20							25					30		
Lys	Ser	Ile	Ala	Pro	Lys	Glu	Gln	Tyr	Glu	Ile	Pro	Phe	Ile	Val	Tyr
	35						40					45			
Ala	Asn	Glu	Pro	Phe	Lys	Glu	Lys	His	Ser	Ile	Ile	Gln	Thr	Gln	Thr
	50						55				60				
Pro	Ile	Asn	Gln	Asn	Val	Ile	Phe	His	Ser	Val	Leu	Gly	Val	Phe	Leu
65				70					75					80	
Asp	Phe	Lys	Asn	Pro	Ser	Val	Val	Tyr	Arg	Pro	Ser	Leu	Asp	Leu	Leu
			85					90					95		
Lys	His	Lys	Lys	Glu											
			100												

```

Gln Asn Ala Asp Ala Leu Cys Arg Thr Leu Glu His Val Glu Lys His
195                200                205
Phe Arg Pro Tyr Leu Glu Asn Met Ala Trp Val Asn Phe Gly Gly Gly
210                215                220
His His Ile Thr Lys Ser Asp Tyr Asp Val Asn Leu Leu Ile Gln Thr
225                230                235                240
Ile Lys Asp Phe Lys Glu Arg Tyr His Asn Ile Glu Val Ile Leu Glu
245                250                255
Pro Gly Glu Ala Ile Gly Trp Gln Cys Gly Phe Leu Ile Ala Ser Val
260                265                270
Ile Asp Ile Val Gln Asn Asp Gln Glu Ile Ala Ile Leu Asp Ala Ser
275                280                285
Phe Ser Ala His Met Pro Asp Cys Leu Glu Met Pro Tyr Arg Pro Ser
290                295                300
Ile Phe Lys Val Ser Val Glu Asn Asp Glu Glu Leu Ile Glu Val Glu
305                310                315                320
Lys Gly Glu Asn Gln Gly Ala Phe Ser Tyr Phe Leu Gly Gly Pro Thr
325                330                335
Cys Leu Ala Gly Asp Phe Met Gly Ser Phe Ser Phe Glu Thr Pro Leu
340                345                350
Lys Arg Gly Asp Lys Ile Val Phe Gln Asp Met Leu His Tyr Thr Ile
355                360                365
Val Lys Asn Asn Ser Phe Asn Gly Val Pro Leu Pro Ser Leu Ala Arg
370                375                380
Leu Asp Gln Gln Gly Phe Lys Ile Leu Lys Asn Phe Ser Tyr Glu Asp
385                390                395                400
Tyr Lys Asn Arg Asn
405

```

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 246...548
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

```

GAATCTTTAC TTTATAATTT GCCTGACCTT TTAAAGAAGC ACTCTAATGA AAATGTCTTG      60
CTCATCTTAC ACTTGCAGGC TCGCATGGCC CAACTACGA CAACAAAGTG CCTTTAAATT      120
TTAGGGTGTT TAAGCCTTAT TGCTCAAGCG CTGATCTGTC TTCTTGCTCC AAAGAAAGCC      180
TGATTAACGC CTATGACAAC ACCATTTTTT ACAACGACTA TCTGCTAGAT CGAAAGATCA      240
TTAGC ATG CTT GAA AAC GCC AAG CAG CCC GCC TTA ATG ATC TAT TTA AGC      290
Met Leu Glu Asn Ala Lys Gln Pro Ala Leu Met Ile Tyr Leu Ser

```

GAA ACG CCT TTA AAA AGG GGC GAT AAA ATC GTG TTT CAA GAC ATG CTC 1168
 Glu Thr Pro Leu Lys Arg Gly Asp Lys Ile Val Phe Gln Asp Met Leu
 350 355 360

CAT TAT ACG ATT GTC AAA AAC AAC TCG TTT AAT GGC GTG CCG CTC CCA 1216
 His Tyr Thr Ile Val Lys Asn Asn Ser Phe Asn Gly Val Pro Leu Pro
 365 370 375 380

AGC CTG GCT AGA TTG GAT CAA CAA GGG TTT AAA ATC CTT AAA AAC TTT 1264
 Ser Leu Ala Arg Leu Asp Gln Gln Gly Phe Lys Ile Leu Lys Asn Phe
 385 390 395

TCT TAT GAA GAC TAT AAA AAC AGA AAC TAAAGCTTTT GATTAAGGCT TTTTGGG 1318
 Ser Tyr Glu Asp Tyr Lys Asn Arg Asn
 400 405

GCTTGTA AAA AGNTTACGCA CAACATTCCA AC 1350

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Lys Lys Tyr Ser Thr Ile Pro Thr Pro Cys Tyr Val Leu Glu Ser
 1 5 10 15
 Glu Arg Leu Glu Lys Asn Ala Lys Ile Leu Glu Ile Val Arg Gln Gln
 20 25 30
 Ser Gly Ala Lys Val Leu Leu Ala Leu Lys Gly Tyr Ala Phe Trp Arg
 35 40 45
 Glu Phe Gly Ile Leu Arg Gln Lys Leu Asn Gly Cys Cys Ala Ser Gly
 50 55 60
 Leu Tyr Glu Ala Lys Leu Ala Phe Glu Glu Phe Gly Gly Arg Glu Ser
 65 70 75 80
 His Lys Glu Ile Cys Val Tyr Ser Pro Ala Phe Lys Glu Ala Glu Met
 85 90 95
 Ser Ala Ile Leu Pro Leu Ala Thr Ser Ile Ile Phe Asn Ser Phe Tyr
 100 105 110
 Gln Tyr Ala Thr Tyr Lys Asp Arg Ile Leu Asp Lys Asn Lys Gln Leu
 115 120 125
 Glu Asn Leu Gly Leu Ser Pro Ile Lys Met Gly Leu Arg Ile Asn Pro
 130 135 140
 Leu Tyr Ser Glu Val Thr Pro Ala Ile Tyr Asn Pro Cys Ser Lys Val
 145 150 155 160
 Ser Arg Leu Gly Ile Thr Pro Ser Gly Phe Glu Lys Gly Val Lys Glu
 165 170 175
 His Gly Leu Glu Gly Val Ser Gly Leu His Phe His Thr His Cys Glu
 180 185 190

AAC AAG CAA TTA GAA AAC TTG GGC TTA AGC CCC ATT AAA ATG GGT TTG	496
Asn Lys Gln Leu Glu Asn Leu Gly Leu Ser Pro Ile Lys Met Gly Leu	
125 130 135 140	
AGG ATA AAC CCT CTC TAT AGC GAA GTA ACC CCA GCG ATC TAT AAC CCA	544
Arg Ile Asn Pro Leu Tyr Ser Glu Val Thr Pro Ala Ile Tyr Asn Pro	
145 150 155	
TGC TCT AAA GTG AGC CGG TTA GGG ATT ACG CCT AGC GGA TTT GAA AAG	592
Cys Ser Lys Val Ser Arg Leu Gly Ile Thr Pro Ser Gly Phe Glu Lys	
160 165 170	
GGG GTG AAA GAG CAT GGC TTA GAG GGG GTG AGC GGG TTG CAT TTC CAT	640
Gly Val Lys Glu His Gly Leu Glu Gly Val Ser Gly Leu His Phe His	
175 180 185	
ACG CAT TGC GAG CAA AAC GCT GAC GCT TTG TGC CGG ACT TTA GAG CAT	688
Thr His Cys Glu Gln Asn Ala Asp Ala Leu Cys Arg Thr Leu Glu His	
190 195 200	
GTA GAA AAG CAT TTC AGG CCC TAT TTA GAA AAC ATG GCG TGG GTG AAT	736
Val Glu Lys His Phe Arg Pro Tyr Leu Glu Asn Met Ala Trp Val Asn	
205 210 215 220	
TTT GGT GGG GGG CAT CAT ATC ACT AAG AGC GAT TAT GAT GTG AAT TTG	784
Phe Gly Gly Gly His His Ile Thr Lys Ser Asp Tyr Asp Val Asn Leu	
225 230 235	
CTC ATC CAA ACG ATT AAG GAT TTC AAA GAA CGC TAT CAT AAT ATA GAA	832
Leu Ile Gln Thr Ile Lys Asp Phe Lys Glu Arg Tyr His Asn Ile Glu	
240 245 250	
GTG ATT TTA GAG CCT GGG GAA GCC ATA GGG TGG CAA TGC GGG TTT TTA	880
Val Ile Leu Glu Pro Gly Glu Ala Ile Gly Trp Gln Cys Gly Phe Leu	
255 260 265	
ATC GCA AGC GTG ATA GAC ATC GTT CAA AAC GAT CAA GAA ATT GCG ATT	928
Ile Ala Ser Val Ile Asp Ile Val Gln Asn Asp Gln Glu Ile Ala Ile	
270 275 280	
CTA GAC GCT TCT TTT AGC GCT CAC ATG CCC GAT TGC TTA GAA ATG CCT	976
Leu Asp Ala Ser Phe Ser Ala His Met Pro Asp Cys Leu Glu Met Pro	
285 290 295 300	
TAT CGC CCT AGC ATT TTT AAA GTC TCC GTA GAA AAT GAT GAA GAG CTT	1024
Tyr Arg Pro Ser Ile Phe Lys Val Ser Val Glu Asn Asp Glu Glu Leu	
305 310 315	
ATT GAA GTT GAA AAG GGC GAA AAT CAA GGG GCG TTT TCT TAT TTT TTA	1072
Ile Glu Val Glu Lys Gly Glu Asn Gln Gly Ala Phe Ser Tyr Phe Leu	
320 325 330	
GGC GGC CCT ACT TGT TTA GCG GGG GAT TTT ATG GGG AGT TTT AGC TTT	1120
Gly Gly Pro Thr Cys Leu Ala Gly Asp Phe Met Gly Ser Phe Ser Phe	
335 340 345	

Lys Ala Pro Ser Leu Ala Asn Trp Phe Met Gly Ile Phe

65 70 75
85 90

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 77...1291
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

TGAAGGCCGA	60	60	TGATTTTCA	112	112	TCCAACTCT	160	160	ACCCCAAAGA	208	208	CATCCAGCGA	256	256	GTGGTTAAGC	304	304				
AATTTTTTGA	112	112	ATTAGC	160	160	ATG AAA	208	208	AAA TAC	256	256	AGC ACT	304	304	ATC CCC	352	352	ACC CCT	400	400	TGC TAC
			Met			Lys Lys			Tyr Ser		Thr Ile		Pro Thr		Pro Cys		Tyr				
			1						5				10								
GTG TTA	160	160	GAG AGC	208	208	GAA CGC	256	256	TTA GAA	304	304	AAA AAC	352	352	GCC AAG	400	400	ATT TTA	448	448	GAA ATC
Val Leu	208	208	Glu Ser	256	256	Glu Arg	304	304	Leu Glu	352	352	Lys Asn	400	400	Ala Lys	448	448	Ile Leu	496	496	Glu Ile
			15						20						25						
GTG CGC	208	208	CAA CAA	256	256	AGT GGG	304	304	GCA AAG	352	352	GTC TTG	400	400	CTT GCT	448	448	TTA AAG	496	496	GGG TAT
Val Arg	256	256	Gln Gln	304	304	Ser Gly	352	352	Ala Lys	400	400	Val Leu	448	448	Leu Leu	496	496	Ala Lys	544	544	Gly Tyr
			30						35						40						
GCG TTT	256	256	TGG CGT	304	304	GAG TTT	352	352	GGG ATT	400	400	TTG AGG	448	448	CAA AAA	496	496	TTG AAC	544	544	GGG TGT
Ala Phe	304	304	Trp Arg	352	352	Glu Phe	400	400	Gly Ile	448	448	Leu Arg	496	496	Gln Lys	544	544	Leu Asn	592	592	Gly Cys
			45			50						55									60
TGC GCG	304	304	AGC GGT	352	352	CTT TAT	400	400	GAG GCT	448	448	AAG CTC	496	496	GCT TTT	544	544	GAA GAA	592	592	TTT GGG
Cys Ala	352	352	Ser Gly	400	400	Leu Tyr	448	448	Glu Ala	496	496	Lys Leu	544	544	Ala Phe	592	592	Glu Glu	640	640	Phe Gly
				65								70						75			
GGG CGA	352	352	GAG AGC	400	400	CAC AAA	448	448	GAA ATT	496	496	TGC TGC	544	544	TAT AGC	592	592	CCG GCT	640	640	TTC AAA
Gly Arg	400	400	Glu Ser	448	448	His Lys	496	496	Glu Ile	544	544	Cys Val	592	592	Tyr Tyr	640	640	Ser Pro	688	688	Ala Phe
				80								85						90			
GAG GCT	400	400	GAA ATG	448	448	AGC GCG	496	496	ATT TTA	544	544	CCC CTA	592	592	GCG ACA	640	640	AGC ATT	688	688	ATT TTT
Glu Ala	448	448	Glu Met	496	496	Ser Ala	544	544	Ile Leu	592	592	Pro Leu	640	640	Ala Thr	688	688	Ser Ile	736	736	Ile Phe
				95								100						105			
AAC TCT	448	448	TTT TAC	496	496	CAA TAC	544	544	GCT ACC	592	592	TAT TAT	640	640	AAA GAC	688	688	AGG ATT	736	736	TTA GAT
Asn Ser	496	496	Phe Tyr	544	544	Gln Tyr	592	592	Ala Thr	640	640	Tyr Tyr	688	688	Lys Asp	736	736	Arg Ile	784	784	Leu Asp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

```

TAAAGATAAA AACCACCCCT TTTGACCCCC TTTTAGAGGA TTTTATGGT TTTTGTGAGA      60
TAATAAAGAC TTATAAAGTT AATTAAAATT AAACAGAAGG GTTTTG ATG TCC GCT      115
                                     Met Ser Ala
                                     1

CAT TTT TTA AAA ATC GTT TTT TTA GTA GGC ATG TGC GTT TCA AGT TTG      163
His Phe Leu Lys Ile Val Phe Leu Val Gly Met Cys Val Ser Ser Leu
   5                10                15

TTC GCT GAA GGT TTA GAG GGG TTT TTT AAC GCC CTA GAA GCC CAG CTC      211
Phe Ala Glu Gly Leu Glu Gly Phe Phe Asn Ala Leu Glu Ala Gln Leu
  20                25                30                35

AAA AGC CCC ATC GCT AAG GGG ATT TTA ATG GTG ATT TTC ATA GGG ATC      259
Lys Ser Pro Ile Ala Lys Gly Ile Leu Met Val Ile Phe Ile Gly Ile
                40                45                50

GCT ATT TAT GTG TGG AGG AAT TTG GAC CGG TGG AAA GAG ATC TTA TTC      307
Ala Ile Tyr Val Trp Arg Asn Leu Asp Arg Trp Lys Glu Ile Leu Phe
   55                60                65

ACG ATC CTT GGC GTG GTG TTT GGG ATT TTT TTA TTC TTT AAA GCT CCG      355
Thr Ile Leu Gly Val Val Phe Gly Ile Phe Leu Phe Phe Lys Ala Pro
   70                75                80

AGT TTA GCG AAT TGG TTT ATG GGA ATT TTT TAATGATTAT CCTGTCAGCG AGC      408
Ser Leu Ala Asn Trp Phe Met Gly Ile Phe
   85                90

GTGAAGAATT TCGTGAAAT TTCGGTTAAA GAAAAATTTT TA      450

```

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

```

Met Ser Ala His Phe Leu Lys Ile Val Phe Leu Val Gly Met Cys Val
  1                5                10                15
Ser Ser Leu Phe Ala Glu Gly Leu Glu Gly Phe Phe Asn Ala Leu Glu
   20                25                30
Ala Gln Leu Lys Ser Pro Ile Ala Lys Gly Ile Leu Met Val Ile Phe
   35                40                45
Ile Gly Ile Ala Ile Tyr Val Trp Arg Asn Leu Asp Arg Trp Lys Glu
   50                55                60
Ile Leu Phe Thr Ile Leu Gly Val Val Phe Gly Ile Phe Leu Phe Phe

```

160

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

```

Met Gly Asn Val Asn Pro Pro Lys Thr Ser Tyr Lys Glu Ser Leu Ser
 1           5           10           15
Thr Ile Ala Ser Ile Glu Tyr Ala Ile Ala His Val Gly Val Gln Asn
          20           25           30
Leu Ile Ile Cys Gly His Ser Asp Cys Gly Ala Cys Gly Ser Val His
          35           40           45
Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile Ala Asn
          50           55           60
Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn His Pro
65           70           75           80
Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu Arg Leu
          85           90           95
Asn Ala Arg Leu Gln Leu Asn Asn Leu Leu Ser Tyr Asp Phe Ile Gln
          100          105          110
Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His Tyr Ile
          115          120          125
Ile Glu Thr Gly Arg Ile Tyr Asn Tyr Asn Phe Glu Ser His Phe Phe
          130          135          140
Glu Pro Ile Gly Glu Thr Ile Lys Gln Arg Lys Ser His Glu Asn Phe
145          150          155          160

```

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 107...385
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 250...729
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

```

TTTAGCTATG ATAAGCGTTT TAAAAACAAA CGAATTTTAA TCAAAATGAG ATTTAAGGGT      60
TAAAGAGTGA AAGCGTTTTT AGGAGCGTTA GAGTTTCAAG AGAATGAATA TGAAGAGCTT      120
AAAGAGCTTT ATGAGAGCTT AAAAACCAAG CAAAAGCCCC ACACTTTGTT CATTTCTTGT      180
GTGGATTACAC GAGTCGTGCC TAATTTAATC ACTGGCACCA AACCGGGCGA ATTGTATGTG      240
ATTTGCAAC ATG GGC AAT GTG AAC CCC CCT AAA ACA AGC TAT AAA GAG TCC      291
    Met Gly Asn Val Asn Pro Pro Lys Thr Ser Tyr Lys Glu Ser
        1             5             10

CTT TCT ACC ATT GCG AGC ATT GAA TAC GCT ATC GCG CAT GTG GGC GTT      339
Leu Ser Thr Ile Ala Ser Ile Glu Tyr Ala Ile Ala His Val Gly Val
    15             20             25             30

CAA AAC TTA ATC ATT TGC GGG CAT AGC GAT TGT GGG GCT TGC GGG AGC      387
Gln Asn Leu Ile Ile Cys Gly His Ser Asp Cys Gly Ala Cys Gly Ser
        35             40             45

GTT CAT TTA ATC CAT GAT GAA ACC ACC AAA GCT AAA ACC CCT TAC ATT      435
Val His Leu Ile His Asp Glu Thr Thr Lys Ala Lys Thr Pro Tyr Ile
        50             55             60

GCA AAC TGG ATA CAA TTT TTA GAG CCT GTT AAA GAA GAG TTA AAA AAC      483
Ala Asn Trp Ile Gln Phe Leu Glu Pro Val Lys Glu Glu Leu Lys Asn
        65             70             75

CAC CCG CAA TTC AGC AAC CAT TTC GCC AAG CGT TCA TGG CTT ACA GAG      531
His Pro Gln Phe Ser Asn His Phe Ala Lys Arg Ser Trp Leu Thr Glu
        80             85             90

CGT TTG AAT GCG CGC TTG CAA CTC AAC AAC CTC TTA AGC TAT GAT TTC      579
Arg Leu Asn Ala Arg Leu Gln Leu Asn Asn Leu Leu Ser Tyr Asp Phe
        95             100            105            110

ATT CAA GAG AAA GCG AGC AAG AAT GAA TTA AAA ATT TTT GGT TGG CAC      627
Ile Gln Glu Lys Ala Ser Lys Asn Glu Leu Lys Ile Phe Gly Trp His
        115            120            125

TAC ATC ATA GAA ACA GGC AGG ATT TAT AAT TAT AAT TTT GAA AGC CAT      675
Tyr Ile Ile Glu Thr Gly Arg Ile Tyr Asn Tyr Asn Phe Glu Ser His
        130            135            140

TTT TTT GAG CCG ATT GGA GAA ACC ATT AAA CAA AGG AAA AGT CAT GAA      723
Phe Phe Glu Pro Ile Gly Glu Thr Ile Lys Gln Arg Lys Ser His Glu
        145            150            155

AAC TTC TAAACAAAA ACCCCTAAAT CCGTTTAAAT CGCTGGGCCA TCGTCATTG A      780
Asn Phe

```



```

Val Glu Gly Val Phe Phe Ser Ile Tyr Ile Phe Tyr Ser Gly Leu Asn
      35              40              45
Glu Asp Asp Leu Asn Arg Leu Gln Glu Thr Ile Lys Pro Phe Lys His
      50              55              60
Phe Ala Ala Leu Lys Cys Gln Asp Ile Ser Ala Thr Leu Asp Ser Leu
      65              70              75              80
Pro Thr Ile Thr Asp Ser Ala Trp Val Asn Arg Tyr Ser Arg Met Ile
      85              90              95
Leu Val Lys Tyr Leu Leu Pro Ser Leu Phe Pro Gln Tyr Ser Lys Met
      100             105             110
Ile Trp Ser Asp Val Asp Val Val Phe Cys Arg Ala Phe Ala Asp Asp
      115             120             125
Phe Ile Ala Leu Asp Thr Ser Glu Ser Phe His Leu Ser Gly Val Ile
      130             135             140
Ser Leu Val Ser Gln Ser Val Thr Glu Gly Phe Trp Phe Cys Asn Leu
      145             150             155             160
Asp Tyr Met Arg Lys His Ser Phe Thr Gln Gln Val Leu Glu Lys Phe
      165             170             175
Lys Ile Gln Val Met Arg Pro Tyr Phe Lys Glu Pro Thr Leu Ile His
      180             185             190
His Leu His Ala Tyr Ile Lys Glu Leu Pro Leu His Tyr Cys Val Leu
      195             200             205
Pro Tyr Tyr Tyr Gln Glu Glu Leu Asp Asp Leu Arg His Lys Ala Ser
      210             215             220
Leu Pro Ile Arg Phe Glu Ile Ile His Gln Asp Lys Pro Asn Glu Phe
      225             230             235             240
Ile His Arg Gln Gln Ile Pro Tyr Glu Ile Ser Gln Ile Gln Asn Ile
      245             250             255
Leu Ser Asn Pro Ile Ile Met His Tyr Glu Ser Asp Lys Asp Ala Leu
      260             265             270
Gly Ile Tyr Asn Gly Lys Pro Trp Glu Phe Pro Leu Gly Asn Gln Tyr
      275             280             285
His Leu Trp Leu Glu Met Leu Ala His Thr Pro Phe Trp Lys Asp Phe
      290             295             300
Thr Leu Glu Met Gln Lys Lys Arg Ile Glu Tyr Arg Asp Ile Ala Gln
      305             310             315             320
Lys Ile His Tyr Phe Ser Gln Asp Lys Arg Leu Tyr Glu Val Ser Ile
      325             330             335
Arg Ser Ile Lys Val Phe Ala Ser His Tyr Tyr Asn Leu Val Val Lys
      340             345             350
Glu Arg Trp Ser Lys Pro Ile Lys Thr Phe Phe Gln Lys Asn Phe Phe
      355             360             365
Gln Lys Lys Phe
      370

```

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

```

TTT GAA ATC ATC CAC CAA GAC AAA CCC AAT GAA TTT ATC CAT CGC CAG      777
Phe Glu Ile Ile His Gln Asp Lys Pro Asn Glu Phe Ile His Arg Gln
    230                      235                      240

CAA ATC CCC TAT GAG ATC TCT CAA ATT CAA AAC ATT CTT TCA AAC CCT      825
Gln Ile Pro Tyr Glu Ile Ser Gln Ile Gln Asn Ile Leu Ser Asn Pro
    245                      250                      255                      260

ATT ATC ATG CAC TAT GAA TCT GAT AAA GAT GCT CTT GGA ATC TAC AAT      873
Ile Ile Met His Tyr Glu Ser Asp Lys Asp Ala Leu Gly Ile Tyr Asn
    265                      270                      275

GGC AAA CCT TGG GAG TTC CCT TTG GGG AAT CAA TAC CAC CTG TGG TTA      921
Gly Lys Pro Trp Glu Phe Pro Leu Gly Asn Gln Tyr His Leu Trp Leu
    280                      285                      290

GAG ATG CTT GCA CAC ACT CCA TTT TGG AAA GAC TTC ACT CTG GAA ATG      969
Glu Met Leu Ala His Thr Pro Phe Trp Lys Asp Phe Thr Leu Glu Met
    295                      300                      305

CAA AAA AAA CGC ATA GAA TAC CGA GAT ATT GCT CAA AAA ATC CAT TAT      1017
Gln Lys Lys Arg Ile Glu Tyr Arg Asp Ile Ala Gln Lys Ile His Tyr
    310                      315                      320

TTT TCT CAA GAT AAG CGT CTT TAT GAA GTG AGC ATA CGC TCC ATT AAG      1065
Phe Ser Gln Asp Lys Arg Leu Tyr Glu Val Ser Ile Arg Ser Ile Lys
    325                      330                      335                      340

GTT TTT GCA TCT CAT TAC TAT AAT TTA GTG GTT AAA GAA CGA TGG TCT      1113
Val Phe Ala Ser His Tyr Tyr Asn Leu Val Val Lys Glu Arg Trp Ser
    345                      350                      355

AAA CCA ATA AAA ACT TTC TTT CAA AAA AAT TTT TTT CAA AAA AAG TTC T      1162
Lys Pro Ile Lys Thr Phe Phe Gln Lys Asn Phe Phe Gln Lys Lys Phe
    360                      365                      370

AATTTGTTGG AATCACAAGG CGAAACCAAA TCCCTAATAC TTATGCTTTC TCAGG      1217

```

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

```

Met Gln His Glu Ile Pro Ile Ala Phe Ala Phe Asp Lys Asn Tyr Leu
 1           5           10           15
Lys Thr Gly Ala Val Ala Leu Tyr Ser Leu Leu His Ala His Arg Ala
    20           25           30

```

ATC CCT ATT GCC TTT GCC TTT GAT AAA AAC TAC CTA AAA ACA GGG GCT	105
Ile Pro Ile Ala Phe Ala Phe Asp Lys Asn Tyr Leu Lys Thr Gly Ala	
5 10 15 20	
GTG GCT CTC TAC TCT TTA TTG CAT GCC CAT CGT GCA GTT GAA GGG GTA	153
Val Ala Leu Tyr Ser Leu Leu His Ala His Arg Ala Val Glu Gly Val	
25 30 35	
TTT TTC AGT ATC TAT ATA TTC TAT AGC GGT TTG AAT GAA GAT GAT TTA	201
Phe Phe Ser Ile Tyr Ile Phe Tyr Ser Gly Leu Asn Glu Asp Asp Leu	
40 45 50	
AAC AGG CTC CAA GAA ACT ATC AAA CCT TTC AAA CAT TTT GCC GCT TTA	249
Asn Arg Leu Gln Glu Thr Ile Lys Pro Phe Lys His Phe Ala Ala Leu	
55 60 65	
AAA TGC CAA GAT ATT AGC GCC ACT CTT GAT TCT TTG CCC ACC ATC ACG	297
Lys Cys Gln Asp Ile Ser Ala Thr Leu Asp Ser Leu Pro Thr Ile Thr	
70 75 80	
GAT AGT GCA TGG GTT AAT CGC TAT TCT AGA ATG ATT TTG GTC AAA TAC	345
Asp Ser Ala Trp Val Asn Arg Tyr Ser Arg Met Ile Leu Val Lys Tyr	
85 90 95 100	
CTT CTC CCT AGT TTA TTC CCC CAA TAC AGC AAA ATG ATT TGG TCT GAT	393
Leu Leu Pro Ser Leu Phe Pro Gln Tyr Ser Lys Met Ile Trp Ser Asp	
105 110 115	
GTG GAT GTG GTC TTT TGC AGA GCT TTC GCT GAT GAT TTT ATC GCT TTA	441
Val Asp Val Val Phe Cys Arg Ala Phe Ala Asp Asp Phe Ile Ala Leu	
120 125 130	
GAC ACA AGC GAA TCT TTT CAT TTG AGT GGT GTG ATA AGT TTA GTA TCA	489
Asp Thr Ser Glu Ser Phe His Leu Ser Gly Val Ile Ser Leu Val Ser	
135 140 145	
CAA TCA GTT ACA GAG GGG TTT TGG TTT TGC AAT TTG GAT TAC ATG CGA	537
Gln Ser Val Thr Glu Gly Phe Trp Phe Cys Asn Leu Asp Tyr Met Arg	
150 155 160	
AAG CAC TCT TTC ACC CAA CAG GTC TTA GAA AAA TTT AAA ATT CAA GTA	585
Lys His Ser Phe Thr Gln Gln Val Leu Glu Lys Phe Lys Ile Gln Val	
165 170 175 180	
ATG CGT CCA TAT TTT AAA GAA CCT ACA TTA ATA CAC CAT TTG CAT GCT	633
Met Arg Pro Tyr Phe Lys Glu Pro Thr Leu Ile His His Leu His Ala	
185 190 195	
TAT ATT AAA GAA CTT CCC TTA CAC TAT TGC GTT CTG CCT TAT TAT TAT	681
Tyr Ile Lys Glu Leu Pro Leu His Tyr Cys Val Leu Pro Tyr Tyr Tyr	
200 205 210	
CAA GAA GAA CTT GAT GAT TTG AGA CAT AAA GCT TCC TTA CCC ATT CGG	729
Gln Glu Glu Leu Asp Asp Leu Arg His Lys Ala Ser Leu Pro Ile Arg	
215 220 225	

755	760	765
Gln Asn Phe Gly Leu Ala Asp Leu His Gln Leu Arg Gly Arg Val Gly		
770	775	780
Arg Gly Lys Lys Glu Gly Phe Cys Tyr Phe Leu Ile Glu Asp Gln Lys		
785	790	795
Ser Leu Asn Glu Gln Ala Leu Lys Arg Leu Leu Ala Leu Glu Lys Asn		
805	810	815
Ser Tyr Leu Gly Ser Gly Glu Ser Val Ala Tyr His Asp Leu Glu Ile		
820	825	830
Arg Gly Gly Gly Asn Leu Leu Gly Gln Asp Gln Ser Gly His Ile Lys		
835	840	845
Asn Ile Gly Tyr Ala Leu Tyr Thr Arg Met Leu Glu Asp Ala Ile Tyr		
850	855	860
Glu Leu Ser Gly Gly Lys Lys Arg Leu Glu Lys Ser Val Glu Ile Gln		
865	870	875
Leu Gly Val Ser Ala Phe Leu Asn Pro Glu Leu Ile Ala Ser Asp Ser		
885	890	895
Leu Arg Leu Asp Leu Tyr Arg Arg Leu Ser Leu Cys Glu Asn Thr Asp		
900	905	910
Glu Val Gly Gln Ile His Glu Glu Ile Glu Asp Arg Phe Gly Lys Ile		
915	920	925
Asp Asp Leu Ser Ala Gln Phe Leu Gln Ile Ile Thr Leu Lys Ile Leu		
930	935	940
Ala Asn Gln Leu Gly Ile Ile Lys Leu Ser Asn Phe Asn Gln Asn Ile		
945	950	955
Thr Ile Thr Tyr Ser Asp Glu Lys Lys Glu Ser Leu Lys Ala Pro Ser		
965	970	975
Lys Asp Asp Asn Asp Ile Leu Glu Thr Leu Leu Lys His Leu Arg Ala		
980	985	990
Gln Ile Ser Leu Lys Arg Arg		
995	1	

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...1161
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

AGGCTATGAT ATAGTTTATT TTCACAAAAT CTCCAAGGAA AATTG ATG CAA CAT GAA 57
 Met Gln His Glu
 1

```

Met Glu Cys Val Ile Ala Pro Phe Val Leu Asn Phe Lys Thr Pro Asp
      325                      330                      335
Gly Ile Phe Ile Ser Leu Asn Ser Phe Glu Arg Lys Lys Lys Arg Gln
      340                      345                      350
Lys Ser Lys Leu Ala Leu Asn Glu Leu Asn Pro Gly Glu Trp Val Val
      355                      360                      365
His Asp Asp Tyr Gly Val Gly Val Phe Ser Gln Leu Val Gln His Ser
      370                      375                      380
Val Leu Gly Ser Lys Arg Asp Phe Leu Glu Ile Ala Tyr Leu Gly Glu
      385                      390                      395                      400
Asp Lys Leu Leu Leu Pro Val Glu Asn Leu His Leu Ile Ala Arg Tyr
      405                      410                      415
Val Ala Gln Ser Asp Ser Val Pro Ala Lys Asp Arg Leu Gly Lys Gly
      420                      425                      430
Ser Phe Leu Lys Leu Lys Ala Lys Val Arg Thr Lys Leu Leu Glu Ile
      435                      440                      445
Ala Ser Lys Ile Ile Glu Leu Ala Ala Glu Arg Asn Leu Ile Leu Gly
      450                      455                      460
Lys Lys Met Asp Val His Leu Ala Glu Leu Glu Val Phe Lys Ser His
      465                      470                      475                      480
Ala Gly Phe Glu Tyr Thr Ser Asp Gln Glu Lys Ala Ile Ala Glu Ile
      485                      490                      495
Ser Lys Asp Leu Ser Ser His Arg Val Met Asp Arg Leu Leu Ser Gly
      500                      505                      510
Asp Val Gly Phe Gly Lys Thr Glu Val Ala Met His Ala Ile Phe Cys
      515                      520                      525
Ala Phe Leu Asn Gly Phe Gln Ser Ala Leu Val Val Pro Thr Thr Leu
      530                      535                      540
Leu Ala His Gln His Phe Glu Thr Leu Arg Ala Arg Phe Glu Asn Phe
      545                      550                      555                      560
Gly Val Lys Val Ala Arg Leu Asp Arg Tyr Ala Ser Glu Lys Asn Lys
      565                      570                      575
Leu Leu Lys Ala Val Glu Leu Gly Gln Val Asp Ala Leu Ile Gly Thr
      580                      585                      590
His Ala Ile Leu Gly Ala Lys Phe Lys Asn Leu Gly Leu Val Val Val
      595                      600                      605
Asp Glu Glu His Lys Phe Gly Val Lys Gln Lys Glu Ala Leu Lys Glu
      610                      615                      620
Leu Ser Lys Ser Val His Phe Leu Ser Met Ser Ala Thr Pro Ile Pro
      625                      630                      635                      640
Arg Thr Leu Asn Met Ala Leu Ser Gln Ile Lys Gly Ile Ser Ser Leu
      645                      650                      655
Lys Thr Pro Pro Thr Asp Arg Lys Pro Ser Arg Thr Phe Leu Lys Glu
      660                      665                      670
Lys Asn Asp Glu Leu Leu Lys Glu Ile Ile Tyr Arg Glu Leu Arg Arg
      675                      680                      685
Asn Gly Gln Ile Phe Tyr Ile His Asn His Ile Ala Ser Ile Leu Lys
      690                      695                      700
Val Lys Thr Lys Leu Glu Asp Leu Ile Pro Lys Leu Lys Ile Ala Ile
      705                      710                      715                      720
Leu His Ser Gln Ile Asn Ala Asn Glu Ser Glu Glu Ile Met Leu Glu
      725                      730                      735
Phe Ala Lys Gly Asn Tyr Gln Val Leu Leu Cys Thr Ser Ile Val Glu
      740                      745                      750
Ser Gly-Ile His Leu Pro Asn Ala Asn Thr Ile Ile Ile Asp Asn Ala

```

AAAAGATTAT TAA

3101

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

```

Met Ile Gln Ser Ser Leu Tyr Arg Ala Leu Asn Lys Gly Phe Asp Tyr
 1           5           10           15
Gln Ile Leu Ala Cys Lys Asp Phe Lys Glu Ser Glu Leu Ala Lys Glu
 20           25           30
Val Ile Ser Tyr Phe Lys Pro Asn Thr Lys Ala Ile Leu Phe Pro Glu
 35           40           45
Phe Arg Ala Lys Lys Asn Asp Asp Leu Arg Ser Phe Phe Glu Glu Phe
 50           55           60
Leu Gln Leu Leu Gly Gly Leu Arg Glu Phe Tyr Gln Ala Leu Glu Asn
 65           70           75           80
Lys Gln Glu Thr Ile Ile Ile Ala Pro Ile Ser Ala Leu Leu His Pro
 85           90           95
Leu Pro Lys Lys Glu Leu Leu Glu Ser Phe Lys Ile Thr Leu Leu Glu
100          105          110
Lys Tyr Asn Leu Lys Asp Leu Lys Asp Lys Leu Phe Tyr Tyr Gly Tyr
115          120          125
Glu Ile Leu Asp Leu Val Glu Val Glu Gly Glu Ala Ser Phe Arg Gly
130          135          140
Asp Ile Val Asp Ile Tyr Ala Pro Asn Ser Lys Ala Tyr Arg Leu Ser
145          150          155          160
Phe Phe Asp Thr Glu Cys Glu Ser Ile Lys Glu Phe Asp Pro Ile Thr
165          170          175
Gln Met Ser Leu Lys Glu Asp Leu Leu Glu Ile Glu Ile Pro Pro Thr
180          185          190
Leu Phe Ser Leu Asp Glu Ser Ser Tyr Lys Asp Leu Lys Thr Lys Val
195          200          205
Glu Gln Ser Pro Leu Asn Ser Phe Ser Lys Asp Leu Thr Ser Phe Gly
210          215          220
Leu Trp Phe Leu Gly Glu Lys Ala Gln Asp Leu Leu Ile Val Tyr Lys
225          230          235          240
Ser Ile Ile Ser Pro Arg Ala Leu Glu Glu Ile Gln Glu Leu Ala Ser
245          250          255
Leu Asn Glu Leu Asp Cys Glu Arg Phe Lys Phe Leu Lys Val Leu Glu
260          265          270
Asn Ala Gln Gly Tyr Glu Asp Leu Glu Ile His Ala His Ala Leu Glu
275          280          285
Gly Phe Ile Ala Leu His Ser Asn His Lys Ile Thr Leu Leu Ala Pro
290          295          300
Asn Lys Thr Ile Leu Asp Asn Ala Ile Ser Ala Leu Asp Ala Gly Asn
305          310          315          320

```

GGT AAA AAA GAA GGC TTT TGT TAT TTC CTC ATA GAA GAT CAA AAA AGT	2456
Gly Lys Lys Glu Gly Phe Cys Tyr Phe Leu Ile Glu Asp Gln Lys Ser	
790 795 800	
TTG AAT GAA CAG GCT TTA AAA CGC TTG CTC GCT TTG GAA AAA AAT TCA	2504
Leu Asn Glu Gln Ala Leu Lys Arg Leu Leu Ala Leu Glu Lys Asn Ser	
805 810 815	
TAT TTA GGC AGC GGG GAG AGT GTC GCT TAT CAT GAT TTA GAA ATC AGG	2552
Tyr Leu Gly Ser Gly Glu Ser Val Ala Tyr His Asp Leu Glu Ile Arg	
820 825 830	
GGG GGC GGG AAT TTG CTC GGG CAA GAT CAG AGC GGG CAT ATT AAA AAC	2600
Gly Gly Gly Asn Leu Leu Gly Gln Asp Gln Ser Gly His Ile Lys Asn	
835 840 845	
ATT GGT TAT GCA CTC TAT ACG CGC ATG CTT GAA GAC GCG ATT TAT GAA	2648
Ile Gly Tyr Ala Leu Tyr Thr Arg Met Leu Glu Asp Ala Ile Tyr Glu	
850 855 860 865	
TTG AGT GGG GGG AAG AAA AGG CTT GAA AAG AGC GTA GAA ATC CAA CTT	2696
Leu Ser Gly Gly Lys Lys Arg Leu Glu Lys Ser Val Glu Ile Gln Leu	
870 875 880	
GGC GTG AGC GCT TTT TTA AAC CCT GAA CTC ATT GCA AGC GAT AGT TTG	2744
Gly Val Ser Ala Phe Leu Asn Pro Glu Leu Ile Ala Ser Asp Ser Leu	
885 890 895	
AGA TTG GAT TTA TAC CGC CGT TTG AGT TTG TGT GAA AAT ACA GAT GAG	2792
Arg Leu Asp Leu Tyr Arg Arg Leu Ser Leu Cys Glu Asn Thr Asp Glu	
900 905 910	
GTG GGG CAA ATC CAT GAA GAA ATA GAA GAC AGG TTT GGC AAA ATA GAC	2840
Val Gly Gln Ile His Glu Glu Ile Glu Asp Arg Phe Gly Lys Ile Asp	
915 920 925	
GAT TTG AGC GCT CAA TTT TTG CAA ATC ATT ACG CTT AAA ATT CTA GCC	2888
Asp Leu Ser Ala Gln Phe Leu Gln Ile Ile Thr Leu Lys Ile Leu Ala	
930 935 940 945	
AAC CAG CTT GGC ATC ATC AAA CTT TCT AAT TTC AAT CAA AAC ATC ACC	2936
Asn Gln Leu Gly Ile Ile Lys Leu Ser Asn Phe Asn Gln Asn Ile Thr	
950 955 960	
ATC ACT TAT AGC GAT GAA AAG AAA GAA AGC CTG AAA GCC CCA AGC AAA	2984
Ile Thr Tyr Ser Asp Glu Lys Lys Glu Ser Leu Lys Ala Pro Ser Lys	
965 970 975	
GAC GAT AAC GAT ATT TTA GAA ACC CTT TTG AAA CAT TTG CGC GCT CAA	3032
Asp Asp Asn Asp Ile Leu Glu Thr Leu Leu Lys His Leu Arg Ala Gln	
980 985 990	
ATT TCT TTA AAG CGG CGT TAAAAGCGTT TGATTTTAGC GTTAATTTTG TTATTTTA	3088
Ile Ser Leu Lys Arg Arg	
995 1	

GTT AAA GTG GCT CGT TTG GAC AGG TAT GCG AGC GAA AAA AAC AAG CTT	1784
Val Lys Val Ala Arg Leu Asp Arg Tyr Ala Ser Glu Lys Asn Lys Leu	
565 570 575	
TTA AAG GCG GTG GAA TTA GGG CAA GTT GAT GCG CTA ATA GGC ACG CAT	1832
Leu Lys Ala Val Glu Leu Gly Gln Val Asp Ala Leu Ile Gly Thr His	
580 585 590	
GCG ATT TTA GGC GCG AAA TTC AAA AAC CTG GGC TTG GTG GTG GTG GAT	1880
Ala Ile Leu Gly Ala Lys Phe Lys Asn Leu Gly Leu Val Val Val Asp	
595 600 605	
GAA GAG CAT AAA TTT GGC GTG AAA CAA AAA GAA GCT TTA AAA GAA TTG	1928
Glu Glu His Lys Phe Gly Val Lys Gln Lys Glu Ala Leu Lys Glu Leu	
610 615 620 625	
AGT AAG AGC GTG CAT TTT TTA AGC ATG TCC GCT ACG CCT ATC CCG CGC	1976
Ser Lys Ser Val His Phe Leu Ser Met Ser Ala Thr Pro Ile Pro Arg	
630 635 640	
ACT CTA AAC ATG GCG CTC TCT CAA ATT AAG GGC ATT AGT TCT TTA AAA	2024
Thr Leu Asn Met Ala Leu Ser Gln Ile Lys Gly Ile Ser Ser Leu Lys	
645 650 655	
ACC CCG CCC ACA GAC AGA AAG CCC AGC CGC ACT TTT TTG AAA GAA AAG	2072
Thr Pro Pro Thr Asp Arg Lys Pro Ser Arg Thr Phe Leu Lys Glu Lys	
660 665 670	
AAT GAC GAA CTC TTA AAA GAG ATT ATT TAC AGA GAA TTA CGC CGT AAC	2120
Asn Asp Glu Leu Leu Lys Glu Ile Ile Tyr Arg Glu Leu Arg Arg Asn	
675 680 685	
GGG CAA ATT TTT TAC ATC CAT AAC CAC ATC GCT AGC ATT TTA AAA GTC	2168
Gly Gln Ile Phe Tyr Ile His Asn His Ile Ala Ser Ile Leu Lys Val	
690 695 700 705	
AAA ACC AAG CTA GAA GAT TTA ATC CCT AAA CTC AAA ATC GCT ATT TTG	2216
Lys Thr Lys Leu Glu Asp Leu Ile Pro Lys Leu Lys Ile Ala Ile Leu	
710 715 720	
CAT TCC CAG ATT AAC GCT AAT GAG AGC GAA GAA ATC ATG CTA GAG TTT	2264
His Ser Gln Ile Asn Ala Asn Glu Ser Glu Glu Ile Met Leu Glu Phe	
725 730 735	
GCC AAG GGA AAT TAT CAG GTT TTA TTA TGC ACT TCT ATT GTG GAA TCA	2312
Ala Lys Gly Asn Tyr Gln Val Leu Leu Cys Thr Ser Ile Val Glu Ser	
740 745 750	
GGG ATT CAT TTG CCT AAC GCT AAC ACG ATC ATT ATA GAT AAT GCG CAA	2360
Gly Ile His Leu Pro Asn Ala Asn Thr Ile Ile Ile Asp Asn Ala Gln	
755 760 765	
AAT TTC GGG CTG GCT GAT TTG CAC CAA TTG AGA GGG CGT GTG GGG AGA	2408
Asn Phe Gly Leu Ala Asp Leu His Gln Leu Arg Gly Arg Val Gly Arg	
770 775 780 785	

ATT TTT ATT TCG CTC AAT TCT TTT GAA AGG AAG AAA AAA CGC CAA AAA	1112
Ile Phe Ile Ser Leu Asn Ser Phe Glu Arg Lys Lys Lys Arg Gln Lys	
340 345 350	
TCC AAG CTC GCT TTG AAT GAG TTG AAT CCG GGC GAA TGG GTG GTG CAT	1160
Ser Lys Leu Ala Leu Asn Glu Leu Asn Pro Gly Glu Trp Val Val His	
355 360 365	
GAT GAT TAT GGG GTG GGC GTG TTT TCT CAA TTA GTC CAG CAC AGC GTT	1208
Asp Asp Tyr Gly Val Gly Val Phe Ser Gln Leu Val Gln His Ser Val	
370 375 380 385	
TTA GGG AGC AAG AGG GAT TTT TTA GAA ATC GCT TAT TTG GGC GAA GAC	1256
Leu Gly Ser Lys Arg Asp Phe Leu Glu Ile Ala Tyr Leu Gly Glu Asp	
390 395 400	
AAA CTG CTG TTA CCG GTA GAA AAC TTG CAT CTC ATC GCT CGC TAT GTG	1304
Lys Leu Leu Leu Pro Val Glu Asn Leu His Leu Ile Ala Arg Tyr Val	
405 410 415	
GCG CAA AGC GAT AGC GTG CCA GCT AAA GAC CGG CTA GGG AAA GGC AGC	1352
Ala Gln Ser Asp Ser Val Pro Ala Lys Asp Arg Leu Gly Lys Gly Ser	
420 425 430	
TTT CTT AAA TTA AAA GCT AAA GTC AGG ACT AAG CTT TTA GAG ATT GCT	1400
Phe Leu Lys Leu Lys Ala Lys Val Arg Thr Lys Leu Leu Glu Ile Ala	
435 440 445	
AGC AAG ATC ATT GAA TTA GCG GCT GAA CGC AAT TTG ATC TTG GGT AAA	1448
Ser Lys Ile Ile Glu Leu Ala Ala Glu Arg Asn Leu Ile Leu Gly Lys	
450 455 460 465	
AAG ATG GAT GTG CAT TTA GCG GAG TTG GAA GTC TTT AAA TCG CAT GCG	1496
Lys Met Asp Val His Leu Ala Glu Leu Glu Val Phe Lys Ser His Ala	
470 475 480	
GGG TTT GAA TAC ACC AGC GAT CAA GAA AAG GCT ATC GCT GAA ATT TCA	1544
Gly Phe Glu Tyr Thr Ser Asp Gln Glu Lys Ala Ile Ala Glu Ile Ser	
485 490 495	
AAG GAT TTA AGC TCT CAC AGG GTG ATG GAT AGA TTA TTG AGT GGG GAT	1592
Lys Asp Leu Ser Ser His Arg Val Met Asp Arg Leu Leu Ser Gly Asp	
500 505 510	
GTG GGT TTT GGG AAA ACA GAA GTG GCG ATG CAT GCG ATT TTT TGC GCG	1640
Val Gly Phe Gly Lys Thr Glu Val Ala Met His Ala Ile Phe Cys Ala	
515 520 525	
TTT TTG AAC GGC TTT CAA AGC GCT TTA GTT GTG CCT ACC ACT TTA TTA	1688
Phe Leu Asn Gly Phe Gln Ser Ala Leu Val Val Pro Thr Thr Leu Leu	
530 535 540 545	
GCG CAC CAG CAT TTT GAG ACT TTA AGG GCG CGT TTT GAA AAT TTT GGC	1736
Ala His Gln His Phe Glu Thr Leu Arg Ala Arg Phe Glu Asn Phe Gly	
550 555 560	

TAT AAC CTT AAG GAT TTG AAA GAC AAG CTC TTT TAT TAT GGC TAT GAA	440
Tyr Asn Leu Lys Asp Leu Lys Asp Lys Leu Phe Tyr Tyr Gly Tyr Glu	
115 120 125	
ATT TTA GAC TTA GTG GAA GTG GAA GGC GAA GCG AGC TTT AGG GGG GAT	488
Ile Leu Asp Leu Val Glu Val Glu Gly Glu Ala Ser Phe Arg Gly Asp	
130 135 140 145	
ATT GTG GAT ATT TAT GCG CCA AAT TCT AAA GCG TAT CGC TTG AGT TTT	536
Ile Val Asp Ile Tyr Ala Pro Asn Ser Lys Ala Tyr Arg Leu Ser Phe	
150 155 160	
TTT GAC ACC GAG TGT GAG AGC ATT AAG GAA TTT GAT CCC ATT ACT CAA	584
Phe Asp Thr Glu Cys Glu Ser Ile Lys Glu Phe Asp Pro Ile Thr Gln	
165 170 175	
ATG AGC CTT AAA GAA GAT TTG TTA GAA ATT GAA ATC CCC CCC ACG CTT	632
Met Ser Leu Lys Glu Asp Leu Leu Glu Ile Glu Ile Pro Pro Thr Leu	
180 185 190	
TTT AGT TTG GAC GAA TCA TCT TAT AAG GAT CTA AAA ACA AAA GTG GAA	680
Phe Ser Leu Asp Glu Ser Ser Tyr Lys Asp Leu Lys Thr Lys Val Glu	
195 200 205	
CAA AGC CCC TTA AAT AGC TTT TCT AAA GAT TTA ACC AGT TTT GGT TTG	728
Gln Ser Pro Leu Asn Ser Phe Ser Lys Asp Leu Thr Ser Phe Gly Leu	
210 215 220 225	
TGG TTT TTA GGA GAA AAA GCA CAA GAC TTA CTA ATC GTT TAT AAA AGC	776
Trp Phe Leu Gly Glu Lys Ala Gln Asp Leu Leu Ile Val Tyr Lys Ser	
230 235 240	
ATT ATA AGT CCT AGA GCT TTA GAA GAA ATT CAA GAA TTA GCG AGC TTA	824
Ile Ile Ser Pro Arg Ala Leu Glu Glu Ile Gln Glu Leu Ala Ser Leu	
245 250 255	
AAC GAA TTG GAT TGT GAG CGT TTC AAA TTT TTA AAG GTT TTA GAA AAC	872
Asn Glu Leu Asp Cys Glu Arg Phe Lys Phe Leu Lys Val Leu Glu Asn	
260 265 270	
GCG CAA GGC TAT GAA GAT TTA GAA ATC CAT GCG CAT GCC CTA GAA GGC	920
Ala Gln Gly Tyr Glu Asp Leu Glu Ile His Ala His Ala Leu Glu Gly	
275 280 285	
TTT ATC GCT TTG CAT TCA AAT CAT AAA ATC ACG CTC CTA GCC CCC AAT	968
Phe Ile Ala Leu His Ser Asn His Lys Ile Thr Leu Leu Ala Pro Asn	
290 295 300 305	
AAA ACG ATT TTA GAC AAC GCG ATA AGC GCG CTT GAT GCA GGC AAC ATG	1016
Lys Thr Ile Leu Asp Asn Ala Ile Ser Ala Leu Asp Ala Gly Asn Met	
310 315 320	
GAA TGC GTC ATC GCC CCC TTT GTG TTA AAC TTT AAA ACC CCT GAT GGG	1064
Glu Cys Val Ile Ala Pro Phe Val Leu Asn Phe Lys Thr Pro Asp Gly	
325 330 335	

50 55 60
 Leu Ile Asn Ala Leu Asn Lys Ile Lys Lys Gly Leu Leu Val Phe
 65 70 75

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 54...3050
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

```

GGGGGGCGTT GTTAATCAAT GAGCAAGAAA AGAAAATTGA AAATAAATAG GGA ATG      56
                                     Met
                                     1

ATC CAA TCC AGC CTT TAT AGA GCC TTA AAC AAA GGC TTT GAT TAC CAA      104
Ile Gln Ser Ser Leu Tyr Arg Ala Leu Asn Lys Gly Phe Asp Tyr Gln
      5                      10                      15

ATA CTC GCT TGT AAG GAT TTT AAA GAA TCC GAG CTC GCT AAA GAA GTC      152
Ile Leu Ala Cys Lys Asp Phe Lys Glu Ser Glu Leu Ala Lys Glu Val
      20                      25                      30

ATA AGC TAT TTT AAG CCA AAT ACC AAA GCC ATT CTT TTC CCG GAG TTT      200
Ile Ser Tyr Phe Lys Pro Asn Thr Lys Ala Ile Leu Phe Pro Glu Phe
      35                      40                      45

AGG GCT AAA AAA AAC GAC GAT TTG CGT TCG TTT TTT GAA GAA TTT TTA      248
Arg Ala Lys Lys Asn Asp Asp Leu Arg Ser Phe Phe Glu Glu Phe Leu
      50                      55                      60                      65

CAG CTT TTA GGG GGT TTA AGG GAG TTT TAT CAA GCC TTA GAA AAC AAG      296
Gln Leu Leu Gly Gly Leu Arg Glu Phe Tyr Gln Ala Leu Glu Asn Lys
      70                      75                      80

CAA GAA ACT ATC ATC ATT GCC CCG ATT AGC GCG TTA TTG CAC CCT TTA      344
Gln Glu Thr Ile Ile Ile Ala Pro Ile Ser Ala Leu Leu His Pro Leu
      85                      90                      95

CCT AAA AAA GAA CTT TTA GAA AGC TTT AAA ATC ACT CTT TTA GAA AAA      392
Pro Lys Lys Glu Leu Leu Glu Ser Phe Lys Ile Thr Leu Leu Glu Lys
      100                      105                      110

```

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...287
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

TAATTTAATA GTTTAGCTAT CATGGAGCAT TCTAAATTAA AGGCGATCAC	ATG TTT	56
	Met Phe	
	1	
GAA AAA ATA CGC AAG ATT TTA GCG GAT ATT GAA GAT TCG CAA AAT GAA		104
Glu Lys Ile Arg Lys Ile Leu Ala Asp Ile Glu Asp Ser Gln Asn Glu		
5 10 15		
ATT GAA ATG CTT TTA AAA TTA GCG AAT TTG AGT TTG GGG GAT TTT ATT		152
Ile Glu Met Leu Leu Lys Leu Ala Asn Leu Ser Leu Gly Asp Phe Ile		
20 25 30		
GAG ATT AAA AGA GGG AGC ATG GAC ATG CCA AAG GGC GTG AAT GAA GCG		200
Glu Ile Lys Arg Gly Ser Met Asp Met Pro Lys Gly Val Asn Glu Ala		
35 40 45 50		
TTT TTT ACG CAA TTA AGC GAA GAA GTG GAG CGA TTG AAG GAG CTT ATT		248
Phe Phe Thr Gln Leu Ser Glu Glu Val Glu Arg Leu Lys Glu Leu Ile		
55 60 65		
AAC GCT TTG AAT AAA ATC AAA AAA GGG TTA TTG GTG TTT TAAATGTGTG GG		299
Asn Ala Leu Asn Lys Ile Lys Lys Gly Leu Leu Val Phe		
70 75		
ATTGTAGGTT ATATAGGGGA TAGCGAGAAA AAATCCGTTC T		340

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

Met Phe Glu Lys Ile Arg Lys Ile Leu Ala Asp Ile Glu Asp Ser Gln	
1 5 10 15	
Asn Glu Ile Glu Met Leu Leu Lys Leu Ala Asn Leu Ser Leu Gly Asp	
20 25 30	
Phe Ile Glu Ile Lys Arg Gly Ser Met Asp Met Pro Lys Gly Val Asn	
35 40 45	
Glu Ala Phe Phe Thr Gln Leu Ser Glu Glu Val Glu Arg Leu Lys Glu	

```

TTGCCCTTTT CAAAAATATA ATAGCTGTAT TTTAAAAGCT CTATCCATAG  CCT GAG      56
                                     Pro Glu
                                     1

CTT GGT GAT TTC GCA AGA ATT GGG GTT AAT ATC CAC GCC AAA AAG GCA      104
Leu Gly Asp Phe Ala Arg Ile Gly Val Asn Ile His Ala Lys Lys Ala
      5              10              15

GTT TTC AAT AAT GGA TTT TTT AAG ATT AAA AAG TTC TTT TTG GAT GTG      152
Val Phe Asn Asn Gly Phe Phe Lys Ile Lys Lys Phe Phe Leu Asp Val
      20              25              30

GTG GTG GGG GTC GTT TTC GCT ATC TGG TTT TAT GTA GTT AAA GAT TTC      200
Val Val Gly Val Val Phe Ala Ile Trp Phe Tyr Val Val Lys Asp Phe
      35              40              45              50

ACC CGT TGG CGT GTG GTG AAT GAT GAT TTC ATC GTT TTC TAATTTAAGA TC      251
Thr Arg Trp Arg Val Val Asn Asp Asp Phe Ile Val Phe
      55              60

GTAGCGATAC AAGGAAGCAA TAAGTCCTAG CTCATAAGCA A      292

```

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

```

Pro Glu Leu Gly Asp Phe Ala Arg Ile Gly Val Asn Ile His Ala Lys
 1              5              10              15
Lys Ala Val Phe Asn Asn Gly Phe Phe Lys Ile Lys Lys Phe Phe Leu
      20              25              30
Asp Val Val Val Gly Val Val Phe Ala Ile Trp Phe Tyr Val Val Lys
      35              40              45
Asp Phe Thr Arg Trp Arg Val Val Asn Asp Asp Phe Ile Val Phe
      50              55              60

```

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

```

Met Glu Lys Leu Phe Glu Lys Ile Leu His Glu Met Arg Ser Arg Thr
 1             5             10             15
Ser Phe Leu Leu Ala Phe Val Val Ser Leu Ile Val Phe Ile Phe Asn
      20             25             30
Leu Lys Gly Val Phe Gln Leu Ile Phe Glu Ser Ile Phe Gln Tyr Thr
      35             40             45
Gln Asn Lys Ile Leu Ser Phe Ser Leu Ser Phe Phe Phe Ile Phe Phe
      50             55             60
Phe Phe Tyr Ala Ile Phe Leu Ile Phe Tyr Gln Ile Phe Leu Trp Tyr
65             70             75             80
Gly Ala Lys Lys Tyr Lys Gln Asn Gln Arg Asp Ser Glu Ile Val Tyr
      85             90             95
Asn Ile Gln Lys Phe Pro Asn Glu Ile Lys Glu Glu Leu Tyr Arg Cys
      100            105            110
Tyr Ser Lys Lys Gln Asn Lys Ile Leu Arg Thr Lys Lys Leu Asp Asp
      115            120            125
Leu Ile Asp Tyr Leu Asp Leu Ile Gly Phe Phe Lys Ser Arg Asp Phe
      130            135            140
Phe Glu Pro Thr Lys Asp Asp Tyr Ile Val Lys Pro Asp Val Leu Arg
145            150            155            160
Ala Ile Lys Lys Tyr His Lys Ile Ala Phe Lys Ser Val Tyr Trp Gln
      165            170            175
Gln Asn Lys

```

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...239
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

ACCACCTCAC	CGATGAAGAA	ATTAAGATCA	TTGAAGAGGG	GCAGTGA	ATG	GAA	AAG	56
					Met	Glu	Lys	
					1			
TTA	TTT	GAA	AAG	ATA	TTG	CAT	GAA	104
Leu	Phe	Glu	Lys	Ile	Leu	His	Glu	
5					10			
CTT	GCT	TTT	GTC	GTT	TCG	CTT	ATT	152
Leu	Ala	Phe	Val	Val	Ser	Leu	Ile	
20					25			
GTT	TTT	CAA	TTG	ATT	TTT	GAG	TCT	200
Val	Phe	Gln	Leu	Ile	Phe	Glu	Ser	
ATC	CTT	TCT	TTT	TCT	CTT	TCT	TTT	248
Ile	Leu	Ser	Phe	Ser	Leu	Ser	Phe	
GCT	ATT	TTT	CTT	ATT	TTT	TAT	CAA	296
Ala	Ile	Phe	Leu	Ile	Phe	Tyr	Gln	
AAA	TAT	AAA	CAA	AAT	CAA	AGA	GAT	344
Lys	Tyr	Lys	Gln	Asn	Gln	Arg	Asp	
AAA	TTC	CCA	AAT	GAG	ATA	AAA	GAA	392
Lys	Phe	Pro	Asn	Glu	Ile	Lys	Glu	
100								
AAA	CAA	AAT	AAA	ATT	CTT	AGA	ACG	440
Lys	Gln	Asn	Lys	Ile	Leu	Arg	Thr	
TAT	CTT	GAT	TTA	ATA	GGT	TTT	TTT	488
Tyr	Leu	Asp	Leu	Ile	Gly	Phe	Phe	
ACA	AAA	GAC	GAT	TAT	ATT	GTC	AAA	536
Thr	Lys	Asp	Asp	Tyr	Ile	Val	Lys	
AAA	TAC	CAT	AAA	ATT	GCT	TTT	AAA	585
Lys	Tyr	His	Lys	Ile	Ala	Phe	Lys	
AAAAAGCGCT	TGTTCTTTGT	CTAAGAAACA	CCCCCTTTA	AAAAAGGGGG				635

(2) INFORMATION FOR SEQ ID NO:590:

Gly Phe Leu Ile Ala Ile Leu Ala Lys Thr Met Trp Phe Val
 135 140 145

TTCAACCTCA AAGAATTTAA GACCACTAAG AGTGAGCTAG CGCT

534

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

Met	Asp	Ala	Ile	Tyr	Pro	Tyr	Val	Leu	Val	Val	His	Leu	Leu	Cys	Ala
1			5				10						15		
Ile	Ile	Phe	Ile	Gly	Tyr	Leu	Phe	Phe	Asp	Gly	Val	Ile	Phe	Pro	Asn
		20					25						30		
Val	Lys	Lys	Met	Phe	Gly	Glu	Glu	Phe	Ala	Asn	Lys	Ala	Asn	Thr	Gly
		35				40						45			
Ile	Thr	Gln	Arg	Ala	Ile	Lys	Ile	Met	Pro	Leu	Cys	Val	Leu	Gly	Leu
	50					55					60				
Val	Leu	Thr	Gly	Gly	Met	Met	Leu	Ser	Gln	Tyr	Met	Gly	Gly	Asp	Lys
65				70					75					80	
Gly	Trp	Cys	Glu	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Met	Leu	Lys	Val	Ile
			85					90					95		
Leu	Ala	Leu	Ser	Ile	Phe	Leu	Leu	Val	Leu	Phe	Ser	Leu	Ser	Cys	Lys
		100						105					110		
Phe	Leu	Gly	Lys	Lys	Asn	Pro	Ile	Gly	Lys	Tyr	Ile	His	Pro	Ile	Ala
		115					120					125			
Leu	Thr	Phe	Gly	Phe	Leu	Ile	Ala	Ile	Leu	Ala	Lys	Thr	Met	Trp	Phe
	130					135					140				
Val															
145															

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...584
- (D) OTHER INFORMATION:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...481
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

```

AGTAGATTAA AAACCTCTTTA ATTTTCCCAT GAATAAAGGA TTTTAA ATG GAT GCG      55
                                   Met Asp Ala
                                   1

ATT TAT CCT TAT GTG TTG GTT GTT CAT TTA TTG TGC GCC ATT ATT TTT      103
Ile Tyr Pro Tyr Val Leu Val Val His Leu Leu Cys Ala Ile Ile Phe
   5                      10                      15

ATT GGC TAC TTG TTT TTT GAT GGG GTA ATT TTC CCT AAT GTG AAG AAA      151
Ile Gly Tyr Leu Phe Phe Asp Gly Val Ile Phe Pro Asn Val Lys Lys
  20                      25                      30                      35

ATG TTT GGC GAA GAG TTT GCC AAT AAA GCG AAT ACA GGA ATC ACT CAA      199
Met Phe Gly Glu Glu Phe Ala Asn Lys Ala Asn Thr Gly Ile Thr Gln
                40                      45                      50

AGA GCG ATC AAA ATC ATG CCC TTA TGC GTT TTA GGG CTT GTT TTA ACA      247
Arg Ala Ile Lys Ile Met Pro Leu Cys Val Leu Gly Leu Val Leu Thr
                55                      60                      65

GGG GGC ATG ATG CTT AGC CAA TAC ATG GGG GGC GAT AAA GGC TGG TGT      295
Gly Gly Met Met Leu Ser Gln Tyr Met Gly Gly Asp Lys Gly Trp Cys
  70                      75                      80

GAA ACC CCT TTT CAA AAG ATA CTC ATG CTT AAA GTG ATC TTA GCG TTA      343
Glu Thr Pro Phe Gln Lys Ile Leu Met Leu Lys Val Ile Leu Ala Leu
  85                      90                      95

AGC ATT TTT CTT TTG GTG CTT TTT TCT TTA TCG TGT AAG TTT TTG GGC      391
Ser Ile Phe Leu Leu Val Leu Phe Ser Leu Ser Cys Lys Phe Leu Gly
 100                      105                      110                      115

AAG AAA AAC CCT ATT GGT AAA TAT ATC CAC CCT ATC GCT CTA ACT TTT      439
Lys Lys Asn Pro Ile Gly Lys Tyr Ile His Pro Ile Ala Leu Thr Phe
                120                      125                      130

GGC TTT TTA ATC GCC ATT TTA GCC AAA ACG ATG TGG TTT GTT TAAGAGCGT      490

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

```

Met Leu Asn Phe Met Thr Lys Lys Lys Asn Arg Met Gln Asp Cys Lys
 1           5           10           15
Met Val Cys Lys Asn Phe Asn Arg Lys Glu Ser Val Leu Ile Ala Gln
 20           25           30
Ser Leu Asp Ile Ser Lys Lys Gly Ser Val Ile Leu Gly Ala Leu Leu
 35           40           45
Ser Ser Leu Trp Leu Thr Asn Pro Leu Asn Ala His Glu Lys Asn Gly
 50           55           60
Ala Phe Val Gly Ile Ser Leu Glu Val Gly Arg Ala Asp Gln Lys Thr
 65           70           75           80
Asn Ala Tyr Lys Asn Gly Glu Leu Phe Gln Val Pro Phe Gly Asp Val
 85           90           95
Ser Ala Asn Asp Asp Gly Lys Val Pro Asp Gly Gln Thr Gly Gly Cys
100          105          110
Gln Pro Ala Ser Gly Thr Pro Gly Thr Pro Gly Tyr Thr Lys Ala Asn
115          120          125
Cys Val Val Asn Trp Thr Ser Arg Thr Met Leu Ser Thr Asn Lys Asn
130          135          140
Ile Pro Gly Arg Asn Gln Pro Met Tyr Gly Leu Gly Val Met Thr Gly
145          150          155          160
Tyr Lys His Phe Ile Gly Lys Lys Arg Trp Phe Gly Leu Arg Tyr Tyr
165          170          175
Gly Phe Phe Asp Tyr Gly His Thr Asn Phe Ser Asn Ser Arg Ala Ala
180          185          190
Asn Ala Ile Ser Pro Phe Tyr Leu Ser Asp Gln Lys Ala Asp Met Tyr
195          200          205
Thr Tyr Gly Phe Gly Thr Asp Met Leu Phe Asn Ile Ile Asp Lys Pro
210          215          220
Lys Ala Thr Ala Gly Phe Phe Leu Gly Val Asn Phe Ala Gly Asn Thr
225          230          235          240
Trp Thr Asn Asn Arg Val Gly Tyr Phe Lys Asp Gly Tyr Val Tyr Gly
245          250          255
Val Asn Thr Asp Ala Asp Ala Tyr Met Thr Asn Ala Asp Gly Thr Ile
260          265          270
Thr Cys Gly Asp Thr Thr Pro Ala Ser Cys Asn Val Gly Ile Asn Pro
275          280          285
Asn Ser Val Tyr Thr Thr Gly Lys Leu Asn Ala Lys Val Asn His Thr
290          295          300
Ile Phe Gln Phe Leu Val Asn Val Gly Ile Arg Thr Asn Ile Phe Glu
305          310          315          320
His His Gly Ile Glu Phe Gly Ile Lys Ile Pro Thr Leu Pro Asn Tyr
325          330          335
Phe Phe Lys Gly Ser Thr Thr Ile Arg Ala Lys Lys Gln Gly Pro Leu
340          345          350
Glu Asn Gly Gln Pro Thr Thr Ile Thr Gly Ala Glu Thr Asn Phe Ser
355          360          365
Leu Thr Gln Thr Leu Arg Arg Gln Tyr Ser Met Tyr Leu Arg Tyr Val
370          375          380
Tyr Thr Phe
385

```

(2) INFORMATION FOR SEQ ID NO:587:

Ala Thr Ala Gly Phe Phe Leu Gly Val Asn Phe Ala Gly Asn Thr Trp	
230 235 240	
ACT AAT AAT CGT GTG GGG TAT TTT AAG GAC GGG TAT GTT TAT GGC GTC	825
Thr Asn Asn Arg Val Gly Tyr Phe Lys Asp Gly Tyr Val Tyr Gly Val	
245 250 255	
AAT ACG GAC GCT GAC GCT TAC ATG ACT AAC GCT GAT GGC ACA ATC ACT	873
Asn Thr Asp Ala Asp Ala Tyr Met Thr Asn Ala Asp Gly Thr Ile Thr	
260 265 270	
TGC GGG GAC ACG ACG CCG GCG AGT TGC AAT GTG GGG ATT AAC CCT AAT	921
Cys Gly Asp Thr Thr Pro Ala Ser Cys Asn Val Gly Ile Asn Pro Asn	
275 280 285	
AGC GTC TAT ACC ACA GGA AAA TTG AAC GCT AAG GTG AAT CAC ACG ATT	969
Ser Val Tyr Thr Thr Gly Lys Leu Asn Ala Lys Val Asn His Thr Ile	
290 295 300 305	
TTC CAA TTT TTA GTG AAT GTG GGC ATT AGA ACT AAT ATT TTT GAA CAC	1017
Phe Gln Phe Leu Val Asn Val Gly Ile Arg Thr Asn Ile Phe Glu His	
310 315 320	
CAT GGC ATT GAG TTT GGC ATC AAA ATC CCC ACG CTC CCT AAC TAC TTT	1065
His Gly Ile Glu Phe Gly Ile Lys Ile Pro Thr Leu Pro Asn Tyr Phe	
325 330 335	
TTC AAA GGT TCT ACT ACC ATA AGA GCG AAA AAA CAA GGC CCG CTA GAG	1113
Phe Lys Gly Ser Thr Thr Ile Arg Ala Lys Lys Gln Gly Pro Leu Glu	
340 345 350	
AAT GGC CAA CCA ACC ACT ATC ACC GGA GCA GAA ACC AAT TTC AGC TTA	1161
Asn Gly Gln Pro Thr Thr Ile Thr Gly Ala Glu Thr Asn Phe Ser Leu	
355 360 365	
ACC CAA ACC TTA CGC CGT CAG TAT TCT ATG TAT TTG CGC TAT GTT TAT	1209
Thr Gln Thr Leu Arg Arg Gln Tyr Ser Met Tyr Leu Arg Tyr Val Tyr	
370 375 380 385	
ACT TTT TAAGTTTGGT AGGGTTTTTA GGCAAGGCTT AGAGATGAA	1254
Thr Phe	

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

5					10					15						
GTT	TGT	AAA	AAT	TTT	AAT	CGT	AAG	GAA	TCT	GTT	TTG	ATA	GCT	CAA	TCT	153
Val	Cys	Lys	Asn	Phe	Asn	Arg	Lys	Glu	Ser	Val	Leu	Ile	Ala	Gln	Ser	
20					25					30						
TTA	GAT	ATT	TCT	AAA	AAA	GGT	TCG	GTA	ATT	TTA	GGC	GCT	CTT	TTG	AGT	201
Leu	Asp	Ile	Ser	Lys	Lys	Gly	Ser	Val	Ile	Leu	Gly	Ala	Leu	Leu	Ser	
35					40					45						
TCG	TTA	TGG	CTG	ACA	AAC	CCC	TTA	AAT	GCC	CAT	GAA	AAG	AAT	GGC	GCG	249
Ser	Leu	Trp	Leu	Thr	Asn	Pro	Leu	Asn	Ala	His	Glu	Lys	Asn	Gly	Ala	
50					55					60					65	
TTT	GTG	GGG	ATT	AGC	TTG	GAA	GTG	GGT	AGG	GCC	GAT	CAA	AAG	ACA	AAC	297
Phe	Val	Gly	Ile	Ser	Leu	Glu	Val	Gly	Arg	Ala	Asp	Gln	Lys	Thr	Asn	
70					75					80						
GCT	TAT	AAA	AAC	GGC	GAG	TTG	TTT	CAA	GTG	CCT	TTT	GGC	GAT	GTT	TCG	345
Ala	Tyr	Lys	Asn	Gly	Glu	Leu	Phe	Gln	Val	Pro	Phe	Gly	Asp	Val	Ser	
85					90					95						
GCT	AAT	GAT	GAT	GGC	AAA	GTT	CCT	GAC	GGG	CAG	ACC	GGT	GGC	TGT	CAG	393
Ala	Asn	Asp	Asp	Gly	Lys	Val	Pro	Asp	Gly	Gln	Thr	Gly	Gly	Cys	Gln	
100					105					110						
CCA	GCT	TCA	GGG	ACG	CCA	GGA	ACG	CCA	GGC	TAC	ACT	AAA	GCT	AAC	TGC	441
Pro	Ala	Ser	Gly	Thr	Pro	Gly	Thr	Pro	Gly	Tyr	Thr	Lys	Ala	Asn	Cys	
115					120					125						
GTG	GTC	AAT	TGG	ACT	TCG	CGC	ACC	ATG	CTT	AGC	ACC	AAT	AAA	AAC	ATT	489
Val	Val	Asn	Trp	Thr	Ser	Arg	Thr	Met	Leu	Ser	Thr	Asn	Lys	Asn	Ile	
130					135					140					145	
CCT	GGC	CGT	AAC	CAG	CCG	ATG	TAT	GGG	CTA	GGC	GTG	ATG	ACA	GGC	TAT	537
Pro	Gly	Arg	Asn	Gln	Pro	Met	Tyr	Gly	Leu	Gly	Val	Met	Thr	Gly	Tyr	
150					155					160						
AAG	CAT	TTT	ATC	GGT	AAA	AAA	AGA	TGG	TTT	GGG	TTG	CGC	TAT	TAC	GGC	585
Lys	His	Phe	Ile	Gly	Lys	Lys	Arg	Trp	Phe	Gly	Leu	Arg	Tyr	Tyr	Gly	
165					170					175						
TTT	TTT	GAT	TAT	GGG	CAT	ACC	AAT	TTC	TCT	AAC	TCC	AGA	GCC	GCT	AAC	633
Phe	Phe	Asp	Tyr	Gly	His	Thr	Asn	Phe	Ser	Asn	Ser	Arg	Ala	Ala	Asn	
180					185					190						
GCT	ATA	TCG	CCT	TTT	TAT	TTG	AGC	GAT	CAA	AAA	GCC	GAC	ATG	TAT	ACT	681
Ala	Ile	Ser	Pro	Phe	Tyr	Leu	Ser	Asp	Gln	Lys	Ala	Asp	Met	Tyr	Thr	
195					200					205						
TAT	GGT	TTT	GGC	ACA	GAC	ATG	CTT	TTT	AAC	ATT	ATA	GAT	AAG	CCT	AAA	729
Tyr	Gly	Phe	Gly	Thr	Asp	Met	Leu	Phe	Asn	Ile	Ile	Asp	Lys	Pro	Lys	
210					215					220					225	
GCC	ACG	GCC	GGG	TTT	TTT	TTA	GGC	GTG	AAT	TTT	GCG	GGT	AAC	ACT	TGG	777

```

Ile Asp Pro Phe Leu Glu Asp Asp Ala Ala Lys Ser Ile Asp Glu Ala
      100                      105                      110
Lys Arg Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val
      115                      120                      125
Pro Ala Ser Glu Ser Gly Ile Glu Val Val Ser Ala Leu Thr Gln Ala
      130                      135                      140
Ser Ile Pro Val Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly
      145                      150                      155                      160
Glu Ile Ala Gln Ile Leu Ala Lys Glu Ala Gln Lys Arg Ala Val Ile
      165                      170                      175
Ser Val Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro
      180                      185                      190
Lys Asn Leu Gln Ala Gln Ser Gly Ile Ile Asn Ala Thr Glu Cys Tyr
      195                      200                      205
Tyr Gln Ile Asn Gln His Ala Asn Lys Leu Thr Ser Thr Leu Phe Ala
      210                      215                      220
Ser Thr Gly Val Lys Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys
      225                      230                      235                      240
Ala Leu Cys Phe Lys Asn Ser Ile Asn Thr Ala Pro Leu Glu Ala Leu
      245                      250                      255
Asn Ala Tyr Leu Leu Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys
      260                      265                      270
Thr Thr Glu Ile Glu Ala Phe Lys Lys Glu Leu Lys Val His Asn Ile
      275                      280                      285
Asp Leu Glu Asn Thr Ala Gln Lys Leu Leu Lys Glu Gly Leu Ile Ala
      290                      295                      300
Phe Lys Gln Ser Phe Glu Lys Leu Leu Ser Ser Phe
      305                      310                      315

```

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...1215
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

```

AGCTATAATA AAATAATTAA AAAAGTAACA CTTAAGCGGA GACCCTAGAG AGTG ATG      57
                                     Met
                                     1

CTC AAT TTT ATG ACA AAG AAG AAA AAT AGA ATG CAA GAT TGC AAA ATG      105
Leu Asn Phe Met Thr Lys Lys Lys Asn Arg Met Gln Asp Cys Lys Met

```

ATT AAT CAG CAT GCC AAT AAG CTA ACA AGC ACC CTT TTT GCA TCC ACA	728
Ile Asn Gln His Ala Asn Lys Leu Thr Ser Thr Leu Phe Ala Ser Thr	
215 220 225	
GGC GTT AAA TCC AAT TCT TTA GCT AAA GAT TAC TAC ATT AAA GCG CTG	776
Gly Val Lys Ser Asn Ser Leu Ala Lys Asp Tyr Tyr Ile Lys Ala Leu	
230 235 240	
TGT TTT AAA AAC TCT ATC AAT ACA GCC CCT CTA GAG GCT TTA AAC GCT	824
Cys Phe Lys Asn Ser Ile Asn Thr Ala Pro Leu Glu Ala Leu Asn Ala	
245 250 255	
TAT TTG CTT GAC CCA AAC ACC GAG TGT CAA ACC CCT TTA AAG ACT ACA	872
Tyr Leu Leu Asp Pro Asn Thr Glu Cys Gln Thr Pro Leu Lys Thr Thr	
260 265 270	
GAA ATT GAA GCG TTT AAA AAA GAA TTA AAA GTG CAC AAC ATT GAT TTA	920
Glu Ile Glu Ala Phe Lys Lys Glu Leu Lys Val His Asn Ile Asp Leu	
275 280 285 290	
GAA AAC ACC GCT CAA AAA CTC CTT AAA GAA GGC TTG ATA GCG TTC AAA	968
Glu Asn Thr Ala Gln Lys Leu Leu Lys Glu Gly Leu Ile Ala Phe Lys	
295 300 305	
CAA TCC TTT GAA AAG CTT TTA AGC AGT TTT TGATTTTAA GGGTTTTTTG GAT	1021
Gln Ser Phe Glu Lys Leu Leu Ser Ser Phe	
310 315	
AGAATAAGCC CTTATTTTAT TTAAAGGAT	1051

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu	
1 5 10 15	
Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Ala	
20 25 30	
Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe	
35 40 45	
Tyr Lys Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile	
50 55 60	
Tyr Glu Thr Leu Ala Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu	
65 70 75 80	
Met Pro Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu	
85 90 95	

ACCAAGAGGT CGTTAAAAGC TATTACCAAC ATTTAAAAACA AGGATAAAAC	ATG CAA Met Gln 1	56
GAA TTC AGT TTG TGG TGC GAT TTT ATA GAA AGG GAT TTT TTA GAA AAC Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu Glu Asn	5 10 15	104
GAC TTT TTA AAG CTC ATT AAT AAG GGG GCT ATT TGC GGG GCA ACG AGT Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Ala Thr Ser	20 25 30	152
AAC CCT AGT TTG TTT TGC GAA GCG ATC ACA AAA AGC GCG TTT TAT AAA Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe Tyr Lys	35 40 45 50	200
GAT GAA ATC GCT AAA CTC AAA GGC AAA AAA GCT AAA GAA ATT TAT GAA Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile Tyr Glu	55 60 65	248
ACT CTG GCG TTA AAG GAT ATT TTA CAA GCT TCT AGC GCG TTG ATG CCT Thr Leu Ala Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu Met Pro	70 75 80	296
TTA TAT GAA AAA GAC CCT AAC AAT GGC TAC ATT AGC CTA GAA ATT GAC Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu Ile Asp	85 90 95	344
CCT TTT TTA GAA GAT GAT GCC GCT AAA AGC ATT GAT GAA GCC AAG CGG Pro Phe Leu Glu Asp Asp Ala Ala Lys Ser Ile Asp Glu Ala Lys Arg	100 105 110	392
TTG TTC AAA ACA TTA AAC CGC CCT AAT GTG ATG ATT AAA GTC CCA GCG Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val Pro Ala	115 120 125 130	440
AGT GAA AGC GGG ATT GAA GTG GTT AGC GCT TTA ACT CAA GCC TCT ATT Ser Glu Ser Gly Ile Glu Val Val Ser Ala Leu Thr Gln Ala Ser Ile	135 140 145	488
CCT GTT AAT GTA ACT TTA GTC TTT TCG CCT AAA ATT GCC GGT GAA ATC Pro Val Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly Glu Ile	150 155 160	536
GCT CAA ATC TTA GCC AAA GAA GCG CAA AAA AGA GCG GTC ATT AGC GTG Ala Gln Ile Leu Ala Lys Glu Ala Gln Lys Arg Ala Val Ile Ser Val	165 170 175	584
TTT GTC TCA CGA TTT GAC AAA GAA ATA GAC CCT TTA GTG CCA AAA AAT Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro Lys Asn	180 185 190	632
TTG CAA GCT CAA AGC GGG ATT ATC AAC GCT ACC GAG TGC TAT TAT CAA Leu Gln Ala Gln Ser Gly Ile Ile Asn Ala Thr Glu Cys Tyr Tyr Gln	195 200 205 210	680

```

AAA AAT AGA GCG CGA AAG CAA ATC CCT AAT ATG CAC CAT GCC GAT AAT      319
Lys Asn Arg Ala Arg Lys Gln Ile Pro Asn Met His His Ala Asp Asn
      40                      45                      50

GTT ATC CTT AGA ACC CTT GCA ATA AGG GTA GCG CGT GAA ATG GCC TTT T      368
Val Ile Leu Arg Thr Leu Ala Ile Arg Val Ala Arg Glu Met Ala Phe
      55                      60                      65

AAAACAATGT CTATATTTTC TTCATAGCTG TTTTCTTCAT CCAAACACAC CATGTCTTTT      428
CGTGGGGTCA TGATTCTTT AG                                           450

```

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

```

Met Asp Leu Leu Phe Phe His Phe Asn Lys Asp Leu Arg Asn Gly Ser
 1           5           10           15
Ala Phe Gly Asp Asp His Phe Pro Asn Asp Leu Ile Glu Ile Met
      20           25           30
His Phe Gly Gly Lys Asn Arg Ala Arg Lys Gln Ile Pro Asn Met His
      35           40           45
His Ala Asp Asn Val Ile Leu Arg Thr Leu Ala Ile Arg Val Ala Arg
      50           55           60
Glu Met Ala Phe
65

```

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...998
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:


```

Val Asn Ala Glu Asn Leu Asn Pro Pro Phe Thr Trp Ser Leu Gly Leu
225                230                235                240
Leu Gln Met Asp Phe Phe Tyr Arg Lys Lys Ser Trp Tyr Ala Gly Gln
                245                250                255
Phe Met Arg Lys Ile Thr Pro Lys Thr Glu Ile Glu Asn Lys Ile Asp
                260                265                270
Leu Arg Ile Ala Asn Tyr Phe Thr Thr Leu Leu Asn Ala Leu Lys Arg
                275                280                285
Pro Leu Leu Ser Val Leu Val Arg Asp Ile Asp Lys Thr Phe Arg Glu
                290                295                300
Gln Lys Ile Gln Leu Pro Leu Lys Pro Thr Ala Lys Thr Gln Thr Leu
305                310                315                320
Asp Gly Ile Asp Phe Asp Phe Met His Thr Leu Ile Asn Ala Leu Met
                325                330                335
Lys Gln Thr Ile Gln Gly Val Ala Gln Tyr Cys Asp Ala Lys Ile Gln
                340                345                350
Ala Thr Lys Glu Val Ile Ser Gln Glu Ala Pro Val Gln Lys Asp Ser
                355                360                365
Leu Phe
370

```

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 164...367
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

```

AATCCAGCAT GCCCTCTAAT TCAAACACGC CCTCTTCAAG CTTGTTTATG CCCTCTTGTT      60
TTAAGTCGTA TTCGTCGCTA ATCTCGCCCA TGATCTCTTC AATGATGTCT TCCATAGTGA      120
GCAACCCGGC TGTGCCGCCG TATTCATCAA TCACCAAAGC GGT ATG GAT TTG CTC      175
                                   Met Asp Leu Leu
                                   1

TTT TTT CAT TTT AAT AAG GAT TTG AGA AAT GGA AGC GCT TTC GGG GAC      223
Phe Phe His Phe Asn Lys Asp Leu Arg Asn Gly Ser Ala Phe Gly Asp
5                10                15                20

GAT GAT CAT TTT CCT AAC GAT TTG ATT GAA ATC ATG CAT TTT GGG GGT      271
Asp Asp His Phe Pro Asn Asp Leu Ile Glu Ile Met His Phe Gly Gly
                25                30                35

```

```

CTA ATG AAG CAA ACC ATT CAA GGC GTG GCT CAA TAC TGC GAC GCT AAA      1239
Leu Met Lys Gln Thr Ile Gln Gly Val Ala Gln Tyr Cys Asp Ala Lys
335                      340                      345                      350

ATA CAA GCT ACA AAA GAG GTT ATC AGC CAA GAA GCG CCC GTT CAA AAA      1287
Ile Gln Ala Thr Lys Glu Val Ile Ser Gln Glu Ala Pro Val Gln Lys
                      355                      360                      365

GAC TCG TTA TTT TAAAAGGGGT TTTAAGCGCG CTAGCTTGTG TTACAATAAA CTAA      1344
Asp Ser Leu Phe
                      370

AATTCGCTTG                                                    1354

```

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

```

Val Arg Ala Ala Thr Asn Asn Gly Ile Lys Gly Phe Ile Ile Asp Asp
 1                      5                      10                      15
Pro Thr Phe Ala Asn Lys Lys Asn Thr Leu Ser Phe Ala Gln Asp Thr
                      20                      25                      30
Phe Thr Val Phe Tyr Gln Lys Gln Pro Tyr Phe Thr Gly Asn Lys Val
                      35                      40                      45
Lys Ile Leu Lys Pro Lys Phe Ala Phe Lys Ser Pro Lys Ile Leu His
 50                      55                      60
Ser Ile Ser Ala Ile Leu Gln Phe Ile Leu Lys Pro Leu Thr Trp Gly
65                      70                      75                      80
Leu Gly Ser Thr Thr Glu Ser Ile Ala Glu Phe Lys Phe Ser Leu Pro
                      85                      90                      95
Leu Lys Pro Thr Ala Asn Ala Gln Thr Leu Glu Asp Ile Asp Phe Asp
                      100                     105                     110
Phe Met Glu Lys Phe Ile Ala Glu Leu Glu Gln Cys Arg Leu Ala Glu
                      115                     120                     125
Leu Glu Gln Cys Arg Leu Ala Glu Leu Gln Ala Tyr Leu Lys Ala Thr
                      130                     135                     140
Gly Leu Glu Asn Thr Thr Leu Ser Asn Asp Glu Glu Asn Ala Leu Asn
145                      150                     155                     160
Val Phe Asn Asn Ser Gly Gly Gly Gly Gly Asn Thr Pro Cys Gly Leu
                      165                     170                     175
Thr Trp Gln Ser Phe Arg Leu Gly Asp Leu Phe Glu Ile Glu Lys Thr
                      180                     185                     190
Leu Ser Phe Asn Lys Asp Ala Leu Thr Gln Gly Glu Asp Tyr Asp Tyr
                      195                     200                     205
Ile Thr Arg Thr Ser Gln Asn Gln Gly Val Leu Gln Thr Thr Gly Phe
210                      215                      220

```

TTT	GAT	TTC	ATG	GAA	AAA	TTC	ATA	GCC	GAA	CTT	GAG	CAG	TGT	CGG	CTC	567
Phe	Asp	Phe	Met	Glu	Lys	Phe	Ile	Ala	Glu	Leu	Glu	Gln	Cys	Arg	Leu	
				115					120					125		
GCC	GAA	CTT	GAG	CAG	TGT	CGG	CTC	GCC	GAA	CTT	CAG	GCT	TAT	TTA	AAA	615
Ala	Glu	Leu	Glu	Gln	Cys	Arg	Leu	Ala	Glu	Leu	Gln	Ala	Tyr	Leu	Lys	
			130					135					140			
GCT	ACA	GGG	CTA	GAA	AAC	ACC	ACC	CTT	TCT	AAC	GAT	GAA	GAA	AAC	GCC	663
Ala	Thr	Gly	Leu	Glu	Asn	Thr	Thr	Leu	Ser	Asn	Asp	Glu	Glu	Asn	Ala	
		145					150					155				
CTT	AAT	GTT	TTC	AAT	AAT	TCT	GGG	GGG	GGG	GGG	GGT	AAT	ACC	CCA	TGC	711
Leu	Asn	Val	Phe	Asn	Asn	Ser	Gly	Gly	Gly	Gly	Gly	Asn	Thr	Pro	Cys	
	160					165					170					
GGC	TTA	ACA	TGG	CAA	AGC	TTT	AGA	TTA	GGG	GAT	TTG	TTT	GAA	ATT	GAA	759
Gly	Leu	Thr	Trp	Gln	Ser	Phe	Arg	Leu	Gly	Asp	Leu	Phe	Glu	Ile	Glu	
175					180					185					190	
AAA	ACC	TTA	AGC	TTT	AAT	AAA	GAC	GCT	TTA	ACG	CAA	GGA	GAA	GAT	TAT	807
Lys	Thr	Leu	Ser	Phe	Asn	Lys	Asp	Ala	Leu	Thr	Gln	Gly	Glu	Asp	Tyr	
			195					200						205		
GAT	TAT	ATT	ACA	AGG	ACT	TCG	CAA	AAT	CAA	GGC	GTT	TTG	CAA	ACT	ACA	855
Asp	Tyr	Ile	Thr	Arg	Thr	Ser	Gln	Asn	Gln	Gly	Val	Leu	Gln	Thr	Thr	
			210				215					220				
GGA	TTT	GTC	AAT	GCA	GAA	AAT	TTA	AAC	CCA	CCA	TTT	ACT	TGG	AGT	TTA	903
Gly	Phe	Val	Asn	Ala	Glu	Asn	Leu	Asn	Pro	Pro	Phe	Thr	Trp	Ser	Leu	
		225					230					235				
GGG	CTT	TTG	CAA	ATG	GAT	TTT	TTC	TAT	CGT	AAA	AAG	TCA	TGG	TAT	GCG	951
Gly	Leu	Leu	Gln	Met	Asp	Phe	Phe	Tyr	Arg	Lys	Lys	Ser	Trp	Tyr	Ala	
	240					245					250					
GGA	CAA	TTC	ATG	CGA	AAA	ATC	ACA	CCA	AAA	ACT	GAA	ATT	GAA	AAT	AAA	999
Gly	Gln	Phe	Met	Arg	Lys	Ile	Thr	Pro	Lys	Thr	Glu	Ile	Glu	Asn	Lys	
255					260					265					270	
ATT	GAT	TTA	CGC	ATA	GCC	AAC	TAC	TTC	ACA	ACG	CTT	TTA	AAC	GCC	TTA	1047
Ile	Asp	Leu	Arg	Ile	Ala	Asn	Tyr	Phe	Thr	Thr	Leu	Leu	Asn	Ala	Leu	
			275						280					285		
AAA	CGC	CCT	TTA	TTA	AGC	GTA	TTG	GTT	AGA	GAT	ATT	GAT	AAA	ACT	TTT	1095
Lys	Arg	Pro	Leu	Leu	Ser	Val	Leu	Val	Arg	Asp	Ile	Asp	Lys	Thr	Phe	
			290					295					300			
AGG	GAG	CAA	AAA	ATC	CAA	CTA	CCC	CTA	AAA	CCC	ACC	GCT	AAA	ACT	CAA	1143
Arg	Glu	Gln	Lys	Ile	Gln	Leu	Pro	Leu	Lys	Pro	Thr	Ala	Lys	Thr	Gln	
		305					310					315				
ACC	CTT	GAT	GGT	ATT	GAT	TTT	GAT	TTC	ATG	CAC	ACC	CTT	ATC	AAC	GCC	1191
Thr	Leu	Asp	Gly	Ile	Asp	Phe	Asp	Phe	Met	His	Thr	Leu	Ile	Asn	Ala	
	320					325					330					

Glu Lys Gly Tyr Thr Leu Gln Ala Asp Val Arg Arg Val Tyr Ala Phe
 225 230 235 240
 Gln Ile Ser Tyr Leu Arg Asp Phe
 245

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 190...1299
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

```

AGTAAGCTTG ATTTTAAAAA ACCAAATGCC CCCAAAGCGA TAGGCCCCCT TAATAGCCAA      60
CTCAACGCTA TTAAGTGGGG CGAGTTCAGA TTGGGGGATT TGTTTGAAGT GTTGTCAAGT      120
AAGAAAATTT ATCATGCCAA CACGATAAAA ATCCATGACA CGCAAATAGA AAACAGCTAC      180
CCTTATGTC GTG CGC GCT GCA ACC AAT AAT GGT ATA AAA GGC TTT ATT ATA      231
      Val Arg Ala Ala Thr Asn Asn Gly Ile Lys Gly Phe Ile Ile
          1              5              10

GAT GAC CCT ACA TTT GCT AAT AAA AAA AAT ACC CTT TCG TTC GCG CAA      279
Asp Asp Pro Thr Phe Ala Asn Lys Lys Asn Thr Leu Ser Phe Ala Gln
15              20              25              30

GAC ACT TTC ACT GTG TTT TAT CAA AAA CAA CCT TAT TTT ACA GGC AAT      327
Asp Thr Phe Thr Val Phe Tyr Gln Lys Gln Pro Tyr Phe Thr Gly Asn
35              40              45

AAG GTT AAA ATT TTA AAA CCA AAA TTT GCT TTC AAA AGC CCT AAA ATT      375
Lys Val Lys Ile Leu Lys Pro Lys Phe Ala Phe Lys Ser Pro Lys Ile
50              55              60

TTA CAT TCT ATA AGC GCG ATT TTA CAA TTT ATT TTA AAA CCC TTA ACT      423
Leu His Ser Ile Ser Ala Ile Leu Gln Phe Ile Leu Lys Pro Leu Thr
65              70              75

TGG GGG CTA GGC TCT ACA ACA GAA AGC ATT GCG GAG TTT AAA TTT TCT      471
Trp Gly Leu Gly Ser Thr Thr Glu Ser Ile Ala Glu Phe Lys Phe Ser
80              85              90

CTA CCC CTA AAA CCC ACC GCT AAC GCT CAA ACC CTT GAG GAT ATT GAT      519
Leu Pro Leu Lys Pro Thr Ala Asn Ala Gln Thr Leu Glu Asp Ile Asp
95              100              105              110

```

```

AAA CAC AAT AGC CTA GAA TTA GGG ATT AAA GTG CCT ACG ATC ACA CAC      678
Lys His Asn Ser Leu Glu Leu Gly Ile Lys Val Pro Thr Ile Thr His
                205                      210                      215

CAG CTT TTC TCT CTT ACC AAC GAA AAG GGA TAC ACC TTA CAG GCT GAT      726
Gln Leu Phe Ser Leu Thr Asn Glu Lys Gly Tyr Thr Leu Gln Ala Asp
                220                      225                      230

GTG CGT AGA GTT TAT GCG TTT CAA ATC AGT TAC TTG AGG GAT TTT TAACC    776
Val Arg Arg Val Tyr Ala Phe Gln Ile Ser Tyr Leu Arg Asp Phe
                235                      240                      245

CCTTTTGTAGA TACAATCACG CCTGAAACTA TCCA                                810

```

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

```

Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser
 1             5             10             15
Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met
                20             25             30
Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro
                35             40             45
Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr
                50             55             60
Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly
                65             70             75             80
Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile
                85             90             95
Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly
                100            105            110
Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn
                115            120            125
Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn
                130            135            140
Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly
                145            150            155            160
Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys
                165            170            175
His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp
                180            185            190
Lys Phe Gly Val Arg Thr His Ile Ala Lys His Asn Ser Leu Glu Leu
                195            200            205
Gly Ile Lys Val Pro Thr Ile Thr His Gln Leu Phe Ser Leu Thr Asn
                210 -            215            220

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

TATCAAAAAA TAAAGGGAAA AGACTGA ATG TTG AAA AGA ATG ATA TTA TTA GGG	54
Met Leu Lys Arg Met Ile Leu Leu Gly	
1 5	
GCT TTG GGT GTT TTA GCG AGC GCT GAA GAG AGT GCG GCT TTT GTG GGA	102
Ala Leu Gly Val Leu Ala Ser Ala Glu Glu Ser Ala Ala Phe Val Gly	
10 15 20 25	
GTC AAT TAC CAG GTG AGC ATG ATA CAA AAT CAG ACT AAA ATG GTG AAT	150
Val Asn Tyr Gln Val Ser Met Ile Gln Asn Gln Thr Lys Met Val Asn	
30 35 40	
GAC AAC GGC TTG CAA AAG CCT TTG ATA AAG TTT CCG CCT TAC GCA GGA	198
Asp Asn Gly Leu Gln Lys Pro Leu Ile Lys Phe Pro Pro Tyr Ala Gly	
45 50 55	
GCG GGT TTT GAA GTG GGC TAT AAG CAA TTT TTT GGT AAG AAA AAA TGG	246
Ala Gly Phe Glu Val Gly Tyr Lys Gln Phe Phe Gly Lys Lys Lys Trp	
60 65 70	
TTT GGC ATG CGT TAT TAT GGG TTT TTT GAC TAC GCG CAC AAC CGC TTT	294
Phe Gly Met Arg Tyr Tyr Gly Phe Phe Asp Tyr Ala His Asn Arg Phe	
75 80 85	
GGC GTG ATG AAA AAG GGC ATT CCG GTG GGC GAT AGT GGG TTT ATT TAC	342
Gly Val Met Lys Lys Gly Ile Pro Val Gly Asp Ser Gly Phe Ile Tyr	
90 95 100 105	
AAT AGT TTT AGT TTT GGA GGG AAC ACT TTA ACG GAA AGG GAT TCC TAT	390
Asn Ser Phe Ser Phe Gly Gly Asn Thr Leu Thr Glu Arg Asp Ser Tyr	
110 115 120	
CAG GGG CAA TAC TAT GTC AAT TTA TTC ACT TAT GGC GTG GGG TTA GAT	438
Gln Gly Gln Tyr Tyr Val Asn Leu Phe Thr Tyr Gly Val Gly Leu Asp	
125 130 135	
ACG CTG TGG AAT TTT GTG AAT AAA GAA AAC ATG GTT TTT GGT TTT GTG	486
Thr Leu Trp Asn Phe Val Asn Lys Glu Asn Met Val Phe Gly Phe Val	
140 145 150	
GTG GGG ATC CAA TTA GCG GGG GAT AGT TGG GCA ACG AGC ATC AGT AAA	534
Val Gly Ile Gln Leu Ala Gly Asp Ser Trp Ala Thr Ser Ile Ser Lys	
155 160 165	
GAA ATC GCT CAT TAT GCA AAA CAC CAC AGC AAT TCC AGT TAT AGC CCG	582
Glu Ile Ala His Tyr Ala Lys His His Ser Asn Ser Ser Tyr Ser Pro	
170 175 180 185	
GCC AAT TTC CAG TTT TTA TGG AAG TTT GGG GTC CGC ACC CAT ATC GCT	630
Ala Asn Phe Gln Phe Leu Trp Lys Phe Gly Val Arg Thr His Ile Ala	
190 195 200	

```

TTG ACG CTA ACC CCT ATA AAA CGA TTT TTG GAG AAA GGA AAT AAT CAT      106
Leu Thr Leu Thr Pro Ile Lys Arg Phe Leu Glu Lys Gly Asn Asn His
      5                      10                      15

GAG AGC TAC GGC GAT AAA AAT CTT TTC ACT CTC ATC AGC ATT AGC CCT      154
Glu Ser Tyr Gly Asp Lys Asn Leu Phe Thr Leu Ile Ser Ile Ser Pro
      20                      25                      30

ATT GCT TCA TGG TTG CTT GAG CAT CAA TTT AAA ACA AAT GCT ACC AGA      202
Ile Ala Ser Trp Leu Leu Glu His Gln Phe Lys Thr Asn Ala Thr Arg
      35                      40                      45                      50

GAT CAG AAC TTA CGA TTT GAA TGC GAG TTC TTT TGAAATCACG CAATGCGCTA      255
Asp Gln Asn Leu Arg Phe Glu Cys Glu Phe Phe
      55                      60

AACCTTTGAC TGAAGTGAGG CTCATTAGTA TTTTG      290

```

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

```

Ile Asn Leu Thr Leu Thr Pro Ile Lys Arg Phe Leu Glu Lys Gly Asn
  1                      5                      10                      15
Asn His Glu Ser Tyr Gly Asp Lys Asn Leu Phe Thr Leu Ile Ser Ile
      20                      25                      30
Ser Pro Ile Ala Ser Trp Leu Leu Glu His Gln Phe Lys Thr Asn Ala
      35                      40                      45
Thr Arg Asp Gln Asn Leu Arg Phe Glu Cys Glu Phe Phe
      50                      55                      60

```

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...771
- (D) OTHER INFORMATION:

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

```

Met Phe Asp Lys Lys Leu Ser Ser Asn Asp Trp His Ile Gln Lys Val
 1             5             10             15
Glu Met Asn His Gln Val Tyr Asp Ile Glu Thr Met Leu Ala Asp Ser
          20             25             30
Ala Phe Arg Glu His Glu Glu Glu Gln Asp Ser Ser Leu Asn Thr Ala
          35             40             45
Leu Pro Glu Asp Lys Thr Ala Ile Glu Ala Lys Glu Gln Glu Gln Lys
          50             55             60
Glu Lys Arg Lys Arg Trp Tyr Glu Leu Phe Lys Lys Lys Pro Lys Pro
65             70             75             80
Lys Ser Ser Met Gly Glu Phe Val Phe Asp Gln Lys Glu Asn Arg Ile
          85             90             95
Tyr Gly Lys Gly Tyr Cys Asn Arg Tyr Phe Ala Ser Tyr Val Trp Gln
          100            105            110
Gly Asp Arg His Ile Gly Ile Glu Asp Ser Gly Ile Ser Arg Lys Val
          115            120            125
Cys Lys Asp Glu His Leu Met Ala Phe Glu Leu Glu Phe Met Glu Asn
          130            135            140
Phe Lys Gly Asn Phe Thr Val Thr Lys Gly Lys Asp Thr Leu Ile Leu
145            150            155            160
Asp Asn Gln Lys Met Lys Ile Tyr Leu Lys Thr Pro
          165            170

```

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 53...235
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

```

TTGAGCTTAA GAAACATTGA TAATTTTGTG GAAAAAGGCT CTGCTTTGAT AG ATA AAT      58
                                     Ile Asn
                                     1

```



```

AAAATAAGGA GGAATTGTTT GATTTTACGA TTGGCTGGAG CAAGCGTTTT AACGGCTTGT      60
GTCTTTTCGG GGTGTTTTTT TTTAAAA ATG TTT GAT AAA AAA CTT TCT AGT AAC      114
          Met Phe Asp Lys Lys Leu Ser Ser Asn
              1              5

GAT TGG CAT ATC CAA AAA GTG GAA ATG AAC CAT CAA GTC TAT GAC ATT      162
Asp Trp His Ile Gln Lys Val Glu Met Asn His Gln Val Tyr Asp Ile
10              15              20              25

GAA ACC ATG CTC GCT GAT AGC GCT TTT AGA GAG CAT GAA GAA GAG CAA      210
Glu Thr Met Leu Ala Asp Ser Ala Phe Arg Glu His Glu Glu Glu Gln
              30              35              40

GAT TCC TCT CTA AAT ACC GCT TTG CCT GAA GAT AAA ACA GCG ATT GAA      258
Asp Ser Ser Leu Asn Thr Ala Leu Pro Glu Asp Lys Thr Ala Ile Glu
              45              50              55

GCC AAA GAG CAA GAG CAA AAA GAA AAA AGA AAA CGC TGG TAT GAG CTT      306
Ala Lys Glu Gln Glu Gln Lys Glu Lys Arg Lys Arg Trp Tyr Glu Leu
              60              65              70

TTT AAA AAG AAA CCA AAG CCC AAA AGC TCT ATG GGA GAG TTT GTG TTT      354
Phe Lys Lys Lys Pro Lys Pro Lys Ser Ser Met Gly Glu Phe Val Phe
              75              80              85

GAT CAA AAA GAA AAT CGT ATT TAT GGC AAA GGC TAT TGC AAC CGG TAT      402
Asp Gln Lys Glu Asn Arg Ile Tyr Gly Lys Gly Tyr Cys Asn Arg Tyr
90              95              100              105

TTT GCC AGC TAT GTA TGG CAG GGC GAT AGG CAC ATT GGG ATT GAA GAT      450
Phe Ala Ser Tyr Val Trp Gln Gly Asp Arg His Ile Gly Ile Glu Asp
              110              115              120

AGC GGG ATT TCA AGA AAA GTG TGT AAA GAT GAG CAT TTA ATG GCG TTT      498
Ser Gly Ile Ser Arg Lys Val Cys Lys Asp Glu His Leu Met Ala Phe
              125              130              135

GAA TTG GAA TTT ATG GAG AAT TTT AAG GGT AAT TTT ACG GTA ACT AAG      546
Glu Leu Glu Phe Met Glu Asn Phe Lys Gly Asn Phe Thr Val Thr Lys
              140              145              150

GGC AAG GAC ACG CTC ATT TTA GAC AAC CAA AAA ATG AAA ATT TAT TTG      594
Gly Lys Asp Thr Leu Ile Leu Asp Asn Gln Lys Met Lys Ile Tyr Leu
              155              160              165

AAA ACG CCT TGAGTGGGTT TTTGATTTC AACAATCTA AGATCACTAA ATTAGGGAT      652
Lys Thr Pro
170

TAAAAAGAAA TTTTTAA      669

```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

Met	Ala	Phe	Trp	His	Lys	Arg	Leu	Ala	Val	Gly	Cys	Cys	Ile	Val	Leu
1				5					10					15	
Phe	Ser	Cys	Met	Met	Asn	Ala	Asn	Ser	Ile	Gln	Ile	Val	Arg	Asp	Asp
			20					25					30		
Pro	Pro	Leu	Asp	Pro	Thr	Leu	Pro	Ala	Trp	Val	Tyr	Ser	Val	Ala	Leu
		35					40					45			
Leu	Lys	Val	Tyr	Phe	Ser	Asp	Gly	Thr	Tyr	Lys	Glu	Gly	Tyr	Ala	Thr
	50					55					60				
Leu	Leu	Lys	Asn	Gly	Arg	Tyr	Ile	Ala	Ser	Ser	Glu	Thr	Leu	Tyr	Ser
65					70					75					80
Asn	Gly	Leu	Tyr	Pro	Lys	Thr	Ile	Leu	Ala	Lys	Met	Gln	Asp	Ser	Ser
				85				90						95	
Ala	Lys	Glu	Leu	Ile	Cys	Ile	Ala	Ser	Leu	Arg	Leu	Glu	Ala	Met	Asp
			100					105					110		
Arg	Asn	Gln	Gly	Leu	Ser	Leu	Leu	Lys	Thr	Ala	Asp	Phe	Arg	Asp	Asp
	115							120				125			
Tyr	Cys	His	Lys	Arg	Glu	Glu	Ser	Tyr	Tyr	His	Ala	Arg	Ile	Tyr	Thr
	130					135					140				
Lys	Tyr	Ala	Gln	Thr	Phe	His	Ser	Asn	Pro	Tyr	Thr	Asn	Gln	Lys	Thr
145					150					155					160
Pro	Asn	Ser	Asp	Leu	Tyr	Tyr	Pro	Ala	Leu	Asn	Glu	Gly	Asn	Ser	Phe
			165					170						175	
Ser	Ile	Gln	Ile	Met	Gly	Ile	Ser	Val	Ala	Glu	Leu	Leu	Lys	Ser	Lys
		180						185					190		
Lys	Phe	Leu	Ser	Leu	Asp	Val	Ser	Phe	Lys	Lys	Gly	Ser	Val	Leu	Trp
	195						200					205			
Gly	Gly	Arg	Pro	Tyr	Phe	Ser	Glu	Val	Gly	Glu	Phe	Met	Gly	Met	Ala
	210					215					220				
Ser	Ser	Thr	Leu	Glu	Asn	Gln	Glu	Ser	Leu	Val	Ile	Ile	Pro	Lys	Glu
225					230					235					240
Lys	Ile	Val	Gln	Phe	Leu	Asn	Ala	Leu	Lys	Asn	Gln	Asn	Ile	Phe	Pro
			245					250						255	
Asn	Ile	Pro													

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 88...603
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

CTG ATT TGT ATA GCT AGC CTA CGC CTT GAA GCG ATG GAT AGG AAT CAA	392
Leu Ile Cys Ile Ala Ser Leu Arg Leu Glu Ala Met Asp Arg Asn Gln	
100 105 110 115	
GGG CTT TCG CTT TTA AAA ACC GCC GAT TTT AGA GAC GAT TAT TGC CAT	440
Gly Leu Ser Leu Leu Lys Thr Ala Asp Phe Arg Asp Asp Tyr Cys His	
120 125 130	
AAA AGA GAA GAG AGC TAT TAT CAT GCA AGG ATT TAC ACA AAA TAC GCT	488
Lys Arg Glu Glu Ser Tyr Tyr His Ala Arg Ile Tyr Thr Lys Tyr Ala	
135 140 145	
CAA ACT TTT CAT TCA AAT CCC TAT ACC AAT CAA AAA ACA CCC AAT TCT	536
Gln Thr Phe His Ser Asn Pro Tyr Thr Asn Gln Lys Thr Pro Asn Ser	
150 155 160	
GAT CTC TAC TAC CCA GCG TTA AAT GAG GGG AAT TCT TTT TCT ATA CAG	584
Asp Leu Tyr Tyr Pro Ala Leu Asn Glu Gly Asn Ser Phe Ser Ile Gln	
165 170 175	
ATA ATG GGC ATT TCT GTG GCT GAA CTT TTG AAA TCT AAA AAA TTC CTT	632
Ile Met Gly Ile Ser Val Ala Glu Leu Leu Lys Ser Lys Lys Phe Leu	
180 185 190 195	
TCG CTT GAT GTT TCT TTT AAA AAG GGG AGC GTG TTG TGG GGA GGG AGG	680
Ser Leu Asp Val Ser Phe Lys Lys Gly Ser Val Leu Trp Gly Gly Arg	
200 205 210	
CCT TAT TTT AGC GAA GTG GGG GAG TTT ATG GGG ATG GCT AGC AGC ACT	728
Pro Tyr Phe Ser Glu Val Gly Glu Phe Met Gly Met Ala Ser Ser Thr	
215 220 225	
TTA GAA AAC CAA GAA AGT CTG GTG ATT ATC CCT AAA GAA AAG ATC GTG	776
Leu Glu Asn Gln Glu Ser Leu Val Ile Ile Pro Lys Glu Lys Ile Val	
230 235 240	
CAA TTT TTA AAC GCT CTA AAA AAT CAA AAT ATT TTC CCA AAC ATT CCC T	825
Gln Phe Leu Asn Ala Leu Lys Asn Gln Asn Ile Phe Pro Asn Ile Pro	
245 250 255	
AAGTTTAAGC AAACCTTAAG CTTTCTATGA CTATACTTTC ATTTCTTGT TTCAGCA	882

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

(2) INFORMATION FOR SEO ID NO:571:

(A) LENGTH: 882 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 48...824
(D) OTHER INFORMATION:

CGATAGT	TGTT	GTAGGATA	CT	TTTGAAATTT	AAGCGGTAAG	TTGGATA	ATG	GCG	TTT								56
							Met	Ala	Phe								
							1										
TGG	CAT	AAA	AGA	TTA	GCG	GTT	GGT	TGT	TGT	ATC	GTT	TTA	TTT	TCA	TGC		104
Trp	His	Lys	Arg	Leu	Ala	Val	Gly	Cys	Cys	Ile	Val	Leu	Phe	Ser	Cys		
	5					10				15							
ATG	ATG	AAC	GCT	AAT	AGC	ATT	CAA	ATC	GTT	AGA	GAC	GAT	CCG	CCC	CTT		152
Met	Met	Asn	Ala	Asn	Ser	Ile	Gln	Ile	Val	Arg	Asp	Asp	Pro	Pro	Leu		
20					25				30						35		
GAT	CCA	ACG	CTC	CCT	GCA	TGG	GTT	TAT	TCT	GTT	GCG	TTA	TTA	AAA	GTG		200
Asp	Pro	Thr	Leu	Pro	Ala	Trp	Val	Tyr	Ser	Val	Ala	Leu	Leu	Lys	Val		
				40				45						50			
TAT	TTT	AGC	GAT	GGG	ACT	TAT	AAA	GAA	GGC	TAT	GCG	ACT	TTG	CTC	AAA		248
Tyr	Phe	Ser	Asp	Gly	Thr	Tyr	Lys	Glu	Gly	Tyr	Ala	Thr	Leu	Leu	Lys		
			55				60						65				
AAC	GGG	CGT	TAT	ATC	GCT	TCT	TCT	GAA	ACG	CTT	TAT	TCT	AAC	GGC	TTA		296
Asn	Gly	Arg	Tyr	Ile	Ala	Ser	Ser	Glu	Thr	Leu	Tyr	Ser	Asn	Gly	Leu		
		70					75					80					
TAC	CCT	AAA	ACG	ATT	TTA	GCC	AAA	ATG	CAA	GAC	AGC	AGC	GCT	AAA	GAG		344
Tyr	Pro	Lys	Thr	Ile	Leu	Ala	Lys	Met	Gln	Asp	Ser	Ser	Ala	Lys	Glu		
	85					90				95							

TTA GCT AGG GCT TTA AAA CTC GTT TTA GAA GAC AGA GTC TTT GTA CAT 927
 Leu Ala Arg Ala Leu Lys Leu Val Leu Glu Asp Arg Val Phe Val His
 275 280 285

GAA AAT AAA ACG GTG GTG TTT TGAATGCTTT TAGATTTTCAG CAACCTCAAT GAAG 982
 Glu Asn Lys Thr Val Val Phe
 290

AACCCTTAAA AAAC 996

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

Met	Leu	Glu	Phe	Ile	Leu	Lys	Ile	Gln	Ala	Arg	Asp	Ser	Lys	Gly	Leu	1	5	10	15
Val	Ser	Thr	Ile	Ser	Thr	Thr	Ile	Ala	Asn	Lys	Gly	Tyr	Asn	Ile	Val	20	25	30	
Lys	Asn	Asp	Glu	Phe	Val	Asp	Pro	Leu	Lys	Gln	Arg	Phe	Phe	Met	Arg	35	40	45	
Leu	Lys	Ile	Gln	Lys	Glu	Ile	Lys	Pro	Leu	Asn	Thr	Glu	Ile	Lys	Glu	50	55	60	
Gln	Glu	Glu	Gln	Ser	Leu	Lys	Thr	Ala	Leu	Phe	Lys	Ala	Leu	Glu	Asn	65	70	75	80
Phe	Asn	Glu	Leu	Leu	Ile	Glu	Val	Ile	Leu	Thr	His	Lys	Lys	Asn	Ile	85	90	95	
Ile	Leu	Leu	Ala	Thr	Lys	Glu	Ser	His	Cys	Leu	Gly	Asp	Leu	Leu	Leu	100	105	110	
Arg	Val	Tyr	Gly	Gly	Glu	Leu	Asn	Ala	Gln	Ile	Leu	Gly	Val	Ile	Ser	115	120	125	
Asn	His	Glu	Ile	Leu	Arg	Pro	Leu	Val	Glu	Lys	Phe	Asp	Ile	Pro	Tyr	130	135	140	
Phe	Tyr	Ala	Pro	Cys	Asp	Asn	Gln	Val	Leu	His	Glu	Lys	Glu	Val	Leu	145	150	155	160
Glu	Ile	Ile	Lys	Asn	Leu	Glu	Leu	Lys	His	Lys	Val	Ser	Ala	Asp	Leu	165	170	175	
Leu	Val	Leu	Ala	Lys	Tyr	Met	Arg	Ile	Leu	Ser	His	Asp	Phe	Thr	Lys	180	185	190	
Arg	Tyr	Glu	Asn	Gln	Ile	Leu	Asn	Ile	His	His	Ser	Phe	Leu	Pro	Ala	195	200	205	
Phe	Ile	Gly	Ala	Asn	Pro	Tyr	Gln	Gln	Ala	Phe	Glu	Arg	Gly	Val	Lys	210	215	220	
Val	Ile	Gly	Ala	Thr	Ala	His	Phe	Val	Asn	Glu	Ser	Leu	Asp	Ala	Gly	225	230	235	240
Pro	Ile	Ile	Ile	Gln	Asp	Thr	Leu	Pro	Ile	Asn	His	Asn	Tyr	Ser	Val	245	250	255	

ATG CGG TTA AAA ATC CAA AAA GAA ATC AAG CCC TTG AAT ACT GAA ATT	255
Met Arg Leu Lys Ile Gln Lys Glu Ile Lys Pro Leu Asn Thr Glu Ile	
50 55 60	
AAA GAG CAA GAA GAG CAA TCC TTA AAG ACC GCT CTT TTT AAA GCC CTA	303
Lys Glu Gln Glu Glu Gln Ser Leu Lys Thr Ala Leu Phe Lys Ala Leu	
65 70 75	
GAA AAC TTT AAC GAG TTA TTG ATT GAA GTC ATT TTA ACG CAT AAA AAA	351
Glu Asn Phe Asn Glu Leu Leu Ile Glu Val Ile Leu Thr His Lys Lys	
80 85 90	
AAC ATC ATT CTG CTC GCT ACT AAA GAG AGC CAT TGC TTA GGG GAT TTG	399
Asn Ile Ile Leu Leu Ala Thr Lys Glu Ser His Cys Leu Gly Asp Leu	
95 100 105 110	
CTT TTA AGG GTG TAT GGG GGG GAA TTG AAC GCT CAA ATT TTA GGC GTT	447
Leu Leu Arg Val Tyr Gly Gly Glu Leu Asn Ala Gln Ile Leu Gly Val	
115 120 125	
ATT TCC AAC CAC GAG ATT TTA CGC CCT TTA GTG GAA AAA TTT GAC ATC	495
Ile Ser Asn His Glu Ile Leu Arg Pro Leu Val Glu Lys Phe Asp Ile	
130 135 140	
CCT TAT TTT TAT GCG CCT TGC GAC AAT CAA GTT TTG CAT GAA AAA GAA	543
Pro Tyr Phe Tyr Ala Pro Cys Asp Asn Gln Val Leu His Glu Lys Glu	
145 150 155	
GTT TTA GAA ATC ATT AAA AAC CTG GAA TTA AAG CAC AAA GTG AGT GCA	591
Val Leu Glu Ile Ile Lys Asn Leu Glu Leu Lys His Lys Val Ser Ala	
160 165 170	
GAC TTG CTC GTT TTA GCC AAA TAC ATG CGC ATT TTA AGC CAT GAT TTT	639
Asp Leu Leu Val Leu Ala Lys Tyr Met Arg Ile Leu Ser His Asp Phe	
175 180 185 190	
ACG AAG CGC TAT GAA AAC CAG ATC TTA AAT ATC CAT CAT AGT TTC TTG	687
Thr Lys Arg Tyr Glu Asn Gln Ile Leu Asn Ile His His Ser Phe Leu	
195 200 205	
CCC GCA TTC ATT GGG GCT AAT CCT TAC CAG CAA GCG TTT GAA AGG GGC	735
Pro Ala Phe Ile Gly Ala Asn Pro Tyr Gln Gln Ala Phe Glu Arg Gly	
210 215 220	
GTG AAA GTC ATC GGG GCC ACG GCG CAT TTT GTG AAT GAA AGC CTT GAT	783
Val Lys Val Ile Gly Ala Thr Ala His Phe Val Asn Glu Ser Leu Asp	
225 230 235	
GCT GGG CCG ATT ATC ATA CAA GAC ACT CTG CCC ATT AAC CAC AAT TAC	831
Ala Gly Pro Ile Ile Ile Gln Asp Thr Leu Pro Ile Asn His Asn Tyr	
240 245 250	
AGC GTG GAA AAA ATG CGC CTA GCG GGT AAG GAT ATA GAA AAA CTG GTT	879
Ser Val Glu Lys Met Arg Leu Ala Gly Lys Asp Ile Glu Lys Leu Val	
255 260 265 270	

(2) INFORMATION FOR SEQ ID NO:569:

(A) LENGTH: 996 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 70...948
(D) OTHER INFORMATION:

AAAAGCCACG	CAATCAGCCA	CAAACATCAT	CACACAAGCC	TTTGGCTATC	AATTATTAAT	60
GAGATAAAG	ATG TTA GAA	TTT ATT TTA	AAA ATT CAA	GCT AGA GAC	TCT AAA	111
	Met Leu Glu	Phe Ile Leu	Lys Ile Gln	Ala Arg Asp	Ser Lys	
	1	5	10			
GGC TTG GTG	AGC ACG ATT	AGC ACC ACT	ATC GCT AAC	AAG GGC TAT	AAC	159
Gly Leu Val	Ser Thr Ile	Ser Thr Thr	Ile Ala Asn	Lys Gly Tyr	Asn	
15	20	25	30			
ATC GTC AAA	AAC GAT GAA	TTT GTT GAT	CCC TTA AAA	CAG CGT TTT	TTC	207
Ile Val Lys	Asn Asp Glu	Phe Val Asp	Pro Leu Lys	Gln Arg Phe	Phe	
	35	40	45			

```

Val Pro Ser Asp Val Arg Glu Arg Lys Gly Ala Phe Phe Thr Pro Lys
  290                      295                      300
Ile Trp Val Glu Lys Ser Gln Glu Tyr Leu Ala Lys Ala Leu Gly Gln
  305                      310                      315                      320
Asp Tyr Gln Glu Asp Cys Ile Ile Trp Asp Cys Ala Gly Gly Thr Gly
                      325                      330                      335
Asn Leu Leu Arg Gly Leu Leu Asn Lys Ala Asn Leu Tyr Leu Ser Thr
                      340                      345                      350
Leu Asp His Asn Asp Val Ala Ile Val Lys Asp Leu Ala Ala Lys Asn
                      355                      360                      365
His Leu Lys Leu Leu Glu Asn His Val Phe Gln Phe Asp Phe Leu Asn
                      370                      375                      380
Asp Asp Phe Phe Ser Asp Lys Thr Pro Lys Ser Leu Gln Glu Ile Leu
  385                      390                      395                      400
Lys Asp Lys Glu Lys Arg Lys Lys Leu Ile Ile Tyr Ile Asn Pro Pro
                      405                      410                      415
Tyr Ala Glu Ala Gly Asn Lys Ser Lys Met Ser Gly Thr Gly Glu His
                      420                      425                      430
Lys Ala Lys Val Ala Arg Asp Asn Leu Ile Cys Glu Lys Tyr Lys Asn
                      435                      440                      445
Glu Leu Gly Lys Ala Asn Asn Glu Val Phe Ala Gln Phe Phe Met Arg
  450                      455                      460
Ile Tyr Lys Glu Leu Asn Gly Val Ile Leu Ala Ser Phe Ser Thr Leu
  465                      470                      475                      480
Lys Asn Leu Gln Gly Ser Asn Phe Lys Lys Phe Arg Glu Ile Phe Lys
                      485                      490                      495
Ala Lys Phe Leu Glu Gly Phe Met Val Pro Ala Asp Thr Phe Asp Asn
                      500                      505                      510
Val Arg Gly Gln Phe Pro Ile Gly Phe Leu Val Trp Asp Thr Ser Ser
                      515                      520                      525
Ile Leu Pro Lys Glu Asn Pro Leu Asn Leu Gly Gly Asn Ser Lys Glu
  530                      535                      540
Glu Lys Gln Asn Ser Asn Leu Ile Leu Asp Gln Asp Asn Leu Lys Asp
  545                      550                      555                      560
Asn Pro Leu Lys Glu Arg Phe Cys Leu Leu Asp Ile Asn Ala Pro Asn
                      565                      570                      575
Arg Lys Met Cys Ser Gln Ser Arg Thr Arg Thr Lys Gly Thr Gln Lys
                      580                      585                      590
His Ser Thr Ala Ala Pro Phe Glu Thr Pro Leu His Thr Val Ser Leu
  595                      600                      605
Glu Ile Phe Asp Ser Phe Gly Gly Phe Leu Gly Ser Lys Lys Ile Tyr
  610                      615                      620
Thr His Thr Ile Asp Lys Met Leu Thr Leu Ala Asp Tyr Leu Gln Lys
  625                      630                      635                      640
Phe Gln Pro Thr Lys Arg Asp Thr Ile Phe Gly Tyr Leu Asp Pro Gly
                      645                      650                      655
Arg Asn Ser Phe Gln His Gln Asn Leu Ile His Ile Ser Ile Ile Asp
                      660                      665                      670
Lys Ser Lys Gln Ser His Val Lys Tyr Phe Pro Ile Ile Ala Thr Thr
                      675                      680                      685
Ile Leu Leu Val Ser Val Phe Phe Ser Ile Arg His Cys Ile Lys Ala
  690                      695                      700
Thr Trp Gln Asn Asp Arg Asp Gln Phe Tyr Ala Pro Tyr Asp Asp Ala
  705                      710                      715                      720
Phe Gln Asp Asp Ser Glu Phe Lys Asn Asn Cys Leu Ile Phe Met Leu

```


GAGCAAGCGG TATTTTSTA 2770

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 892 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Met 1	Leu	Leu	Asp	Phe 5	Ser	Asn	Leu	Asn	Glu 10	Glu	Pro	Leu	Lys	Asn 15	Gln
Ile	Lys	Ala	Glu	Phe	Phe	Lys	Asp	Lys	Lys	Phe	Leu	Tyr	Ser	Gly	Asp
			20					25					30		
Lys	Ile	Asp	Phe	Met	Leu	Ser	Tyr	Lys	His	Ser	Asn	Ala	Thr	Leu	Pro
		35					40				45				
Ile	Leu	Trp	Gly	Glu	Ala	Lys	Arg	Gly	Asp	Phe	Asp	Asp	Leu	Asp	Lys
	50					55				60					
Ala	Phe	Thr	Gln	Leu	Leu	Leu	Thr	Ile	Gly	Lys	His	Arg	Leu	Tyr	Thr
65					70					75					80
His	His	Thr	Pro	Pro	Tyr	Leu	Cys	Ala	Phe	Asn	Ala	Phe	Lys	Met	Glu
				85					90					95	
Phe	Ile	Ala	Phe	Asp	Asp	Thr	Ile	Thr	Ser	Phe	Phe	Tyr	Lys	Ser	Asp
			100					105					110		
Ile	Asp	Phe	Ser	Ile	Thr	Pro	Ser	Asn	His	Asn	Thr	Glu	Gly	Phe	Lys
		115					120					125			
His	Ala	Leu	Asp	Ala	Phe	Lys	Ala	Met	Ser	Lys	Ser	His	Lys	Phe	Val
	130					135					140				
Phe	Asp	Phe	Lys	Thr	Gln	Ser	Gln	Glu	Cys	Lys	Glu	Phe	Ile	Lys	Asn
145					150					155					160
Arg	Leu	Asn	Ser	Ser	His	Leu	Leu	Ser	Lys	Ile	Gln	Ile	Asp	Lys	Asn
				165					170					175	
Asn	Phe	Phe	Thr	Ile	Tyr	Gln	Lys	Trp	Leu	Glu	Ile	Val	Lys	Pro	Thr
			180					185					190		
Ile	Asp	Ile	Asn	Trp	Glu	Val	Ala	Lys	Thr	Lys	Asp	Ile	Leu	Asp	Ala
		195					200					205			
Asp	Tyr	Tyr	Leu	Ala	Asp	Leu	Leu	Ser	Asp	Gly	Asp	Lys	Thr	Ile	Ile
	210					215					220				
Glu	Lys	Leu	His	Thr	Ile	Leu	Arg	Ser	Ser	His	Tyr	Lys	Leu	Asn	Arg
225					230					235					240
Gly	Val	Asn	Glu	Leu	Gly	Lys	Met	Asp	Phe	Met	Glu	Val	Gly	Phe	Thr
				245					250					255	
Asp	Ser	Gln	Gln	Ala	His	Gln	Glu	Phe	Trp	Ser	Val	Tyr	Glu	Arg	Pro
			260					265					270		
Pro	Lys	Arg	Glu	Phe	Gln	Ala	Ser	Ile	Leu	Glu	Arg	Arg	Asp	Leu	Leu
		275					280					285			

CAA CAT CAA AAT CTA ATT CAT ATT AGC ATT ATT GAC AAA TCA AAA CAA	2073
Gln His Gln Asn Leu Ile His Ile Ser Ile Ile Asp Lys Ser Lys Gln	
665 670 675	
TCG CAT GTA AAA TAT TTT CCA ATC ATT GCA ACT ACA ATT TTG TTG GTA	2121
Ser His Val Lys Tyr Phe Pro Ile Ile Ala Thr Thr Ile Leu Leu Val	
680 685 690	
TCT GTA TTT TTC TCC ATC CGC CAT TGC ATC AAA GCC ACA TGG CAA AAC	2169
Ser Val Phe Phe Ser Ile Arg His Cys Ile Lys Ala Thr Trp Gln Asn	
695 700 705	
GAT AGG GAT CAA TTT TAC GCC CCC TAT GAC GAT GCG TTC CAA GAC GAC	2217
Asp Arg Asp Gln Phe Tyr Ala Pro Tyr Asp Asp Ala Phe Gln Asp Asp	
710 715 720	
AGC GAG TTT AAA AAC AAT TGT TTG ATT TTC ATG CTT TTT CAC ACC CAG	2265
Ser Glu Phe Lys Asn Asn Cys Leu Ile Phe Met Leu Phe His Thr Gln	
725 730 735 740	
AAC CGC ATC ACT ACC GCT CAA GGG ACT AAC CAT TTT ATC CCC TTT AGC	2313
Asn Arg Ile Thr Thr Ala Gln Gly Thr Asn His Phe Ile Pro Phe Ser	
745 750 755	
GAA ACT GAA GTC AAT GCC AAA GAA AGA TAT TCT AGC CAC GCT CTA TTA	2361
Glu Thr Glu Val Asn Ala Lys Glu Arg Tyr Ser Ser His Ala Leu Leu	
760 765 770	
GAG TTT TTA AAA GGC GAA ATC AAA GAA CTT AAA GAG AAC GAT AGC CTC	2409
Glu Phe Leu Lys Gly Glu Ile Lys Glu Leu Lys Glu Asn Asp Ser Leu	
775 780 785	
TTT TTA AGT GCC AAA AAA GAA AAC AAG CCC CTG AAA TTC AGC CCG AGC	2457
Phe Leu Ser Ala Lys Lys Glu Asn Lys Pro Leu Lys Phe Ser Pro Ser	
790 795 800	
GCT TCA AAG GTG TTT GAC GCT AGC AGA GAG GTT TAT CGC TAT TAC CAC	2505
Ala Ser Lys Val Phe Asp Ala Ser Arg Glu Val Tyr Arg Tyr Tyr His	
805 810 815 820	
ACA CAA GAT TTC ACA AAC CGC CCC TAT AAC GCT AAC GCA AGC CTT TAT	2553
Thr Gln Asp Phe Thr Asn Arg Pro Tyr Asn Ala Asn Ala Ser Leu Tyr	
825 830 835	
GAC ATC AAA GAA TTT TTT CAA GGC CGT AAC AAG CAA GGC AAA TTA AAT	2601
Asp Ile Lys Glu Phe Phe Gln Gly Arg Asn Lys Gln Gly Lys Leu Asn	
840 845 850	
TTA CCC GCT AAA GCT AAA GAT GAA TAT TAC AAA CAG CTT TAC GCT AAT	2649
Leu Pro Ala Lys Ala Lys Asp Glu Tyr Tyr Lys Gln Leu Tyr Ala Asn	
855 860 865	
TTG CAA GAC GCC CTA AAA GAT CTC GCC AAA GAA ATA CAG CCT AAA GTC	2697
Leu Gln Asp Ala Leu Lys Asp Leu Ala Lys Glu Ile Gln Pro Lys Val	
870 875 880	

GCA CGA GAC AAT CTC ATC TGT GAA AAA TAC AAA AAT GAA TTA GGC AAG	1401
Ala Arg Asp Asn Leu Ile Cys Glu Lys Tyr Lys Asn Glu Leu Gly Lys	
440 445 450	
GCT AAT AAT GAA GTT TTT GCA CAA TTT TTC ATG CGT ATT TAC AAA GAA	1449
Ala Asn Asn Glu Val Phe Ala Gln Phe Phe Met Arg Ile Tyr Lys Glu	
455 460 465	
TTA AAC GGT GTT ATC CTT GCA AGT TTT TCA ACT TTG AAA AAC TTG CAA	1497
Leu Asn Gly Val Ile Leu Ala Ser Phe Ser Thr Leu Lys Asn Leu Gln	
470 475 480	
GGA TCT AAT TTT AAA AAA TTC AGA GAA ATC TTT AAA GCT AAA TTT TTA	1545
Gly Ser Asn Phe Lys Lys Phe Arg Glu Ile Phe Lys Ala Lys Phe Leu	
485 490 495 500	
GAG GGG TTT ATG GTG CCA GCA GAC ACT TTT GAT AAT GTT AGG GGG CAA	1593
Glu Gly Phe Met Val Pro Ala Asp Thr Phe Asp Asn Val Arg Gly Gln	
505 510 515	
TTT CCT ATC GGC TTT TTA GTG TGG GAT ACA AGC TCT ATT CTT CCT AAA	1641
Phe Pro Ile Gly Phe Leu Val Trp Asp Thr Ser Ser Ile Leu Pro Lys	
520 525 530	
GAA AAC CCC CTA AAT TTA GGG GGC AAC TCT AAA GAA GAG AAA CAA AAC	1689
Glu Asn Pro Leu Asn Leu Gly Gly Asn Ser Lys Glu Glu Lys Gln Asn	
535 540 545	
TCC AAT TTA ATC TTA GAC CAA GAC AAT TTG AAA GAT AAT CCC TTG AAA	1737
Ser Asn Leu Ile Leu Asp Gln Asp Asn Leu Lys Asp Asn Pro Leu Lys	
550 555 560	
GAG CGT TTT TGC CTT TTA GAC ATA AAC GCT CCT AAT AGG AAG ATG TGT	1785
Glu Arg Phe Cys Leu Leu Asp Ile Asn Ala Pro Asn Arg Lys Met Cys	
565 570 575 580	
TCC CAA AGC AGA ACA AGA ACT AAG GGG ACA CAA AAG CAT TCT ACA GCA	1833
Ser Gln Ser Arg Thr Arg Thr Lys Gly Thr Gln Lys His Ser Thr Ala	
585 590 595	
GCC CCC TTT GAA ACC CCT TTA CAC ACT GTT AGT TTA GAA ATA TTT GAT	1881
Ala Pro Phe Glu Thr Pro Leu His Thr Val Ser Leu Glu Ile Phe Asp	
600 605 610	
AGT TTC GGC GGA TTT TTA GGC AGT AAA AAA ATA TAC ACT CAC ACA ATA	1929
Ser Phe Gly Gly Phe Leu Gly Ser Lys Lys Ile Tyr Thr His Thr Ile	
615 620 625	
GAC AAA ATG CTT ACT TTA GCG GAT TAT TTA CAA AAG TTT CAG CCA ACA	1977
Asp Lys Met Leu Thr Leu Ala Asp Tyr Leu Gln Lys Phe Gln Pro Thr	
630 635 640	
AAA AGA GAC ACT ATT TTT GGC TAT TTA GAT CCT GGT CGC AAT AGT TTT	2025
Lys Arg Asp Thr Ile Phe Gly Tyr Leu Asp Pro Gly Arg Asn Ser Phe	
645 650 655 660	

GCG GAT TTG CTT AGC GAT GGC GAT AAA ACC ATT ATT GAG AAA TTG CAC Ala Asp Leu Leu Ser Asp Gly Asp Lys Thr Ile Ile Glu Lys Leu His 215 220 225	729
ACG ATT TTA AGA TCG AGC CAT TAT AAA TTG AAT AGG GGT GTG AAT GAA Thr Ile Leu Arg Ser Ser His Tyr Lys Leu Asn Arg Gly Val Asn Glu 230 235 240	777
TTA GGC AAA ATG GAT TTT ATG GAA GTT GGT TTC ACA GAC AGC CAA CAA Leu Gly Lys Met Asp Phe Met Glu Val Gly Phe Thr Asp Ser Gln Gln 245 250 255 260	825
GCC CAT CAA GAA TTT TGG AGC GTT TAT GAA CGA CCG CCT AAA AGA GAA Ala His Gln Glu Phe Trp Ser Val Tyr Glu Arg Pro Pro Lys Arg Glu 265 270 275	873
TTT CAA GCC TCT ATT TTA GAG CGG CGC GAC TTG TTA GTA CCA AGC GAT Phe Gln Ala Ser Ile Leu Glu Arg Arg Asp Leu Leu Val Pro Ser Asp 280 285 290	921
GTG AGA GAA AGG AAA GGG GCG TTT TTC ACC CCT AAA ATC TGG GTA GAA Val Arg Glu Arg Lys Gly Ala Phe Phe Thr Pro Lys Ile Trp Val Glu 295 300 305	969
AAG AGT CAA GAA TAT TTA GCT AAA GCT TTG GGG CAA GAT TAT CAA GAG Lys Ser Gln Glu Tyr Leu Ala Lys Ala Leu Gly Gln Asp Tyr Gln Glu 310 315 320	1017
GAT TGT ATC ATT TGG GAT TGC GCT GGG GGG ACT GGG AAT TTG CTT CGA Asp Cys Ile Ile Trp Asp Cys Ala Gly Gly Thr Gly Asn Leu Leu Arg 325 330 335 340	1065
GGT TTA TTG AAT AAG GCT AAT TTG TAT CTA TCC ACT TTA GAT CAT AAC Gly Leu Leu Asn Lys Ala Asn Leu Tyr Leu Ser Thr Leu Asp His Asn 345 350 355	1113
GAT GTG GCA ATC GTT AAA GAT CTG GCT GCA AAA AAC CAC TTA AAA TTA Asp Val Ala Ile Val Lys Asp Leu Ala Ala Lys Asn His Leu Lys Leu 360 365 370	1161
CTG GAA AAT CAT GTT TTC CAA TTT GAC TTT TTA AAC GAT GAT TTT TTC Leu Glu Asn His Val Phe Gln Phe Asp Phe Leu Asn Asp Asp Phe Phe 375 380 385	1209
AGC GAT AAA ACG CCA AAA AGC TTG CAA GAA ATC TTA AAA GAC AAA GAG Ser Asp Lys Thr Pro Lys Ser Leu Gln Glu Ile Leu Lys Asp Lys Glu 390 395 400	1257
AAA CGA AAA AAG CTC ATC ATT TAC ATC AAC CCG CCC TAT GCA GAA GCA Lys Arg Lys Lys Leu Ile Ile Tyr Ile Asn Pro Pro Tyr Ala Glu Ala 405 410 415 420	1305
GGT AAT AAA TCT AAG ATG AGT GGC ACA GGC GAA CAT AAA GCC AAA GTG Gly Asn Lys Ser Lys Met Ser Gly Thr Gly Glu His Lys Ala Lys Val 425 430 435	1353

Met Leu Leu Asp

1

TTC AGC AAC CTC AAT GAA GAA CCC TTA AAA AAC CAA ATC AAA GCC GAG	105
Phe Ser Asn Leu Asn Glu Glu Pro Leu Lys Asn Gln Ile Lys Ala Glu	
5 10 15 20	
TTT TTT AAG GAT AAG AAA TTC CTT TAT AGC GGG GAT AAA ATA GAT TTC	153
Phe Phe Lys Asp Lys Lys Phe Leu Tyr Ser Gly Asp Lys Ile Asp Phe	
25 30 35	
ATG CTA AGC TAT AAG CAT TCT AAC GCC ACC TTA CCC ATT TTA TGG GGC	201
Met Leu Ser Tyr Lys His Ser Asn Ala Thr Leu Pro Ile Leu Trp Gly	
40 45 50	
GAA GCT AAA AGG GGC GAT TTT GAT GAT TTG GAC AAA GCT TTC ACG CAA	249
Glu Ala Lys Arg Gly Asp Phe Asp Asp Leu Asp Lys Ala Phe Thr Gln	
55 60 65	
CTT CTT TTA ACC ATA GGC AAG CAC AGG CTT TAT ACC CAC CAC ACA CCA	297
Leu Leu Leu Thr Ile Gly Lys His Arg Leu Tyr Thr His His Thr Pro	
70 75 80	
CCT TAT TTG TGC GCT TTT AAC GCT TTT AAA ATG GAA TTT ATC GCC TTT	345
Pro Tyr Leu Cys Ala Phe Asn Ala Phe Lys Met Glu Phe Ile Ala Phe	
85 90 95 100	
GAT GAC ACG ATC ACA AGC TTT TTT TAT AAA AGC GAT ATA GAT TTT TCT	393
Asp Asp Thr Ile Thr Ser Phe Phe Tyr Lys Ser Asp Ile Asp Phe Ser	
105 110 115	
ATC ACC CCA AGC AAC CAC AAC ACA GAA GGT TTT AAA CAT GCT TTA GAC	441
Ile Thr Pro Ser Asn His Asn Thr Glu Gly Phe Lys His Ala Leu Asp	
120 125 130	
GCG TTT AAA GCC ATG AGC AAA TCC CAT AAA TTC GTT TTT GAC TTT AAA	489
Ala Phe Lys Ala Met Ser Lys Ser His Lys Phe Val Phe Asp Phe Lys	
135 140 145	
ACC CAA AGC CAA GAA TGC AAA GAA TTT ATC AAA AAC CGT TTA AAT TCT	537
Thr Gln Ser Gln Glu Cys Lys Glu Phe Ile Lys Asn Arg Leu Asn Ser	
150 155 160	
AGC CAT TTA CTC AGC AAA ATC CAA ATT GAC AAA AAC AAT TTC TTT ACG	585
Ser His Leu Leu Ser Lys Ile Gln Ile Asp Lys Asn Asn Phe Phe Thr	
165 170 175 180	
ATC TAT CAA AAG TGG CTT GAA ATT GTC AAA CCC ACC ATT GAC ATA AAT	633
Ile Tyr Gln Lys Trp Leu Glu Ile Val Lys Pro Thr Ile Asp Ile Asn	
185 190 195	
TGG GAG GTG GCT AAA ACT AAA GAC ATT TTA GAC GCA GAC TAT TAT TTA	681
Trp Glu Val Ala Lys Thr Lys Asp Ile Leu Asp Ala Asp Tyr Tyr Leu	
200 205 210	

[illegible]

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2770 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...2721
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GAAGACAGAG TCTTTGTACA TGAAAATAAA ACGGTGGTGT TTTGA ATG CTT TTA GAT

57

```

Met Thr Asp Asn Asn Gln Asn Asn Glu Asn His Glu Asn Ser Ser Glu
 1      5      10      15
Asn Ser Lys Ala Asp Glu Met Arg Ala Gly Ala Phe Glu Arg Phe Thr
 20      25      30
Asn Arg Lys Lys Arg Phe Arg Glu Asn Ala Gln Lys Asn Ala Glu Tyr
 35      40      45
Ser Asn His Glu Ala Ser Ser His His Lys Lys Glu His Arg Pro Asn
 50      55      60
Lys Lys Pro Asn Asn His His Lys Gln Lys His Ala Lys Thr Arg Asn
 65      70      75      80
Tyr Ala Gln Glu Glu Leu Asp Ser Asn Lys Val Glu Gly Val Thr Glu
 85      90      95
Ile Leu His Val Asn Glu Arg Gly Thr Leu Gly Phe His Lys Glu Leu
 100      105      110
Lys Lys Gly Val Glu Ala Asn Asn Lys Ile Gln Val Glu His Leu Asn
 115      120      125
Pro His Tyr Lys Met Asn Leu Asn Ser Lys Ala Ser Val Lys Ile Thr
 130      135      140
Pro Leu Gly Gly Leu Gly Glu Ile Gly Gly Asn Met Met Val Ile Glu
 145      150      155      160
Thr Pro Lys Ser Ala Ile Val Ile Asp Ala Gly Met Ser Phe Pro Lys
 165      170      175
Glu Gly Leu Phe Gly Val Asp Ile Leu Ile Pro Asp Phe Ser Tyr Leu
 180      185      190
His Gln Ile Lys Asp Lys Ile Ala Gly Ile Ile Ile Thr His Ala His
 195      200      205
Glu Asp His Ile Gly Ala Thr Pro Tyr Leu Phe Lys Glu Leu Gln Phe
 210      215      220
Pro Leu Tyr Gly Thr Pro Leu Ser Leu Gly Leu Ile Gly Ser Lys Phe
 225      230      235      240
Asp Glu His Gly Leu Lys Lys Tyr Arg Ser Tyr Phe Lys Ile Val Glu
 245      250      255
Lys Arg Cys Pro Ile Ser Val Gly Glu Phe Ile Ile Glu Trp Ile His
 260      265      270
Ile Thr His Ser Ile Ile Asp Ser Ser Ala Leu Ala Ile Gln Thr Lys
 275      280      285
Ala Gly Thr Ile Ile His Thr Gly Asp Phe Lys Ile Asp His Thr Pro
 290      295      300
Val Asp Asn Leu Pro Thr Asp Leu Tyr Arg Leu Ala His Tyr Gly Glu
 305      310      315      320
Lys Gly Val Met Leu Leu Leu Ser Asp Ser Thr Asn Ser His Lys Ser
 325      330      335
Gly Thr Thr Pro Ser Glu Ser Thr Ile Ala Pro Ala Phe Asp Thr Leu
 340      345      350
Phe Lys Glu Ala Gln Gly Arg Val Ile Met Ser Thr Phe Ser Ser Asn
 355      360      365
Ile His Arg Val Tyr Gln Ala Ile Gln Tyr Gly Ile Lys Tyr Asn Arg
 370      375      380
Lys Ile Ala Val Ile Gly Arg Ser Met Glu Lys Asn Leu Asp Ile Ala
 385      390      395      400
Arg Glu Leu Gly Tyr Ile His Leu Pro Tyr Gln Ser Phe Ile Glu Ala
 405      410      415
Asn Glu Val Ala Lys Tyr Pro Asp Asn Glu Ile Leu Ile Val Thr Thr
 420      425      430
Gly Ser Gln Gly Glu Thr Met Ser Ala Leu Tyr Arg Met Ala Thr Asp

```

GCG CGC CAC AAA CAA ACC GCT ATT TCT TGC GGA GTG CCT GAA AAA AAT	1690
Ala Arg His Lys Gln Thr Ala Ile Ser Cys Gly Val Pro Glu Lys Asn	
535 540 545	
ATC TAT TTA ATG GAG GAT GGC GAT CAG GTG GAG GTT GGC CCT GCG TTC	1738
Ile Tyr Leu Met Glu Asp Gly Asp Gln Val Glu Val Gly Pro Ala Phe	
550 555 560	
ATC AAA AAA GTC GGC ACG ATT AAA AGC GGG AAA AGC TAT GTG GAT AAC	1786
Ile Lys Lys Val Gly Thr Ile Lys Ser Gly Lys Ser Tyr Val Asp Asn	
565 570 575	
CAA AGC AAT TTG AGT ATT GAT ACA AGC ATC GTG CAA CAA AGA GAA GAA	1834
Gln Ser Asn Leu Ser Ile Asp Thr Ser Ile Val Gln Gln Arg Glu Glu	
580 585 590	
GTC GCT AGC GCC GGG GTG TTT GTG GCT ACG ATT TTT GTG AAT AAA AAC	1882
Val Ala Ser Ala Gly Val Phe Val Ala Thr Ile Phe Val Asn Lys Asn	
595 600 605 610	
AAG CAA GCG CTT TTA GAA AGC TCT CAA TTT TCC AGT TTA GGG CTT GTG	1930
Lys Gln Ala Leu Leu Glu Ser Ser Gln Phe Ser Ser Leu Gly Leu Val	
615 620 625	
GGT TTC AAA GAT GAA AAG CCT TTG ATC AAA GAA ATT CAA GGG GGC TTA	1978
Gly Phe Lys Asp Glu Lys Pro Leu Ile Lys Glu Ile Gln Gly Gly Leu	
630 635 640	
GAG GTG TTA TTG AAA TCC AGC AAC GCC GAA ATT TTG AAT AAC CCT AAA	2026
Glu Val Leu Leu Lys Ser Ser Asn Ala Glu Ile Leu Asn Asn Pro Lys	
645 650 655	
AAA TTA GAA GAT CAC ACT CGT AAT TTC ATC AGA AAA GCG CTC TTT AAA	2074
Lys Leu Glu Asp His Thr Arg Asn Phe Ile Arg Lys Ala Leu Phe Lys	
660 665 670	
AAG TTT AGA AAA TAC CCG GCT ATC ATT TGT CAT GCC CAT TCT TTT TGATT	2124
Lys Phe Arg Lys Tyr Pro Ala Ile Ile Cys His Ala His Ser Phe	
675 680 685	
GTAACGCTAT TGCTTCACAA GTTTTAAAAG ATGAAGCGAG CGCGC	2169

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

Asn	Leu	Pro	Thr	Asp	Leu	Tyr	Arg	Leu	Ala	His	Tyr	Gly	Glu	Lys	Gly		
			310					315					320				
GTG	ATG	CTT	CTT	TTA	AGC	GAT	TCC	ACC	AAC	TCC	CAT	AAA	TCC	GGG	ACT	1066	
Val	Met	Leu	Leu	Leu	Ser	Asp	Ser	Thr	Asn	Ser	His	Lys	Ser	Gly	Thr		
		325					330					335					
ACG	CCG	AGT	GAA	AGC	ACC	ATA	GCG	CCG	GCT	TTT	GAT	ACC	CTT	TTT	AAA	1114	
Thr	Pro	Ser	Glu	Ser	Thr	Ile	Ala	Pro	Ala	Phe	Asp	Thr	Leu	Phe	Lys		
	340					345					350						
GAA	GCG	CAA	GGG	AGG	GTG	ATT	ATG	AGC	ACC	TTC	TCT	AGC	AAT	ATC	CAC	1162	
Glu	Ala	Gln	Gly	Arg	Val	Ile	Met	Ser	Thr	Phe	Ser	Ser	Asn	Ile	His		
355					360					365					370		
CGG	GTC	TAT	CAA	GCC	ATA	CAA	TAC	GGC	ATT	AAA	TAC	AAC	CGC	AAG	ATC	1210	
Arg	Val	Tyr	Gln	Ala	Ile	Gln	Tyr	Gly	Ile	Lys	Tyr	Asn	Arg	Lys	Ile		
			375					380						385			
GCT	GTG	ATC	GGG	CGC	TCT	ATG	GAA	AAA	AAC	CTA	GAC	ATC	GCT	AGA	GAA	1258	
Ala	Val	Ile	Gly	Arg	Ser	Met	Glu	Lys	Asn	Leu	Asp	Ile	Ala	Arg	Glu		
		390						395					400				
TTG	GGC	TAT	ATC	CAT	TTG	CCT	TAT	CAA	TCT	TTT	ATT	GAA	GCC	AAT	GAA	1306	
Leu	Gly	Tyr	Ile	His	Leu	Pro	Tyr	Gln	Ser	Phe	Ile	Glu	Ala	Asn	Glu		
	405					410						415					
GTC	GCC	AAA	TAC	CCG	GAC	AAT	GAA	ATC	TTA	ATC	GTA	ACG	ACC	GGC	TCA	1354	
Val	Ala	Lys	Tyr	Pro	Asp	Asn	Glu	Ile	Leu	Ile	Val	Thr	Thr	Gly	Ser		
	420					425					430						
CAA	GGC	GAA	ACC	ATG	AGC	GCG	CTT	TAT	CGC	ATG	GCG	ACT	GAT	GAA	CAC	1402	
Gln	Gly	Glu	Thr	Met	Ser	Ala	Leu	Tyr	Arg	Met	Ala	Thr	Asp	Glu	His		
435					440					445					450		
CGT	CAT	ATT	TCT	ATC	AAA	CCC	AAC	GAT	TTA	GTC	ATC	ATT	TCC	GCT	AAA	1450	
Arg	His	Ile	Ser	Ile	Lys	Pro	Asn	Asp	Leu	Val	Ile	Ile	Ser	Ala	Lys		
			455					460						465			
GCC	ATT	CCT	GGC	AAT	GAA	GCG	AGC	GTT	TCA	GCG	GTG	TTG	AAT	TTC	TTG	1498	
Ala	Ile	Pro	Gly	Asn	Glu	Ala	Ser	Val	Ser	Ala	Val	Leu	Asn	Phe	Leu		
		470						475					480				
ATC	AAA	AAA	GAA	GCT	AAA	GTG	GCT	TAT	CAA	GAA	TTT	GAC	AAT	ATC	CAT	1546	
Ile	Lys	Lys	Glu	Ala	Lys	Val	Ala	Tyr	Gln	Glu	Phe	Asp	Asn	Ile	His		
	485					490						495					
GTG	AGC	GGG	CAT	GCC	GCC	CAA	GAA	GAG	CAA	AAG	CTC	ATG	TTA	AGA	CTC	1594	
Val	Ser	Gly	His	Ala	Ala	Gln	Glu	Glu	Gln	Lys	Leu	Met	Leu	Arg	Leu		
	500					505					510						
ATT	AAG	CCT	AAG	TTT	TTC	TTA	CCC	GTG	CAT	GGG	GAA	TAT	AAC	CAT	GTC	1642	
Ile	Lys	Pro	Lys	Phe	Phe	Leu	Pro	Val	His	Gly	Glu	Tyr	Asn	His	Val		
515					520					525					530		

85	90	95	
CAT GTG AAT GAG AGA GGG ACT TTA GGC TTT CAT AAG GAG TTA AAA AAG His Val Asn Glu Arg Gly Thr Leu Gly Phe His Lys Glu Leu Lys Lys 100 105 110			394
GGC GTT GAA GCG AAT AAC AAG ATC CAA GTG GAG CAT TTA AAC CCG CAT Gly Val Glu Ala Asn Asn Lys Ile Gln Val Glu His Leu Asn Pro His 115 120 125 130			442
TAT AAG ATG AAC TTA AAC TCT AAA GCG AGC GTT AAA ATC ACG CCT TTA Tyr Lys Met Asn Leu Asn Ser Lys Ala Ser Val Lys Ile Thr Pro Leu 135 140 145			490
GGG GGC TTG GGT GAG ATT GGG GGG AAC ATG ATG GTC ATT GAA ACC CCA Gly Gly Leu Gly Glu Ile Gly Gly Asn Met Met Val Ile Glu Thr Pro 150 155 160			538
AAA AGC GCG ATC GTG ATT GAT GCG GGC ATG AGC TTC CCT AAA GAG GGG Lys Ser Ala Ile Val Ile Asp Ala Gly Met Ser Phe Pro Lys Glu Gly 165 170 175			586
CTC TTT GGC GTG GAT ATT TTA ATC CCG GAT TTT TCC TAC TTG CAC CAA Leu Phe Gly Val Asp Ile Leu Ile Pro Asp Phe Ser Tyr Leu His Gln 180 185 190			634
ATC AAG GAC AAA ATC GCT GGC ATT ATC ATC ACC CAT GCC CAT GAA GAT Ile Lys Asp Lys Ile Ala Gly Ile Ile Ile Thr His Ala His Glu Asp 195 200 205 210			682
CAC ATA GGG GCC ACG CCT TAT TTG TTT AAA GAG CTG CAA TTC CCC CTT His Ile Gly Ala Thr Pro Tyr Leu Phe Lys Glu Leu Gln Phe Pro Leu 215 220 225			730
TAT GGC ACG CCC TTG AGT TTG GGG CTG ATT GGG AGC AAG TTT GAT GAA Tyr Gly Thr Pro Leu Ser Leu Gly Leu Ile Gly Ser Lys Phe Asp Glu 230 235 240			778
CAT GGT TTG AAA AAA TAC CGC TCG TAT TTT AAA ATC GTA GAA AAG CGC His Gly Leu Lys Lys Tyr Arg Ser Tyr Phe Lys Ile Val Glu Lys Arg 245 250 255			826
TGT CCC ATT AGC GTG GGC GAA TTT ATC ATT GAA TGG ATC CAC ATC ACG Cys Pro Ile Ser Val Gly Glu Phe Ile Ile Glu Trp Ile His Ile Thr 260 265 270			874
CAT TCT ATC ATT GAC AGC AGC GCT TTA GCG ATC CAA ACT AAA GCC GGA His Ser Ile Ile Asp Ser Ser Ala Leu Ala Ile Gln Thr Lys Ala Gly 275 280 285 290			922
ACG ATC ATC CAC ACC GGC GAT TTT AAA ATC GAT CAC ACC CCG GTG GAT Thr Ile Ile His Thr Gly Asp Phe Lys Ile Asp His Thr Pro Val Asp 295 300 305			970
AAT TTG CCC ACG GAT TTG TAT CGT TTA GCG CAC TAT GGC GAA AAG GGG			1018

Gly	Leu	Arg	Met	Gly	Asp	Lys	His	His	Thr	Leu	Glu	Leu	Ser	Thr	Ser
65					70					75				80	
Val	His	Gly	Asp	Ala	Pro	Ser	Cys	Ser	Leu	Lys	Lys	Leu	Lys	Ser	Cys
			85					90					95		
Glu	Ser	Ala	Arg	Val	Leu	Gln	Ala	Lys	Ile	Pro	Arg	Gly	Ile	Phe	Glu
		100					105						110		
Ser	Tyr	Val	Thr	Trp	Ser	Ala	Asp	Tyr	Val	Tyr	Arg	Phe			
	115					120						125			

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...2119
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

CTTTTAAAAG GCTAATGCCT TTTTAAAAAA TTGAAATAAA GGAATAAAAG TT ATG ACG	58
Met Thr	
1	
GAT AAC AAC CAA AAC AAT GAA AAC CAT GAA AAC AGC AGT GAA AAT TCA	106
Asp Asn Asn Gln Asn Asn Glu Asn His Glu Asn Ser Ser Glu Asn Ser	
5 10 15	
AAA GCT GAT GAG ATG CGA GCC GGA GCG TTT GAG CGC TTC ACC AAC CGC	154
Lys Ala Asp Glu Met Arg Ala Gly Ala Phe Glu Arg Phe Thr Asn Arg	
20 25 30	
AAA AAG CGT TTC AGA GAA AAC GCG CAA AAA AAC GCA GAG TAT TCA AAC	202
Lys Lys Arg Phe Arg Glu Asn Ala Gln Lys Asn Ala Glu Tyr Ser Asn	
35 40 45 50	
CAT GAA GCG TCT TCG CAC CAT AAA AAA GAG CAT CGC CCT AAC AAA AAA	250
His Glu Ala Ser Ser His His Lys Lys Glu His Arg Pro Asn Lys Lys	
55 60 65	
CCA AAC AAC CAC CAC AAA CAA AAA CAT GCC AAA ACA CGA AAT TAC GCC	298
Pro Asn Asn His His Lys Gln Lys His Ala Lys Thr Arg Asn Tyr Ala	
70 75 80	
CAA GAA GAA TTG GAT AGC AAC AAA GTA GAG GGC GTT ACG GAA ATT TTG	346
Gln Glu Glu Leu Asp Ser Asn Lys Val Glu Gly Val Thr Glu Ile Leu	

TAT GAT AAC AAT GTC AAC TTA CAG CTT TTT TAT GGA TTT TTA CAC AAT	104
Tyr Asp Asn Asn Val Asn Leu Gln Leu Phe Tyr Gly Phe Leu His Asn	
5 10 15	
GTG TAT GAA AAT GAG AAG TTT TTC ATC GGT TAT TTT ATA GGG GCT GGG	152
Val Tyr Glu Asn Glu Lys Phe Phe Ile Gly Tyr Phe Ile Gly Ala Gly	
20 25 30	
CTA GGG GGT GAG AGC GTA ACA CCC AAT GTT CTT AAA GAT TTT GGT AAT	200
Leu Gly Gly Glu Ser Val Thr Pro Asn Val Leu Lys Asp Phe Gly Asn	
35 40 45 50	
ATG TTA GCG CAA TTA GTG CAA TTT CAG GGC TAT GGC TCA CTA GGG CTA	248
Met Leu Ala Gln Leu Val Gln Phe Gln Gly Tyr Gly Ser Leu Gly Leu	
55 60 65	
AGG ATG GGC GAT AAA CAC CAC ACG CTA GAA TTG AGC ACG AGC GTT CAT	296
Arg Met Gly Asp Lys His His Thr Leu Glu Leu Ser Thr Ser Val His	
70 75 80	
GGC GAC GCT CCT AGT TGT TCT TTA AAA AAG CTA AAG AGT TGC GAA AGT	344
Gly Asp Ala Pro Ser Cys Ser Leu Lys Lys Leu Lys Ser Cys Glu Ser	
85 90 95	
GCG AGG GTT TTA CAA GCA AAA ATC CCT AGG GGC ATT TTT GAA AGC TAT	392
Ala Arg Val Leu Gln Ala Lys Ile Pro Arg Gly Ile Phe Glu Ser Tyr	
100 105 110	
GTT ACT TGG AGC GCG GAT TAT GTT TAT CGT TTT TAAAAGTTTT TAAAAATTTA	445
Val Thr Trp Ser Ala Asp Tyr Val Tyr Arg Phe	
115 120 125	
ATGGCTTTGT TCCAATTGAA TAGGGGTAAT AAA	478

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

Trp Trp Tyr Asp Asn Asn Val Asn Leu Gln Leu Phe Tyr Gly Phe Leu	
1 5 10 15	
His Asn Val Tyr Glu Asn Glu Lys Phe Phe Ile Gly Tyr Phe Ile Gly	
20 25 30	
Ala Gly Leu Gly Gly Glu Ser Val Thr Pro Asn Val Leu Lys Asp Phe	
35 40 45	
Gly Asn Met Leu Ala Gln Leu Val Gln Phe Gln Gly Tyr Gly Ser Leu	
50 55 60	

Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu Leu Ser
 35 40 45 50
 TAT GGC TTG ACA ATG GCG ACA AGC TGT CAT TAATGAGAGA ACTTTTAAAGC 253
 Tyr Gly Leu Thr Met Ala Thr Ser Cys His
 55 60
 GTTAGAGGGT TTTTTCGCCT TCTTAGAATG 283

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

Met Val Ala Gly Gly Arg Glu Val Val Phe Lys Asp Asn Asp Lys Lys
 1 5 10 15
 Glu Ala Lys Leu Phe Glu Tyr Gly Ile Asn Ala Val Val Leu Gly Asp
 20 25 30
 Tyr Leu Thr Thr Lys Gly Lys Ala Pro Lys Lys Asp Ile Glu Lys Leu
 35 40 45
 Leu Ser Tyr Gly Leu Thr Met Ala Thr Ser Cys His
 50 55 60

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...425
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

CACTTGTTTGG GAGTGCCTAT AGGCATAATA AGTCCTGTTT CTATTTTAA TGG TGG 56
 Trp Trp
 1

(2) INFORMATION FOR SEO ID NO:561:

(A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...230
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

- 869 -

165	170	175	
AAC GAT TTC ATT GAG TGG CTG TAT TCT AAT GTT AAA TTT ATC ACC ATC			633
Asn Asp Phe Ile Glu Trp Leu Tyr Ser Asn Val Lys Phe Ile Thr Ile			
180	185	190	
ATT TGC CCA AAC ATA GAC AAG GCA TTA AGG ATT TTT AAT GTT TTA AAC			681
Ile Cys Pro Asn Ile Asp Lys Ala Leu Arg Ile Phe Asn Val Leu Asn			
195	200	205	210
GCT AGG GGT TTG CCT TTG AAT GCG ACA GAT ATT TTT AAG GGG GAA TTA			729
Ala Arg Gly Leu Pro Leu Asn Ala Thr Asp Ile Phe Lys Gly Glu Leu			
	215	220	225
TTA AAA CAC GCT AAA GAG CAT GAG CGA GAA GAA TTT GTG TCT CGT TGG			777
Leu Lys His Ala Lys Glu His Glu Arg Glu Glu Phe Val Ser Arg Trp			
	230	235	240
AAC GCC TTA AGC CAA AAA TGC TCG GAC AAT GAT TTA ACA ATG GAG ACA			825
Asn Ala Leu Ser Gln Lys Cys Ser Asp Asn Asp Leu Thr Met Glu Thr			
	245	250	255
TTA TTC AGT TGG TAT AAC CTA TCT CAA TCC GGT AAC TTC TAGAGACAAA AT			876
Leu Phe Ser Trp Tyr Asn Leu Ser Gln Ser Gly Asn Phe			
	260	265	270
GGAAAAAGAG CTCGTTACTT GGTTCACAT ACTTAACAAA CCCCCCTAG AATACCTTAA			936
GGGCGTAGAG GATTTTACAC ACGCTTATGG TGAGGTGTTA GAAATGCAAG ATCG			990

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

Met	Ala	Lys	Ile	Glu	Ser	Asn	Asp	Ser	His	Leu	Arg	Gly	Ile	Leu	Lys
1				5				10					15		
Asp	Glu	Leu	Tyr	Tyr	Gln	Ile	Pro	Ile	Tyr	Gln	Arg	Pro	Tyr	Gln	Trp
		20					25					30			
Thr	Glu	Glu	Asn	Cys	Glu	Lys	Leu	Asp	Asp	Leu	Phe	Phe	Asn	Tyr	
		35				40				45					
Glu	Asp	Asp	Arg	Glu	Gly	Asp	Tyr	Phe	Cys	Gly	Ser	Leu	Val	Leu	Ile
	50				55			60							
Ala	Ile	Ser	Lys	Asp	Ser	Lys	Ala	Thr	Thr	Tyr	Asp	Val	Val	Asp	Gly
65				70				75						80	
Gln	Gln	Arg	Leu	Ser	Thr	Phe	Ile	Leu	Leu	Ala	Lys	Val	Leu	Ala	Asp
			85					90					95		
Leu	Tyr	Asn	Asp	Cys	Leu	Asp	Pro	Lys	Asn	Leu	Glu	His	Leu	Gln	Glu

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 52...864
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

AAAAACACTT TTTAATGTTA TAATCTATCC TAAACAATAT AAGGGGTTTT T ATG GCA	57
Met Ala	
1	
AAA ATT GAA AGC AAT GAT TCC CAC CTA AGA GGT ATT TTA AAA GAC GAA	105
Lys Ile Glu Ser Asn Asp Ser His Leu Arg Gly Ile Leu Lys Asp Glu	
5 10 15	
CTC TAC TAT CAA ATC CCC ATC TAC CAA CGC CCT TAT CAA TGG ACA GAA	153
Leu Tyr Tyr Gln Ile Pro Ile Tyr Gln Arg Pro Tyr Gln Trp Thr Glu	
20 25 30	
GAA AAC TGC GAA AAA CTT TTA GAC GAT TTG TTT TTT AAT TAT GAA GAT	201
Glu Asn Cys Glu Lys Leu Leu Asp Asp Leu Phe Phe Asn Tyr Glu Asp	
35 40 45 50	
GAC AGA GAA GGC GAT TAT TTT TGC GGC TCA TTA GTC TTA ATT GCA ATC	249
Asp Arg Glu Gly Asp Tyr Phe Cys Gly Ser Leu Val Leu Ile Ala Ile	
55 60 65	
AGC AAA GAT TCT AAA GCC ACA ACC TAT GAT GTT GTA GAT GGC CAG CAA	297
Ser Lys Asp Ser Lys Ala Thr Thr Tyr Asp Val Val Asp Gly Gln Gln	
70 75 80	
CGC TTA AGC ACT TTC ATT CTG CTT GCA AAA GTT TTA GCC GAT CTT TAT	345
Arg Leu Ser Thr Phe Ile Leu Leu Ala Lys Val Leu Ala Asp Leu Tyr	
85 90 95	
AAT GAT TGT TTA GAC CCT AAG AAT TTA GAA CAT TTA CAA GAG GGT TGG	393
Asn Asp Cys Leu Asp Pro Lys Asn Leu Glu His Leu Gln Glu Gly Trp	
100 105 110	
AAA GAT AGG CAT ACA GAA AGA AAA CGA CTG AGT TTT AAC ACT ATA GGG	441
Lys Asp Arg His Thr Glu Arg Lys Arg Leu Ser Phe Asn Thr Ile Gly	
115 120 125 130	
TCT AAC GCT GAA TAT GAT TTT CAA GAT GCA TTA GAA CAT TTC AAC GAC	489
Ser Asn Ala Glu Tyr Asp Phe Gln Asp Ala Leu Glu His Phe Asn Asp	
135 140 145	
TCT CAA GCA AGC AAG AAT AAA AAT AAT AAG AAC AAT TAC CTA AAA AAT	537
Ser Gln Ala Ser Lys Asn Lys Asn Asn Lys Asn Asn Tyr Leu Lys Asn	
150 155 160	
GCG ATC TGT TTA AAA GAC TAT CTC ATG AAA AAA GAG ATT AAA AAC ATT	585
Ala Ile Cys Leu Lys Asp Tyr Leu Met Lys Lys Glu Ile Lys Asn Ile	

1				5					10					15			
Phe	Gln	Gly	Val	Ile	Phe	Leu	Asn	Pro	Lys	Ile	Val	Ser	Trp	Leu	Leu		
			20					25					30				
Lys	Ala	Tyr	Arg	Met	Ser	Asp	Asn	Leu	Leu	His	Lys	Asp	Ile	Gln	Ala		
		35					40					45					
Leu	Ile	Ala	Arg	Leu	Lys	Arg	Gln	Asp	Leu	Ser	Leu	Gly	Met	Leu	Glu		
	50					55					60						
Lys	Ser	Leu	Ser	Arg	Leu	Ile	His	Asp	Glu	Ile	Asn	Leu	Glu	Tyr	Leu		
65					70					75					80		
Lys	Ala	Cys	Gly	Leu	Asn	Phe	Ile	Glu	Thr	Ser	Glu	Asn	Leu	Ile	Thr		
				85					90					95			
Leu	Lys	Asn	Leu	Lys	Thr	Pro	Leu	Lys	Asp	Glu	Val	Phe	Ser	Phe	Ile		
			100					105					110				
Asp	Leu	Glu	Thr	Thr	Gly	Ser	Cys	Pro	Ile	Lys	His	Glu	Ile	Leu	Glu		
		115					120					125					
Ile	Gly	Ala	Val	Gln	Val	Lys	Gly	Gly	Glu	Ile	Ile	Asn	Arg	Phe	Glu		
	130					135					140						
Thr	Leu	Val	Lys	Val	Lys	Ser	Val	Pro	Asp	Tyr	Ile	Ala	Glu	Leu	Thr		
145					150					155					160		
Gly	Ile	Thr	Tyr	Glu	Asp	Thr	Leu	Asn	Ala	Pro	Ser	Ala	His	Glu	Ala		
				165					170					175			
Leu	Gln	Glu	Leu	Arg	Leu	Phe	Leu	Gly	Asn	Ser	Val	Phe	Val	Ala	His		
			180					185					190				
Asn	Ala	Asn	Phe	Asp	Tyr	Asn	Phe	Leu	Gly	Arg	Tyr	Phe	Val	Glu	Lys		
		195					200					205					
Leu	His	Cys	Pro	Leu	Leu	Asn	Leu	Lys	Leu	Cys	Thr	Leu	Asp	Leu	Ser		
	210					215					220						
Lys	Arg	Ala	Ile	Leu	Ser	Met	Arg	Tyr	Ser	Leu	Ser	Phe	Leu	Lys	Glu		
225						230				235					240		
Leu	Leu	Gly	Phe	Gly	Ile	Glu	Val	Ser	His	Arg	Ala	Tyr	Ala	Asp	Ala		
				245					250					255			
Leu	Ala	Ser	Tyr	Lys	Leu	Phe	Glu	Ile	Cys	Leu	Leu	Asn	Leu	Pro	Ser		
			260					265					270				
Tyr	Ile	Lys	Thr	Thr	Met	Asp	Leu	Ile	Asp	Phe	Ser	Lys	Cys	Ala	Asn		
		275					280					285					
Thr	Leu	Ile	Lys	Arg	Pro	Pro	Lys	Ala	Arg	Tyr	Gln	Glu	Ile	Pro	Ser		
	290					295					300						
Pro	Phe	Ser	Leu	Phe	Glu	Lys	Thr	Lys	Gly	Leu	Phe	Asn	His	Lys	Ser		
305					310				315						320		
Asn	Gln	Leu	Asn	Glu	Ser	Cys	Leu	Met	Gly	Phe	Met	Gly	Thr	Glu	Ile		
				325					330					335			
Leu	Ala	Ser	Leu	Phe	Asp	Thr	Phe	Glu	Cys	Cys	Leu	Val	Phe				
			340					345					350				

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

Asn Phe Asp Tyr Asn Phe Leu Gly Arg Tyr Phe Val Glu Lys Leu His	
195 200 205 210	
TGC CCT TTA TTG AAT TTA AAG CTT TGC ACT CTG GAT TTA TCC AAA CGA	728
Cys Pro Leu Leu Asn Leu Lys Leu Cys Thr Leu Asp Leu Ser Lys Arg	
215 220 225	
GCC ATT TTG TCC ATG CGT TAT TCT TTG AGC TTT TTA AAA GAG CTT TTA	776
Ala Ile Leu Ser Met Arg Tyr Ser Leu Ser Phe Leu Lys Glu Leu Leu	
230 235 240	
GGG TTT GGT ATA GAA GTC AGC CAT AGA GCC TAT GCG GAC GCT TTA GCG	824
Gly Phe Gly Ile Glu Val Ser His Arg Ala Tyr Ala Asp Ala Leu Ala	
245 250 255	
AGC TAT AAA CTC TTT GAA ATA TGC CTG TTA AAC TTG CCC AGC TAC ATC	872
Ser Tyr Lys Leu Phe Glu Ile Cys Leu Leu Asn Leu Pro Ser Tyr Ile	
260 265 270	
AAA ACG ACA ATG GAT TTG ATT GAT TTT TCT AAA TGT GCT AAC ACG CTA	920
Lys Thr Thr Met Asp Leu Ile Asp Phe Ser Lys Cys Ala Asn Thr Leu	
275 280 285 290	
ATC AAA AGA CCC CCA AAA GCC AGA TAC CAA GAG ATT CCA TCG CCA TTT	968
Ile Lys Arg Pro Pro Lys Ala Arg Tyr Gln Glu Ile Pro Ser Pro Phe	
295 300 305	
TCT CTT TTT GAA AAG ACA AAG GGC TTG TTC AAT CAT AAA AGC AAC CAG	1016
Ser Leu Phe Glu Lys Thr Lys Gly Leu Phe Asn His Lys Ser Asn Gln	
310 315 320	
TTA AAC GAA AGC TGT TTA ATG GGG TTT ATG GGG ACT GAA ATT TTA GCA	1064
Leu Asn Glu Ser Cys Leu Met Gly Phe Met Gly Thr Glu Ile Leu Ala	
325 330 335	
TCT CTA TTT GAT ACT TTT GAA TGT TGC CTA GTA TTT TGATTTTATC GGTTAC	1116
Ser Leu Phe Asp Thr Phe Glu Cys Cys Leu Val Phe	
340 345 350	
TTCGCACTCA TCGTATATCT TTTTGTATTC TTGTATG	1153

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

Met Ile Lys Ile Ser Leu Asn Ser Asn Lys Arg Ala Trp Met Trp Trp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GATCAAACGC	TACAACCCTA	GCTGTCTTTT	AGAAGTGGAT	GGGGGCGTGA	ATG ATA	56
					Met Ile	
					1	
AAA ATA TCT TTG AAC TCC AAC AAG CGG GCG TGG ATG TGG TGG TTT CAG	104					
Lys Ile Ser Leu Asn Ser Asn Lys Arg Ala Trp Met Trp Trp Phe Gln						
5 10 15						
GGA GTT ATA TTT TTA AAT CCA AAG ATC GTA AGC TGG CTA TTG AAG GCT	152					
Gly Val Ile Phe Leu Asn Pro Lys Ile Val Ser Trp Leu Leu Lys Ala						
20 25 30						
TAC AGA ATG TCA GAC AAT CTC TTG CAT AAA GAC ATC CAA GCC CTA ATC	200					
Tyr Arg Met Ser Asp Asn Leu Leu His Lys Asp Ile Gln Ala Leu Ile						
35 40 45 50						
GCT CGC TTA AAG CGC CAG GAC TTA AGC TTG GGC ATG CTA GAA AAA TCG	248					
Ala Arg Leu Lys Arg Gln Asp Leu Ser Leu Gly Met Leu Glu Lys Ser						
55 60 65						
CTC TCT CGC CTT ATT CAT GAT GAA ATC AAT TTG GAG TAT TTG AAG GCG	296					
Leu Ser Arg Leu Ile His Asp Glu Ile Asn Leu Glu Tyr Leu Lys Ala						
70 75 80						
TGC GGG CTC AAT TTC ATA GAA ACG AGC GAA AAT TTA ATC ACG CTC AAA	344					
Cys Gly Leu Asn Phe Ile Glu Thr Ser Glu Asn Leu Ile Thr Leu Lys						
85 90 95						
AAC CTT AAA ACC CCC CTT AAA GAT GAG GTT TTT TCC TTT ATT GAT TTA	392					
Asn Leu Lys Thr Pro Leu Lys Asp Glu Val Phe Ser Phe Ile Asp Leu						
100 105 110						
GAA ACC ACC GGA TCT TGC CCC ATA AAG CAT GAG ATT TTA GAA ATT GGG	440					
Glu Thr Thr Gly Ser Cys Pro Ile Lys His Glu Ile Leu Glu Ile Gly						
115 120 125 130						
GCC GTG CAA GTG AAA GGG GGG GAA ATT ATC AAT CGT TTT GAA ACC CTT	488					
Ala Val Gln Val Lys Gly Gly Glu Ile Ile Asn Arg Phe Glu Thr Leu						
135 140 145						
GTG AAA GTC AAA AGC GTG CCT GAT TAT ATC GCT GAG CTT ACA GGC ATC	536					
Val Lys Val Lys Ser Val Pro Asp Tyr Ile Ala Glu Leu Thr Gly Ile						
150 155 160						
ACT TAT GAA GAC ACC CTA AAC GCC CCA AGC GCG CAT GAA GCT TTG CAA	584					
Thr Tyr Glu Asp Thr Leu Asn Ala Pro Ser Ala His Glu Ala Leu Gln						
165 170 175						
GAA TTG CGG CTT TTT TTA GGC AAT AGC GTG TTT GTG GCC CAC AAC GCT	632					
Glu Leu Arg Leu Phe Leu Gly Asn Ser Val Phe Val Ala His Asn Ala						
180 185 190						
AAT TTT GAT TAC AAC TTT TTG GGG CGT TAT TTT GTA GAA AAA TTG CAT	680					

Met	Glu	Ile	Arg	Thr	Phe	Leu	Glu	Arg	Ala	Leu	Lys	Glu	Asp	Leu	Gly
1				5					10					15	
His	Gly	Asp	Leu	Phe	Glu	Arg	Val	Leu	Glu	Lys	Asp	Phe	Lys	Ala	Thr
		20						25					30		
Ala	Phe	Val	Arg	Ala	Lys	Gln	Glu	Gly	Val	Phe	Ser	Gly	Glu	Lys	Tyr
		35					40					45			
Ala	Leu	Glu	Leu	Leu	Glu	Met	Thr	Gly	Ile	Glu	Cys	Val	Gln	Thr	Ile
	50					55					60				
Lys	Asp	Lys	Glu	Arg	Phe	Lys	Pro	Lys	Asp	Ala	Leu	Met	Glu	Ile	Arg
65				70						75				80	
Gly	Asp	Phe	Ser	Met	Leu	Leu	Lys	Val	Glu	Arg	Thr	Leu	Leu	Asn	Leu
				85					90					95	
Leu	Gln	His	Ser	Ser	Gly	Ile	Ala	Thr	Leu	Thr	Ser	Arg	Phe	Val	Glu
			100					105					110		
Ala	Leu	Asn	Ser	His	Lys	Val	Arg	Leu	Leu	Asp	Thr	Arg	Lys	Thr	Arg
		115					120					125			
Pro	Leu	Leu	Arg	Ile	Phe	Glu	Lys	Tyr	Ser	Val	Leu	Asn	Gly	Gly	Ala
	130					135					140				
Ser	Asn	His	Arg	Leu	Gly	Leu	Asp	Asp	Ala	Leu	Met	Leu	Lys	Asp	Thr
145				150					155					160	
His	Leu	Arg	His	Val	Lys	Asp	Leu	Lys	Ser	Phe	Leu	Thr	His	Ala	Arg
			165						170					175	
Lys	Asn	Leu	Pro	Phe	Thr	Ala	Lys	Ile	Glu	Ile	Glu	Cys	Glu	Ser	Phe
		180					185					190			
Glu	Glu	Ala	Lys	Asn	Ala	Met	Asn	Ala	Gly	Ala	Asp	Ile	Val	Met	Cys
		195					200					205			
Asp	Asn	Leu	Ser	Val	Leu	Glu	Thr	Lys	Glu	Ile	Ala	Ala	Tyr	Arg	Asp
	210					215					220				
Ala	His	Tyr	Pro	Phe	Val	Leu	Leu	Glu	Ala	Ser	Gly	Asn	Ile	Ser	Leu
225					230					235				240	
Glu	Ser	Ile	Asn	Ala	Tyr	Ala	Lys	Ser	Gly	Val	Asp	Ala	Ile	Ser	Val
			245						250					255	
Gly	Ala	Leu	Ile	His	Gln	Ala	Thr	Phe	Ile	Asp	Met	His	Met	Lys	Met
			260					265					270		

Ala

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1100
- (D) OTHER INFORMATION:

AAA GTG CGT TTG TTG GAC ACG AGA AAA ACG AGA CCC CTT TTA AGG ATC	438
Lys Val Arg Leu Leu Asp Thr Arg Lys Thr Arg Pro Leu Leu Arg Ile	
120 125 130	
TTT GAA AAA TAT TCC GTG CTT AAT GGG GGA GCG AGC AAC CAC CGC TTA	486
Phe Glu Lys Tyr Ser Val Leu Asn Gly Gly Ala Ser Asn His Arg Leu	
135 140 145	
GGG CTA GAT GAC GCT TTA ATG CTT AAA GAC ACG CAT TTA AGG CAT GTG	534
Gly Leu Asp Asp Ala Leu Met Leu Lys Asp Thr His Leu Arg His Val	
150 155 160 165	
AAA GAT CTC AAA AGC TTT TTA ACG CAT GCC AGA AAA AAC TTG CCT TTC	582
Lys Asp Leu Lys Ser Phe Leu Thr His Ala Arg Lys Asn Leu Pro Phe	
170 175 180	
ACG GCT AAA ATT GAA ATT GAA TGC GAA AGC TTT GAA GAG GCC AAA AAC	630
Thr Ala Lys Ile Glu Ile Glu Cys Glu Ser Phe Glu Glu Ala Lys Asn	
185 190 195	
GCC ATG AAT GCG GGA GCG GAT ATT GTG ATG TGC GAT AAT TTG AGC GTT	678
Ala Met Asn Ala Gly Ala Asp Ile Val Met Cys Asp Asn Leu Ser Val	
200 205 210	
TTA GAG ACT AAA GAA ATT GCC GCT TAT AGA GAT GCG CAT TAT CCC TTT	726
Leu Glu Thr Lys Glu Ile Ala Ala Tyr Arg Asp Ala His Tyr Pro Phe	
215 220 225	
GTT TTA CTG GAA GCG AGC GGG AAC ATT TCA CTA GAG AGC ATT AAC GCT	774
Val Leu Leu Glu Ala Ser Gly Asn Ile Ser Leu Glu Ser Ile Asn Ala	
230 235 240 245	
TAC GCT AAA AGC GGC GTG GAT GCC ATT AGC GTA GGG GCT TTA ATC CAT	822
Tyr Ala Lys Ser Gly Val Asp Ala Ile Ser Val Gly Ala Leu Ile His	
250 255 260	
CAA GCC ACT TTT ATT GAC ATG CAC ATG AAA ATG GCT TAAAGACTTT AAAAAG	874
Gln Ala Thr Phe Ile Asp Met His Met Lys Met Ala	
265 270	
GGGTTATTAA CATGCTAAAA GAATATTTAG AAAGCATTAA AGATCTTACG CCTGAAAAGA	934
ATGAACTCAC GCACCGCCCT TCTTTATACA ACTTGCTTAA TCAGTTAAAA AACCAT	990

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Gln Lys Glu Tyr Leu Lys His Tyr His Glu Leu Asn Pro Ser Glu Gln
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...858
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

```

GGCCAACTC GCTTTAACTA AAATGATGGA GTTATCTTA ATG GAG ATT AGA ACC      54
                                   Met Glu Ile Arg Thr
                                   1         5

TTT TTA GAA CGC GCT TTA AAA GAA GAT TTA GGG CAT GGG GAT TTG TTT      102
Phe Leu Glu Arg Ala Leu Lys Glu Asp Leu Gly His Gly Asp Leu Phe
      10              15              20

GAA AGG GTG TTA GAA AAA GAT TTT AAG GCC ACA GCG TTT GTT AGG GCT      150
Glu Arg Val Leu Glu Lys Asp Phe Lys Ala Thr Ala Phe Val Arg Ala
      25              30              35

AAA CAA GAG GGC GTG TTT TCA GGC GAA AAA TAC GCT TTA GAG TTG TTG      198
Lys Gln Glu Gly Val Phe Ser Gly Glu Lys Tyr Ala Leu Glu Leu Leu
      40              45              50

GAA ATG ACC GGC ATT GAA TGC GTT CAA ACG ATT AAG GAT AAA GAA CGC      246
Glu Met Thr Gly Ile Glu Cys Val Gln Thr Ile Lys Asp Lys Glu Arg
      55              60              65

TTC AAG CCT AAA GAC GCT TTA ATG GAA ATT AGG GGG GAT TTT AGC ATG      294
Phe Lys Pro Lys Asp Ala Leu Met Glu Ile Arg Gly Asp Phe Ser Met
      70              75              80              85

CTT TTA AAG GTT GAG CGC ACC CTT TTA AAC CTT TTG CAA CAC AGC AGC      342
Leu Leu Lys Val Glu Arg Thr Leu Leu Asn Leu Leu Gln His Ser Ser
      90              95              100

GGG ATT GCT ACT TTA ACG AGC CGT TTT GTA GAG GCT TTA AAT TCT CAT      390
Gly Ile Ala Thr Leu Thr Ser Arg Phe Val Glu Ala Leu Asn Ser His
      105              110              115

```

195	200	205	
CCT GAT TTT AAC TCG CCC ACC TGG TAT GAA GAA TTA CAA GAA CGC ATG			730
Pro Asp Phe Asn Ser Pro Thr Trp Tyr Glu Glu Leu Gln Glu Arg Met			
210	215	220	
CAA AAA GAG TAT TTA AAA CAC TAT CAT GAA TTA AAC CCT AGC GAA CAA TGA			781
Gln Lys Glu Tyr Leu Lys His Tyr His Glu Leu Asn Pro Ser Glu Gln			
225	230	235	240
AGCTTTTTTGA CTACGCTCCT TTGAGTTTGG CTTGGCGGGA GTTTTTTGCAA AGCGAATTTA			841
AAAAGCCTTA TTTTITTAGAA ATAGAAAAAC GCTACCTAGA AGCCCTAAAA ATCCCTAAA			900

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Met	Lys	Ser	Asn	Lys	Lys	Ser	Asn	Arg	Leu	Arg	Ala	Ile	Tyr	Arg	Ala
1				5					10					15	
Leu	Val	Ile	Ala	Ile	Gly	Leu	Ala	Val	Ile	Ile	Val	Phe	Asn	Tyr	Phe
			20					25					30		
Asn	Arg	Lys	Asn	Asn	Asn	Ala	Arg	Ser	Ser	Arg	Arg	Ala	Cys	Ser	Cys
		35				40					45				
Phe	Phe	Ser	Leu	Thr	Gly	Val	Asn	Leu	Glu	Lys	Ile	Gly	Thr	Phe	Asp
	50				55					60					
Thr	Asp	Ala	Lys	Leu	Ile	Val	Leu	Asn	His	Gln	Ser	Leu	Leu	Asp	Ile
65				70					75					80	
Ile	Tyr	Leu	Glu	Ala	Tyr	His	Pro	Arg	Asn	Ile	Cys	Trp	Ile	Ala	Lys
				85				90					95		
Lys	Glu	Leu	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	His	Ala	Leu	Thr	Asp	Thr
		100					105					110			
Gly	Met	Ile	Leu	Ile	Asp	Arg	Glu	Asp	Lys	Lys	Gly	Ile	Val	Ser	Leu
	115					120					125				
Leu	Lys	Ala	Cys	Lys	Glu	Lys	Leu	Asp	Gln	Asn	Arg	Pro	Leu	Val	Ile
	130					135					140				
Phe	Pro	Glu	Gly	Thr	Arg	Gly	Lys	Gly	Gly	Glu	Lys	Phe	Leu	Pro	Phe
145				150						155				160	
Lys	Gln	Gly	Ala	Lys	Ile	Ile	Ala	Glu	Lys	Phe	Gln	Leu	Lys	Ile	Gln
			165					170					175		
Pro	Met	Val	Leu	Ile	Asn	Ser	Ile	Lys	Ile	Phe	Asn	Ser	Lys	Pro	Leu
		180						185					190		
Glu	Ala	Tyr	Lys	Ala	Arg	Thr	Arg	Leu	Val	Met	Leu	Glu	Ser	Tyr	Thr
	195					200				205					
Pro	Asp	Phe	Asn	Ser	Pro	Thr	Trp	Tyr	Glu	Glu	Leu	Gln	Glu	Arg	Met
210						215					220				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

CATGATGATT ATTATAAAAT CCTAACGCCG CATGAACAAA TAGGATGGGT CAAAAAAG	58
ATG AAG TCA AAT AAA AAG TCC AAT CGT TTA AGA GCG ATT TAT AGA GCT Met Lys Ser Asn Lys Lys Ser Asn Arg Leu Arg Ala Ile Tyr Arg Ala 1 5 10 15	106
TTA GTG ATC GCT ATA GGA CTA GCT GTT ATC ATC GTT TTC AAT TAC TTT Leu Val Ile Ala Ile Gly Leu Ala Val Ile Ile Val Phe Asn Tyr Phe 20 25 30	154
AAC CGC AAA AAC AAT AAC GCC CGC TCC AGC CGT AGG GCT TGT TCG TGC Asn Arg Lys Asn Asn Asn Ala Arg Ser Ser Arg Arg Ala Cys Ser Cys 35 40 45	202
TTT TTT TCC CTT ACC GGG GTT AAT TTA GAA AAA ATA GGC ACT TTT GAT Phe Phe Ser Leu Thr Gly Val Asn Leu Glu Lys Ile Gly Thr Phe Asp 50 55 60	250
ACG GAC GCT AAA CTC ATT GTC TTA AAC CAC CAA AGC TTA CTA GAC ATC Thr Asp Ala Lys Leu Ile Val Leu Asn His Gln Ser Leu Leu Asp Ile 65 70 75 80	298
ATT TAT TTA GAA GCC TAC CAC CCT AGA AAT ATT TGC TGG ATC GCT AAA Ile Tyr Leu Glu Ala Tyr His Pro Arg Asn Ile Cys Trp Ile Ala Lys 85 90 95	346
AAA GAG CTG GGC GAA ATC CCT TTT TAT GGG CAT GCC TTA ACG GAT ACC Lys Glu Leu Gly Glu Ile Pro Phe Tyr Gly His Ala Leu Thr Asp Thr 100 105 110	394
GGA ATG ATT TTA ATT GAC AGA GAG GAT AAA AAG GGG ATT GTG AGC CTT Gly Met Ile Leu Ile Asp Arg Glu Asp Lys Lys Gly Ile Val Ser Leu 115 120 125	442
TTG AAA GCG TGT AAA GAA AAA TTA GAC CAA AAC CGC CCT TTA GTG ATT Leu Lys Ala Cys Lys Glu Lys Leu Asp Gln Asn Arg Pro Leu Val Ile 130 135 140	490
TTC CCT GAA GGC ACT AGA GGC AAA GGA GGA GAA AAA TTC CTC CCT TTC Phe Pro Glu Gly Thr Arg Gly Lys Gly Gly Glu Lys Phe Leu Pro Phe 145 150 155 160	538
AAG CAA GGG GCT AAA ATC ATC GCC GAA AAA TTC CAG CTC AAA ATC CAA Lys Gln Gly Ala Lys Ile Ile Ala Glu Lys Phe Gln Leu Lys Ile Gln 165 170 175	586
CCC ATG GTG TTA ATC AAT TCC ATT AAA ATC TTT AAT TCC AAG CCT CTA Pro Met Val Leu Ile Asn Ser Ile Lys Ile Phe Asn Ser Lys Pro Leu 180 185 190	634
GAA GCC TAT AAA GCG CGC ACC CGT TTA GTC ATG CTA GAA AGC TAT ACG Glu Ala Tyr Lys Ala Arg Thr Arg Leu Val Met Leu Glu Ser Tyr Thr	682

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Met	Arg	Val	Met	Ala	Lys	Ile	Glu	Leu	Leu	Ala	Lys	Phe	Thr	Gln	Ile
1				5					10					15	
Ala	Leu	Pro	Asn	Ser	His	Pro	Leu	Leu	Lys	Lys	Val	Leu	Asn	Tyr	Ala
			20					25					30		
Lys	Lys	His	Phe	Ser	Gln	Cys	His	Met	Leu	Ser	Ser	Ser	Leu	Leu	Ile
		35					40					45			
Leu	Asn	Asp	Thr	Glu	Cys	Phe	Lys	Lys	Asn	Tyr	Leu	Leu	Asn	Trp	Val
	50					55					60				
Tyr	His	Ala	Leu	Glu	Cys	Val	His	Glu	Lys	Asp	Ile	Ser	Ala	His	Ser
65					70					75				80	
Leu	Glu	Glu	Val	Leu	Gln	Lys	Ser	His	Leu	Pro	Ile	Arg	Ile	Lys	Ile
				85					90				95		
Met	Ala	Gln	Asn	Thr	Leu	Leu	Glu	Lys	Ile	Glu	Val	Lys	Val	Leu	Thr
			100					105					110		
Phe	Gly	Ala	Glu	Tyr	Ala	Leu	Phe	Ile	Thr	Lys	His	Pro	Ile	Ala	Lys
		115						120				125			
Arg	Phe	Leu	Arg	Gln	Lys	Phe	Ser	Gly	Cys	Val	Phe	Leu	Glu	Thr	Gln
	130					135					140				
Asp	Glu	Leu	His	Ile	Arg	Gly	Asp	Ser	Glu	Arg	Phe	Trp	Glu	Leu	Ile
145					150					155				160	
Val	Thr	Leu	Asn	Glu	Asn	Arg	Ile	Val	His	Asn	Ala	Cys	Leu	Asp	Phe
			165					170					175		
Ile	Tyr	Pro	Asn	Gly	Phe	Gly	Lys	Asp	Ser	Tyr	Thr	Thr	Met	Ala	Glu
		180						185					190		
Arg	Lys	Leu	Lys	Glu	Cys	Tyr	Lys	Thr	Leu	Gly	Phe	Ile	Lys	His	Glu
		195					200					205			
Asp	Phe	Ser	Glu	Val	Lys	Lys	Arg	Tyr	Leu	Glu	Leu	Ala	Lys	Thr	Tyr
	210					215					220				
His	Pro	Asp	Leu	Cys	Asp	Leu	Lys	Glu	Lys	Lys	Ala	Leu	Tyr	Ala	Lys
225					230					235				240	
Arg	Phe	Ala	Ile	Ile	Gln	Glu	Ala	Tyr	Arg	His	Ile	Lys	Lys	His	Ala
			245					250					255		

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 59...778
 (D) OTHER INFORMATION:

80	85	90	
ATC AAA ATC ATG GCT CAA AAC ACG CTT TTA GAA AAG ATA GAA GTG AAA			338
Ile Lys Ile Met Ala Gln Asn Thr Leu Leu Glu Lys Ile Glu Val Lys			
95	100	105	
GTT TTA ACC TTT GGG GCG GAA TAT GCG CTT TTT ATC ACC AAA CAC CCT			386
Val Leu Thr Phe Gly Ala Glu Tyr Ala Leu Phe Ile Thr Lys His Pro			
110	115	120	125
ATC GCC AAG CGG TTT TTA CGC CAA AAA TTT AGC GGC TGT GTG TTT TTA			434
Ile Ala Lys Arg Phe Leu Arg Gln Lys Phe Ser Gly Cys Val Phe Leu			
	130	135	140
GAA ACC CAA GAT GAA TTG CAT ATA AGA GGC GAT TCA GAG CGT TTT TGG			482
Glu Thr Gln Asp Glu Leu His Ile Arg Gly Asp Ser Glu Arg Phe Trp			
	145	150	155
GAA CTC ATT GTA ACG CTC AAT GAA AAT AGA ATC GTC CAT AAC GCA TGC			530
Glu Leu Ile Val Thr Leu Asn Glu Asn Arg Ile Val His Asn Ala Cys			
	160	165	170
TTA GAT TTC ATC TAC CCT AAT GGC TTT GGC AAG GAC AGC TAC ACC ACT			578
Leu Asp Phe Ile Tyr Pro Asn Gly Phe Gly Lys Asp Ser Tyr Thr Thr			
	175	180	185
ATG GCT GAA CGC AAA TTA AAA GAA TGC TAT AAA ACG CTA GGG TTT ATC			626
Met Ala Glu Arg Lys Leu Lys Glu Cys Tyr Lys Thr Leu Gly Phe Ile			
190	195	200	205
AAG CAT GAA GAT TTC AGC GAA GTC AAA AAG CGC TAT TTA GAA TTG GCT			674
Lys His Glu Asp Phe Ser Glu Val Lys Lys Arg Tyr Leu Glu Leu Ala			
	210	215	220
AAA ACC TAC CAC CCT GAT TTA TGC GAT CTC AAA GAA AAA AAG GCT CTT			722
Lys Thr Tyr His Pro Asp Leu Cys Asp Leu Lys Glu Lys Lys Ala Leu			
	225	230	235
TAT GCC AAA CGC TTC GCT ATC ATT CAA GAG GCG TAT CGC CAC ATT AAA			770
Tyr Ala Lys Arg Phe Ala Ile Ile Gln Glu Ala Tyr Arg His Ile Lys			
	240	245	250
AAA CAC GCC TAAACCCCTA AACTAGCCCT AATCGCGCTA G			810
Lys His Ala			
255			

(2) INFORMATION FOR SEQ ID NO:552:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

```

Leu Lys Ile Pro Arg Asn Ala Arg Asp Lys Gln Thr Phe Ala Phe Arg
  290                      295                      300
Asn Glu Gly Val Lys His Pro Glu Ser Ser Tyr Arg Gly Ser Leu Ile
305                      310                      315                      320
Val Glu Leu Gln Val Ile Tyr Pro Lys Ser Leu Asn Lys Glu Gln Gln
                      325                      330                      335
Glu Leu Leu Glu Lys Leu His Ala Ser Phe Gly Tyr Glu Gly Glu Pro
                      340                      345                      350
His Lys Ser Val Leu Glu Thr Cys Ile Ser Lys Ile Lys Asp Trp Phe
                      355                      360                      365
Lys

```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 12...779
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

```

CGCATGGAGA A ATG AGG GTA ATG GCC AAA ATT GAA TTG TTA GCC AAA TTC      50
      Met Arg Val Met Ala Lys Ile Glu Leu Leu Ala Lys Phe
              1              5              10

ACG CAA ATC GCG CTC CCT AAC AGC CAC CCT TTA TTG AAA AAA GTT TTA      98
Thr Gln Ile Ala Leu Pro Asn Ser His Pro Leu Leu Lys Lys Val Leu
      15              20              25

AAC TAC GCC AAA AAG CAT TTC AGC CAG TGC CAC ATG CTC TCT TCA TCG     146
Asn Tyr Ala Lys Lys His Phe Ser Gln Cys His Met Leu Ser Ser Ser
      30              35              40              45

TTA CTC ATC TTA AAC GAC ACG GAA TGC TTT AAA AAA AAC TAC TTG CTT     194
Leu Leu Ile Leu Asn Asp Thr Glu Cys Phe Lys Lys Asn Tyr Leu Leu
              50              55              60

AAT TGG GTC TAT CAT GCC CTT GAA TGC GTG CAT GAA AAA GAT ATT AGC     242
Asn Trp Val Tyr His Ala Leu Glu Cys Val His Glu Lys Asp Ile Ser
              65              70              75

GCG CAT TCT TTA GAA GAG GTT TTA CAA AAA AGC CAC CTG CCC ATA CGC     290
Ala His Ser Leu Glu Glu Val Leu Gln Lys Ser His Leu Pro Ile Arg

```

ACC TGT ATT TCT AAA ATT AAA GAC TGG TTC AAA TAAAAGGTTG TTGATGCATG 1162
 Thr Cys Ile Ser Lys Ile Lys Asp Trp Phe Lys
 360 365

AGTTTCTAAA AGCTTTTAAA GACGCTTTCC CTCATACCAT TT 1204

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

Val	Glu	Leu	Ser	Tyr	Tyr	Glu	Ile	Leu	Glu	Val	Glu	Lys	His	Ser	Asn	1	5	10	15
Gln	Glu	Thr	Ile	Lys	Lys	Ser	Tyr	Arg	Lys	Leu	Ala	Leu	Lys	Tyr	His	20	25	30	
Pro	Asp	Arg	Asn	Ala	Gly	Asp	Lys	Glu	Ala	Glu	Glu	Lys	Phe	Lys	Leu	35	40	45	
Ile	Asn	Glu	Ala	Tyr	Gly	Val	Leu	Ser	Asp	Glu	Lys	Lys	Arg	Ala	Leu	50	55	60	
Tyr	Asp	Arg	Tyr	Gly	Lys	Gly	Leu	Asn	Gln	Ala	Gly	Ala	Ser	Gln		65	70	75	80
Gly	Asp	Phe	Ser	Asp	Phe	Phe	Glu	Asp	Leu	Gly	Ser	Phe	Phe	Glu	Asp	85	90	95	
Ala	Phe	Gly	Phe	Gly	Ala	Arg	Gly	Ser	Lys	Arg	Gln	Lys	Ser	Ser	Ile	100	105	110	
Ala	Pro	Asp	Tyr	Leu	Gln	Thr	Leu	Glu	Leu	Ser	Phe	Lys	Glu	Ala	Val	115	120	125	
Phe	Gly	Cys	Lys	Lys	Thr	Ile	Lys	Val	Gln	Tyr	Gln	Ser	Val	Cys	Glu	130	135	140	
Ser	Cys	Asp	Gly	Thr	Gly	Ala	Lys	Asp	Lys	Ala	Leu	Glu	Thr	Cys	Lys	145	150	155	160
Gln	Cys	Asn	Gly	Gln	Gly	Gln	Val	Phe	Met	Arg	Gln	Gly	Phe	Met	Ser	165	170	175	
Phe	Ala	Gln	Thr	Cys	Gly	Ala	Cys	Gln	Gly	Lys	Gly	Lys	Ile	Val	Lys	180	185	190	
Thr	Pro	Cys	Gln	Ala	Cys	Lys	Gly	Lys	Thr	Tyr	Ile	Leu	Lys	Asp	Glu	195	200	205	
Glu	Ile	Asp	Ala	Ile	Ile	Pro	Glu	Gly	Ile	Asp	Asp	Gln	Asn	Arg	Met	210	215	220	
Val	Leu	Lys	Asn	Lys	Gly	Asn	Glu	Tyr	Glu	Lys	Gly	Lys	Arg	Gly	Asp	225	230	235	240
Leu	Tyr	Leu	Glu	Ala	Gln	Val	Lys	Glu	Asp	Glu	His	Phe	Lys	Arg	Glu	245	250	255	
Gly	Cys	Asp	Leu	Phe	Ile	Lys	Ala	Pro	Val	Phe	Phe	Thr	Thr	Ile	Ala	260	265	270	
Leu	Gly	His	Thr	Ile	Lys	Val	Pro	Ser	Leu	Lys	Gly	Asp	Glu	Leu	Glu	275	280	285	

Ile Lys Val Gln Tyr Gln Ser Val Cys Glu Ser Cys Asp Gly Thr Gly	
135 140 145 150	
GCT AAA GAC AAA GCC CTA GAG ACT TGC AAG CAA TGC AAT GGG CAG GGG	533
Ala Lys Asp Lys Ala Leu Glu Thr Cys Lys Gln Cys Asn Gly Gln Gly	
155 160 165	
CAG GTG TTT ATG CGT CAA GGT TTT ATG AGT TTT GCG CAA ACT TGT GGG	581
Gln Val Phe Met Arg Gln Gly Phe Met Ser Phe Ala Gln Thr Cys Gly	
170 175 180	
GCG TGT CAA GGC AAG GGC AAG ATC GTT AAA ACC CCA TGC CAA GCG TGC	629
Ala Cys Gln Gly Lys Gly Lys Ile Val Lys Thr Pro Cys Gln Ala Cys	
185 190 195	
AAG GGT AAA ACC TAT ATC CTT AAA GAT GAA GAA ATT GAT GCG ATA ATC	677
Lys Gly Lys Thr Tyr Ile Leu Lys Asp Glu Glu Ile Asp Ala Ile Ile	
200 205 210	
CCT GAG GGC ATT GAT GAT CAA AAC CGC ATG GTG CTT AAA AAT AAA GGC	725
Pro Glu Gly Ile Asp Asp Gln Asn Arg Met Val Leu Lys Asn Lys Gly	
215 220 225 230	
AAT GAA TAC GAG AAG GGA AAA AGA GGG GAT TTG TAT TTA GAA GCG CAA	773
Asn Glu Tyr Glu Lys Gly Lys Arg Gly Asp Leu Tyr Leu Glu Ala Gln	
235 240 245	
GTC AAA GAA GAT GAG CAT TTC AAG CGC GAA GGC TGC GAT TTA TTC ATT	821
Val Lys Glu Asp Glu His Phe Lys Arg Glu Gly Cys Asp Leu Phe Ile	
250 255 260	
AAA GCG CCG GTG TTT TTC ACC ACT ATC GCT TTA GGG CAT ACG ATT AAA	869
Lys Ala Pro Val Phe Phe Thr Thr Ile Ala Leu Gly His Thr Ile Lys	
265 270 275	
GTG CCG TCT TTA AAA GGG GAC GAA CTG GAA TTA AAA ATC CCT AGA AAC	917
Val Pro Ser Leu Lys Gly Asp Glu Leu Glu Leu Lys Ile Pro Arg Asn	
280 285 290	
GCC AGA GAC AAG CAG ACT TTT GCG TTT AGA AAC GAG GGC GTG AAA CAC	965
Ala Arg Asp Lys Gln Thr Phe Ala Phe Arg Asn Glu Gly Val Lys His	
295 300 305 310	
CCT GAA AGC TCT TAT AGA GGG AGT TTG ATC GTG GAA TTG CAA GTG ATT	1013
Pro Glu Ser Ser Tyr Arg Gly Ser Leu Ile Val Glu Leu Gln Val Ile	
315 320 325	
TAC CCT AAA AGT TTG AAT AAA GAG CAG CAA GAA TTG TTG GAA AAA TTG	1061
Tyr Pro Lys Ser Leu Asn Lys Glu Gln Gln Glu Leu Leu Glu Lys Leu	
330 335 340	
CAT GCG AGT TTT GGC TAT GAG GGC GAG CCG CAT AAA AGC GTT TTA GAA	1109
His Ala Ser Phe Gly Tyr Glu Gly Glu Pro His Lys Ser Val Leu Glu	
345 350 355	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 36...1142
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```

AAAATAAGCG TTTTGATGCC ATTTTGGAG CGATC GTG GAA TTG AGT TAT TAT      53
                               Val Glu Leu Ser Tyr Tyr
                               1           5

GAA ATT TTA GAA GTG GAA AAA CAC AGC AAC CAA GAG ACC ATT AAA AAG      101
Glu Ile Leu Glu Val Glu Lys His Ser Asn Gln Glu Thr Ile Lys Lys
                10                15                20

TCT TAC AGA AAG CTG GCT TTA AAA TAC CAC CCA GAC AGA AAC GCC GGC      149
Ser Tyr Arg Lys Leu Ala Leu Lys Tyr His Pro Asp Arg Asn Ala Gly
                25                30                35

GAT AAA GAA GCC GAA GAA AAA TTC AAG CTC ATC AAT GAA GCC TAT GGG      197
Asp Lys Glu Ala Glu Glu Lys Phe Lys Leu Ile Asn Glu Ala Tyr Gly
                40                45                50

GTG TTA AGC GAT GAA AAG AAG CGG GCC TTA TAC GAC AGG TAT GGT AAA      245
Val Leu Ser Asp Glu Lys Lys Arg Ala Leu Tyr Asp Arg Tyr Gly Lys
                55                60                65                70

AAA GGC TTA AAC CAA GCC GGC GCA AGC CAA GGC GAT TTT TCT GAT TTT      293
Lys Gly Leu Asn Gln Ala Gly Ala Ser Gln Gly Asp Phe Ser Asp Phe
                75                80                85

TTT GAA GAT TTA GGC TCG TTT TTT GAA GAC GCT TTT GGG TTT GGC GCT      341
Phe Glu Asp Leu Gly Ser Phe Phe Glu Asp Ala Phe Gly Phe Gly Ala
                90                95                100

AGG GGG AGT AAA AGG CAA AAA AGC TCT ATC GCA CCG GAT TAT TTG CAA      389
Arg Gly Ser Lys Arg Gln Lys Ser Ser Ile Ala Pro Asp Tyr Leu Gln
                105                110                115

ACC CTT GAA TTG AGT TTC AAA GAA GCG GTT TTT GGC TGT AAA AAA ACC      437
Thr Leu Glu Leu Ser Phe Lys Glu Ala Val Phe Gly Cys Lys Lys Thr
                120                125                130

ATT AAA-GTC CAA TAC CAG AGC GTT TGT GAA AGT TGC GAT GGC ACG GGC      485

```

35	40	45	50	
TTG ACG ACA GCG GCT CGT GTG GGC GAT TTT AAT GCG CAC CGC CAT GTT				248
Leu Thr Thr Ala Ala Arg Val Gly Asp Phe Asn Ala His Arg His Val				
	55	60	65	
TTT GCA TAT TTG CAA AAC AAA GAA GCC ACC CAC AAG CTT GTA ACT GAA				296
Phe Ala Tyr Leu Gln Asn Lys Glu Ala Thr His Lys Leu Val Thr Glu				
	70	75	80	
ATC GCG CCC AAA TAC GCG CAA AGG AAT GGC GGA TAC ACC AGG ATC CAA				344
Ile Ala Pro Lys Tyr Ala Gln Arg Asn Gly Gly Tyr Thr Arg Ile Gln				
	85	90	95	
CGC ACC ACT TTT AGA AGA GGG GAC GCT TCC ACT CTA GCC ACC ATT GAA				392
Arg Thr Thr Phe Arg Arg Gly Asp Ala Ser Thr Leu Ala Thr Ile Glu				
	100	105	110	
TTT GTA TGAAATTTGA TGAAGTGCTA GCCAAGATTT AGTCTTGGTT GGTGGTTATC GC				450
Phe Val				
115				
T				451

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

Met	Arg	His	Lys	His	Gly	Tyr	Arg	Lys	Leu	Gly	Arg	Thr	Ser	Ser	His
1				5					10					15	
Arg	Lys	Ala	Leu	Leu	Lys	Asn	Leu	Ala	Ile	Ala	Leu	Ile	Glu	His	Asn
			20					25					30		
Lys	Ile	Glu	Thr	Gly	Ile	Tyr	Lys	Ala	Lys	Glu	Leu	Arg	Ser	Tyr	Ile
		35					40					45			
Glu	Lys	Leu	Thr	Thr	Ala	Ala	Arg	Val	Gly	Asp	Phe	Asn	Ala	His	Arg
	50					55				60					
His	Val	Phe	Ala	Tyr	Leu	Gln	Asn	Lys	Glu	Ala	Thr	His	Lys	Leu	Val
65					70					75				80	
Thr	Glu	Ile	Ala	Pro	Lys	Tyr	Ala	Gln	Arg	Asn	Gly	Gly	Tyr	Thr	Arg
			85					90					95		
Ile	Gln	Arg	Thr	Thr	Phe	Arg	Arg	Gly	Asp	Ala	Ser	Thr	Leu	Ala	Thr
			100					105					110		
Ile	Glu	Phe	Val												
			115												

(2) INFORMATION FOR SEQ ID NO:549:

```

Leu Ser Tyr Ala Tyr Val Ala Tyr Gln Trp Lys Leu Asn Ala Asp Val
65              70              75              80
Ile Leu Cys Leu Phe Leu Tyr Met Pro Val Thr Ile Tyr Gly Leu Phe
85              90              95
Ala Trp Lys Lys Thr Glu Gln His Glu Gly Val Ile Lys Ala Gln Lys
100            105            110
Leu Ser Lys Asn Trp Arg Phe Ile Leu Ile Leu Gly Val Gly Val Leu
115            120            125
Thr Cys Val Ser Ala Leu Phe Phe Lys Glu Ile Lys Thr Asn Phe Leu
130            135            140
Trp Ala Glu Ser Phe Asn Phe Val Ile Phe Ile Ile Ala Phe Ile Leu
145            150            155            160
Gln Val Leu Arg Tyr Ile Glu Asn Tyr Ala Leu Val Thr Leu Gly Asn
165            170            175
Ile Val Ser Ile Ile Val Trp Phe Cys Ile Phe Gln Ile Ser Thr Glu
180            185            190
Ser Leu Val Gln Leu Phe Thr Thr Ile Leu Tyr Leu Phe Ile Gly Leu
195            200            205
Tyr Tyr Phe Asn Arg Trp Asn Lys Ser Cys Lys Gln
210            215            220

```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...398
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

```

AGTTTAAAGA AAAGATTAGA AAAATTAGAA GATAAAGGAG GTAACGACTG  ATG AGA      56
                                                                Met Arg
                                                                1
CAC AAA CAC GGA TAC CGC AAG CTT GGG AGA ACC AGC TCG CAC AGA AAG      104
His Lys His Gly Tyr Arg Lys Leu Gly Arg Thr Ser Ser His Arg Lys
5              10              15
GCG TTA TTA AAG AAT TTA GCG ATC GCT TTG ATT GAG CAT AAC AAA ATT      152
Ala Leu Leu Lys Asn Leu Ala Ile Ala Leu Ile Glu His Asn Lys Ile
20            25            30
GAA ACA GGG ATT TAT AAG GCT AAG GAA TTG CGC AGT TAC ATT GAG AAA      200
Glu Thr Gly Ile Tyr Lys Ala Lys Glu Leu Arg Ser Tyr Ile Glu Lys

```


Lys	Lys	Thr	Glu	Gln	His	Glu	Gly	Val	Ile	Lys	Ala	Gln	Lys	Leu	Ser		
100						105					110						
AAA	AAT	TGG	CGT	TTT	ATA	CTC	ATT	TTA	GGC	GTA	GGG	GTT	TTA	ACT	TGT	442	
Lys	Asn	Trp	Arg	Phe	Ile	Leu	Ile	Leu	Gly	Val	Gly	Val	Leu	Thr	Cys		
115					120				125						130		
GTG	AGC	GCT	TTG	TTT	TTT	AAA	GAG	ATT	AAA	ACG	AAT	TTT	TTA	TGG	GCA	490	
Val	Ser	Ala	Leu	Phe	Phe	Lys	Glu	Ile	Lys	Thr	Asn	Phe	Leu	Trp	Ala		
				135					140						145		
GAG	AGT	TTT	AAT	TTC	GTC	ATC	TTT	ATT	ATT	GCT	TTT	ATT	TTA	CAG	GTT	538	
Glu	Ser	Phe	Asn	Phe	Val	Ile	Phe	Ile	Ile	Ala	Phe	Ile	Leu	Gln	Val		
			150					155					160				
TTG	CGC	TAT	ATA	GAA	AAT	TAT	GCG	CTA	GTA	ACT	TTG	GGG	AAT	ATC	GTA	586	
Leu	Arg	Tyr	Ile	Glu	Asn	Tyr	Ala	Leu	Val	Thr	Leu	Gly	Asn	Ile	Val		
		165					170					175					
TCC	ATT	ATC	GTG	TGG	TTT	TGT	ATT	TTT	CAA	ATT	TCT	ACA	GAG	AGC	TTG	634	
Ser	Ile	Ile	Val	Trp	Phe	Cys	Ile	Phe	Gln	Ile	Ser	Thr	Glu	Ser	Leu		
	180					185					190						
GTG	CAA	CTC	TTC	ACA	ACG	ATC	CTA	TAC	CTT	TTT	ATT	GGC	TTG	TAT	TAT	682	
Val	Gln	Leu	Phe	Thr	Thr	Ile	Leu	Tyr	Leu	Phe	Ile	Gly	Leu	Tyr	Tyr		
195					200				205					210			
TTT	AAC	CGG	TGG	AAT	AAG	TCA	TGC	AAG	CAG	TGATTTTAGC	GAATGGGGAG	TTT	735				
Phe	Asn	Arg	Trp	Asn	Lys	Ser	Cys	Lys	Gln								
			215					220									
CCTAAATCTC	AAAAATGCTT	AGACCTTTTA	AAAAACGCTC	CCTTTTAAAT	CGCATGCGAT	795											
GGGGCTGTTA	CCTCA					810											

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

Met	Leu	Ile	Thr	Thr	Gln	Leu	Ser	Lys	Arg	Phe	Tyr	Ala	Thr	Leu	Ala
1				5				10						15	
Leu	Ser	Cys	Val	Phe	Leu	Thr	Ile	Thr	Asn	Ile	Leu	Val	Lys	Gly	Ser
			20					25					30		
Phe	Ile	Asn	Leu	Leu	Ala	Gly	Leu	Ser	Gly	Val	Leu	Tyr	Ala	Phe	Phe
		35				40					45				
Ala	Gly	Glu	Arg	Gln	Thr	Ile	Cys	Phe	Val	Phe	Gly	Leu	Val	Tyr	Asn
	50					55					60				

130	135	140
Leu Val Cys Val Phe Gly Ile Cys Ser Arg Leu Cys Ala Lys Leu Gly		
145	150	155
Trp		160

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...712
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

TGAGATCAAA CCCGTAGAAC TTGTCAAGGT AATTCTTGCG TAAGGAAATA GC ATG TTA	58
Met Leu	
1	
ATA ACC ACC CAA CTA TCC AAA CGA TTT TAC GCC ACA CTC GCT CTT TCT	106
Ile Thr Thr Gln Leu Ser Lys Arg Phe Tyr Ala Thr Leu Ala Leu Ser	
5 10 15	
TGC GTG TTT TTA ACC ATC ACT AAC ATT CTT GTC AAA GGC TCG TTT ATC	154
Cys Val Phe Leu Thr Ile Thr Asn Ile Leu Val Lys Gly Ser Phe Ile	
20 25 30	
AAT CTT TTA GCA GGG CTT AGT GGG GTT TTG TAT GCG TTT TTT GCC GGA	202
Asn Leu Leu Ala Gly Leu Ser Gly Val Leu Tyr Ala Phe Phe Ala Gly	
35 40 45 50	
GAA AGG CAA ACG ATT TGC TTT GTG TTT GGT CTT GTT TAT AAT TTG AGT	250
Glu Arg Gln Thr Ile Cys Phe Val Phe Gly Leu Val Tyr Asn Leu Ser	
55 60 65	
TAC GCT TAT GTC GCT TAT CAG TGG AAA TTA AAC GCT GAT GTG ATT TTA	298
Tyr Ala Tyr Val Ala Tyr Gln Trp Lys Leu Asn Ala Asp Val Ile Leu	
70 75 80	
TGC CTT TTT TTG TAT ATG CCA GTA ACG ATT TAT GGG CTG TTC GCA TGG	346
Cys Leu Phe Leu Tyr Met Pro Val Thr Ile Tyr Gly Leu Phe Ala Trp	
85 90 95	
AAA AAG ACA GAG CAG CAT GAA GGC GTT ATC AAG GCT CAA AAA CTT TCC	394

Cys	Tyr	Lys	Ser	Phe	Gln	Val	Arg	Tyr	Pro	Arg	Phe	Leu	Lys	Ala	Ile	
		75					80					85				
TTT	AAG	GCT	AGG	TTT	TTT	GGC	GCG	TTT	TAT	AAC	GCT	GTG	TTA	GGA	TCA	342
Phe	Lys	Ala	Arg	Phe	Phe	Gly	Ala	Phe	Tyr	Asn	Ala	Val	Leu	Gly	Ser	
	90					95				100						
AGG	CTA	AGG	GAT	TTT	TAT	GTG	ATG	CTT	TTA	ACG	ATA	CCC	TTT	ATT	GCC	390
Arg	Leu	Arg	Asp	Phe	Tyr	Val	Met	Leu	Leu	Thr	Ile	Pro	Phe	Ile	Ala	
105					110					115					120	
GCT	ATC	CAT	GAG	GTT	TCG	GCG	TAT	TAC	GGG	CAT	CCT	AGC	AAC	TTC	CTT	438
Ala	Ile	His	Glu	Val	Ser	Ala	Tyr	Tyr	Gly	His	Pro	Ser	Asn	Phe	Leu	
				125					130					135		
ATA	GAG	GGT	TTG	GTC	ATT	CTT	GGC	CTT	GTG	TGT	GTT	TTT	GGG	ATT	TGT	486
Ile	Glu	Gly	Leu	Val	Ile	Leu	Gly	Leu	Val	Cys	Val	Phe	Gly	Ile	Cys	
			140					145					150			
TCT	AGG	CTT	TGC	GCT	AAA	TTA	GGG	TGG	TGATT	TAACT	CAA	ATAGCAT	TAA	ATGG		540
Ser	Arg	Leu	Cys	Ala	Lys	Leu	Gly	Trp								
		155					160									
AGGGGGGAGT	AAAAAATTA															559

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

Met	Asn	Val	Lys	Asn	Arg	Leu	Ser	Asp	Trp	Glu	Tyr	Gln	Trp	Ala	Val	
1				5				10						15		
Ala	Leu	Val	Tyr	Thr	Ile	Cys	Ile	Ser	Ile	Asn	Ala	Arg	Ile	Phe	Tyr	
		20						25					30			
Asp	Ile	Asp	Gly	Ser	Ala	Ser	Asp	Ser	Ile	Phe	Asp	Pro	Lys	Asn	Ser	
	35					40					45					
Tyr	Tyr	Met	Trp	Leu	Val	Gly	Leu	Ile	Ala	Ala	Leu	Leu	Ser	Asn	Leu	
	50				55						60					
Leu	Phe	Asp	Pro	Arg	Gly	Arg	Asp	Cys	Tyr	Lys	Ser	Phe	Gln	Val	Arg	
65				70					75					80		
Tyr	Pro	Arg	Phe	Leu	Lys	Ala	Ile	Phe	Lys	Ala	Arg	Phe	Phe	Gly	Ala	
			85					90						95		
Phe	Tyr	Asn	Ala	Val	Leu	Gly	Ser	Arg	Leu	Arg	Asp	Phe	Tyr	Val	Met	
		100					105						110			
Leu	Leu	Thr	Ile	Pro	Phe	Ile	Ala	Ala	Ile	His	Glu	Val	Ser	Ala	Tyr	
	115					120					125					
Tyr	Gly	His	Pro	Ser	Asn	Phe	Leu	Ile	Glu	Gly	Leu	Val	Ile	Leu	Gly	

290		295		300
Pro Gly Val Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala				
305		310		315
Val Tyr Glu Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu				
	325		330	335
Leu Cys Gln Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala				
	340		345	350
Leu Ala Tyr Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile				
	355		360	365
Ile Val Val Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val				
	370		375	380
Tyr Asn Ala Leu Lys Gly Gly Leu Lys				
385		390		

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...513
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

CAGGTAGCTT TGGGCGAGAA AGGAGAGAGC	ATG AAT GTC AAA AAT CGT TTG AGC	54
	Met Asn Val Lys Asn Arg Leu Ser	
	1 5	
GAT TGG GAA TAT CAA TGG GCA GTG GCT CTA GTC TAT ACG ATA TGT ATC		102
Asp Trp Glu Tyr Gln Trp Ala Val Ala Leu Val Tyr Thr Ile Cys Ile		
10 15 20		
TCC ATA AAC GCT AGG ATT TTT TAT GAC ATA GAT GGT TCA GCT AGC GAT		150
Ser Ile Asn Ala Arg Ile Phe Tyr Asp Ile Asp Gly Ser Ala Ser Asp		
25 30 35 40		
TCG ATT TTT GAC CCT AAA AAT AGC TAT TAT ATG TGG CTA GTG GGT CTA		198
Ser Ile Phe Asp Pro Lys Asn Ser Tyr Tyr Met Trp Leu Val Gly Leu		
45 50 55		
ATA GCG GCT TTG TTG TCT AAC CTT TTA TTT GAC CCA CGA GGT AGG GAT		246
Ile Ala Ala Leu Leu Ser Asn Leu Leu Phe Asp Pro Arg Gly Arg Asp		
60 65 70		
TGT TAT AAA TCT TTC CAA GTA AGA TAC CCT AGG TTT CTC AAA GCC ATT		294

165	170	175	
AAG GAC ACG CAT TAT TTG CTA GGC ACA GCC GCC GGG CCA CAC CCT TAC			632
Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro His Pro Tyr			
180	185	190	195
CCC ACA ATG GTT AAA ACC TTT CAA AAA ATG ATA GGC GAT GAG GTT AAA			680
Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp Glu Val Lys			
200	205		210
AGC CAG ATT TTA GAA AAA GAA AAC CGC TTG CCT GAT TAT GTG ATC GCA			728
Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr Val Ile Ala			
215	220		225
TGC GTT GGA GGG GGG TCT AAC GCT ATA GGG ATA TTC AGC GCA TTT TTA			776
Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser Ala Phe Leu			
230	235		240
AAC GAC AAA GAA GTT AAA CTC ATA GGC GTA GAG CCG GCG GGT TTA GGG			824
Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala Gly Leu Gly			
245	250		255
CTA GAA ACC AAT AAG CAT GGG GCG ACT TTG AAT AAG GGG CGT GTG GGG			872
Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly Arg Val Gly			
260	265	270	275
ATT TTG CAT GGG AAT AAA ACC TAT CTT TTA CAA GAT GAT GAA GGC CAG			920
Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp Glu Gly Gln			
280	285		290
ATT GCA GAA AGC CAT AGC ATT AGC GCC GGG CTT GAT TAT CCA GGA GTG			968
Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val			
295	300		305
GGG CCA GAA CAC AGC TAT TTA AAA GAA AGT GGG CGT GCG GTT TAT GAA			1016
Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala Val Tyr Glu			
310	315		320
AGC GCA AGC GAT GCT GAA GCG CTA GAA GCC TTC AAG TTG TTG TGC CAA			1064
Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu Leu Cys Gln			
325	330		335
AAA GAA GGC ATT ATC CCA GCG CTA GAA AGC TCA CAC GCC TTA GCG TAT			1112
Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Leu Ala Tyr			
340	345	350	355
GCC TTA AAG CTC GCT CAA AAA TGC GAA GAA GAA AGC ATC ATC GTA GTG			1160
Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile Ile Val Val			
360	365		370
AAT TTA AGC GGC AGA GGG GAT AAG GAT TTA AGC ACC GTT TAT AAC GCT			1208
Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val Tyr Asn Ala			
375	380		385
TTA AAA GGA GGT TTA AAA TGAGGTATCA AAACATGTTT GAAACCTTAA AAAAACAC			1264

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 48...1226
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

TAAGGATAAA ATCAAGCGAT TAGCCCGAAT TTTAAGAGAG TATTAAG	ATG AAT AAA	56
	Met Asn Lys	
	1	
AAA GCG TAT TTT GGG GAG TTT GGA GGG AGT TTT GTT TCG GAG TTG TTA		104
Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu		
5 10 15		
GTG CCT GCA TTA AGA GAA TTA GAA CAG GCG TTT GAT GCG TGT TTG AAA		152
Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys		
20 25 30 35		
GAT GAA AAA TTC CAA AAA GAA TAT TTT CGT CTT TTA AAG GAT TTT GTG		200
Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys Asp Phe Val		
40 45 50		
GGC CGT CCT AGC CCT TTA ACC TTG TGT CAA AAT ATC GTT TCT AAC CCT		248
Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val Ser Asn Pro		
55 60 65		
AAA GTC AAG CTT TAT TTA AAA CGA GAG GAT TTA ATC CAT GGC GGG GCG		296
Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His Gly Gly Ala		
70 75 80		
CAT AAG ACT AAT CAA GCC TTA GGG CAA GCC CTT TTA GCG AAA AAA ATG		344
His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala Lys Lys Met		
85 90 95		
GGT AAA ACA AGG ATC ATC GCT GAA ACA GGC GCC GGT CAG CAT GGC GTG		392
Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Val		
100 105 110 115		
GCG ACG GCT ATC GCT TGC GCA TTA TTG AAC TTA AAA TGC GTG GTT TTT		440
Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys Val Val Phe		
120 125 130		
ATG GGA TCT AAA GAC ATC AAG CGC CAG GAA ATG AAT GTT TTT AGA ATG		488
Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val Phe Arg Met		
135 140 145		
CAC TTA TTA GGC GCT GAA GTG AGA GAG GTT AAT TCA GGG AGC GCG ACG		536
His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly Ser Ala Thr		
150 155 160		
CTT AAA GAC GCT GTG AAT GAA GCC TTA AGA GAT TGG GCG AGC AGT TAC		584
Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala Ser Ser Tyr		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

```

Met Ser Ala Tyr Ile Ile Glu Thr Leu Ile Lys Ile Leu Ile Leu Val
 1           5           10           15
Ala Val Phe Ser Ala Leu Gly Gly Phe Ala Thr Tyr Ile Glu Arg Lys
 20           25           30
Val Leu Ala Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro
 35           40           45
Phe Gly Leu Leu Gln Val Ala Ala Asp Gly Ile Lys Leu Phe Thr Lys
 50           55           60
Glu Asp Ile Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala
 65           70           75           80
Pro Ile Ile Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro
 85           90           95
Phe Phe Pro Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile
 100          105          110
Ser Asp Ile Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala
 115          120          125
Gly Ile Tyr Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr
 130          135          140
Ser Leu Ile Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu
 145          150          155          160
Val Val Ser Thr Leu Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser
 165          170          175
Leu Ser Leu Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp
 180          185          190
Trp Leu Val Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala
 195          200          205
Ser Tyr Ala Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu
 210          215          220
Ala Glu Ile Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp
 225          230          235          240
Gly Met Phe Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe
 245          250          255
Val Ile Ser Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile
 260          265          270
Pro Gly Gly Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu
 275          280          285
Ser Met Trp Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu
 290          295          300
Met Asp Met Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile
 305          310          315          320
Val Leu Thr Gly Ile Ile Ile Leu Ile
 325

```

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

165	170	175	
GTG GAA ATC AAT CAT TAC CAA AGC GGT GGG TTT TTA GAC TGG CTT GTG			631
Val Glu Ile Asn His Tyr Gln Ser Gly Gly Phe Leu Asp Trp Leu Val			
180	185	190	195
TTT AAG CAG CCT CTA GCG TTT GTT TTG TTT TTG ATC GCA AGT TAT GCC			679
Phe Lys Gln Pro Leu Ala Phe Val Leu Phe Leu Ile Ala Ser Tyr Ala			
	200	205	210
GAA TTG AAT CGA ACC CCC TTT GAC TTG CTA GAG CAT GAA GCC GAG ATC			727
Glu Leu Asn Arg Thr Pro Phe Asp Leu Leu Glu His Glu Ala Glu Ile			
	215	220	225
GTG GCG GGG TAT TGC ACC GAA TAC AGC GGC TTG AAA TGG GGC ATG TTC			775
Val Ala Gly Tyr Cys Thr Glu Tyr Ser Gly Leu Lys Trp Gly Met Phe			
	230	235	240
TTT TTA GCG GAA TAC GCG CAT TTA TTC GCT TTT TCT TTT GTG ATT TCT			823
Phe Leu Ala Glu Tyr Ala His Leu Phe Ala Phe Ser Phe Val Ile Ser			
	245	250	255
ATT GTG TTT TTT GGC GGG TTT AAC GCA TGG GGC TTT ATC CCT GGA GGC			871
Ile Val Phe Phe Gly Gly Phe Asn Ala Trp Gly Phe Ile Pro Gly Gly			
	260	265	270
ATA GCG ATT TTG ATT AAA GCG GGC TTT TTT GTC TTT TTA TCC ATG TGG			919
Ile Ala Ile Leu Ile Lys Ala Gly Phe Phe Val Phe Leu Ser Met Trp			
	280	285	290
GTT AGA GCG ACT TAT CCG CAT GTG CGC CCA GAC CAA CTG ATG GAT ATG			967
Val Arg Ala Thr Tyr Pro His Val Arg Pro Asp Gln Leu Met Asp Met			
	295	300	305
TGC TGG AAA ATC ATG CTG CCT TTA GCG TTA TTG AAC ATT GTG CTA ACG			1015
Cys Trp Lys Ile Met Leu Pro Leu Ala Leu Leu Asn Ile Val Leu Thr			
	310	315	320
GGC ATT ATC ATT TTA ATT TAAAGGAGGT TTTATGGCCA AACAAGAATA CAAGCAAC			1071
Gly Ile Ile Ile Leu Ile			
	325		
TTCCTAAAC			1080

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 47...1033
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

TTTTTAGAGA GGGCGTGTTT GATAGCGTGG ATTTAAAGGA GCAAGC ATG AGC GCT	55
Met Ser Ala	
1	
TAT ATC ATT GAA ACC CTG ATT AAA ATT TTG ATT TTA GTC GCT GTT TTT	103
Tyr Ile Ile Glu Thr Leu Ile Lys Ile Leu Ile Leu Val Ala Val Phe	
5 10 15	
TCG GCT TTA GGA GGC TTT GCC ACT TAT ATT GAA AGG AAA GTG TTA GCC	151
Ser Ala Leu Gly Gly Phe Ala Thr Tyr Ile Glu Arg Lys Val Leu Ala	
20 25 30 35	
TAT TTC CAA CGC CGT TTA GGG CCT TGT TAT GTG GGG CCT TTT GGG CTT	199
Tyr Phe Gln Arg Arg Leu Gly Pro Cys Tyr Val Gly Pro Phe Gly Leu	
40 45 50	
TTG CAA GTC GCA GCA GAC GGC ATT AAG CTT TTC ACT AAA GAA GAC ATT	247
Leu Gln Val Ala Ala Asp Gly Ile Lys Leu Phe Thr Lys Glu Asp Ile	
55 60 65	
ATC CCT CAA GGC GCG AAC AAA TTC ATT TTC ACG CTA GCG CCC ATT ATT	295
Ile Pro Gln Gly Ala Asn Lys Phe Ile Phe Thr Leu Ala Pro Ile Ile	
70 75 80	
GCG ATG GTG AGT GCG TTT GTG TCC ATG GCG CCT ATC CCC TTT TTC CCT	343
Ala Met Val Ser Ala Phe Val Ser Met Ala Pro Ile Pro Phe Phe Pro	
85 90 95	
AAT TTC ACT CTG TTT GGC TAT GAG ATC AAG CCC CTT ATT TCT GAC ATC	391
Asn Phe Thr Leu Phe Gly Tyr Glu Ile Lys Pro Leu Ile Ser Asp Ile	
100 105 110 115	
AAC ATT GGC TTT TTG TTT TTC TTA GCC GTG GGT TCG GCA GGG ATT TAT	439
Asn Ile Gly Phe Leu Phe Phe Leu Ala Val Gly Ser Ala Gly Ile Tyr	
120 125 130	
GCG CCT ATT TTA GCC GGG CTT GCC TCT AAT AAC AAA TAC TCT TTA ATT	487
Ala Pro Ile Leu Ala Gly Leu Ala Ser Asn Asn Lys Tyr Ser Leu Ile	
135 140 145	
GGC TCC GCA AGA GCG ACG ATC CAA CTG CTC AGC TTT GAA GTG GTC AGC	535
Gly Ser Ala Arg Ala Thr Ile Gln Leu Leu Ser Phe Glu Val Val Ser	
150 155 160	
ACT TTA ACC ATT CTA GCC CCC TTA ATG GTG GTA GGA TCG CTC TCT TTA	583
Thr Leu -Thr Ile Leu Ala Pro Leu Met Val Val Gly Ser Leu Ser Leu	

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

```

Met Lys Leu Lys Ser Phe Gly Val Phe Gly Asn Pro Ile Lys His Ser
 1           5           10           15
Lys Ser Pro Leu Ile His Asn Ala Cys Phe Leu Thr Phe Gln Lys Glu
          20           25           30
Leu Arg Phe Leu Gly His Tyr His Pro Ile Leu Leu Pro Leu Glu Ser
          35           40           45
His Ile Lys Ser Glu Phe Leu His Leu Gly Leu Ser Gly Ala Asn Val
          50           55           60
Thr Leu Pro Phe Lys Glu Arg Ala Phe Gln Val Cys Asp Lys Ile Lys
65           70           75           80
Gly Ile Ala Leu Glu Cys Gly Ala Val Asn Thr Leu Val Leu Glu Asn
          85           90           95
Asp Glu Leu Val Gly Tyr Asn Thr Asp Ala Leu Gly Phe Tyr Leu Ser
          100          105          110
Leu Lys Gln Lys Asn Tyr Gln Asn Ala Leu Ile Leu Gly Ala Gly Gly
          115          120          125
Ser Ala Lys Ala Leu Ala Cys Glu Leu Lys Lys Gln Gly Leu Gln Val
          130          135          140
Ser Val Leu Asn Arg Ser Ser Arg Gly Leu Asp Phe Phe Gln Arg Leu
145          150          155          160
Gly Cys Asp Cys Phe Met Glu Pro Pro Lys Ser Ala Phe Asp Leu Ile
          165          170          175
Ile Asn Ala Thr Ser Ala Ser Leu His Asn Glu Leu Pro Leu Asn Lys
          180          185          190
Glu Val Leu Lys Gly Tyr Phe Lys Glu Gly Lys Leu Ala Tyr Asp Leu
          195          200          205
Ala Tyr Gly Phe Leu Thr Pro Phe Leu Ser Leu Ala Lys Glu Leu Lys
          210          215          220
Thr Pro Phe Gln Asp Gly Lys Asp Met Leu Ile Tyr Gln Ala Ala Leu
225          230          235          240
Ser Phe Glu Lys Phe Ser Ala Ser Gln Ile Pro Tyr Ser Lys Ala Phe
          245          250          255
Glu Val Met Arg Ser Val Phe
          260

```

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

TTT CAA GTT TGC GAT AAA ATC AAA GGT ATC GCG CTT GAA TGC GGA GCG	354
Phe Gln Val Cys Asp Lys Ile Lys Gly Ile Ala Leu Glu Cys Gly Ala	
75 80 85	
GTC AAT ACG CTT GTT TTA GAA AAT GAT GAG CTT GTG GGT TAC AAT ACC	402
Val Asn Thr Leu Val Leu Glu Asn Asp Glu Leu Val Gly Tyr Asn Thr	
90 95 100	
GAC GCT TTA GGG TTT TAT CTT TCT TTA AAG CAA AAA AAC TAT CAA AAC	450
Asp Ala Leu Gly Phe Tyr Leu Ser Leu Lys Gln Lys Asn Tyr Gln Asn	
105 110 115 120	
GCT TTG ATT TTA GGA GCT GGG GGG AGC GCT AAA GCC CTA GCG TGT GAA	498
Ala Leu Ile Leu Gly Ala Gly Gly Ser Ala Lys Ala Leu Ala Cys Glu	
125 130 135	
TTG AAA AAA CAA GGC TTA CAA GTG AGC GTG TTG AAC CGC TCT TCT AGG	546
Leu Lys Lys Gln Gly Leu Gln Val Ser Val Leu Asn Arg Ser Ser Arg	
140 145 150	
GGA TTG GAT TTT TTC CAA CGC CTG GGC TGT GAT TGT TTT ATG GAG CCT	594
Gly Leu Asp Phe Phe Gln Arg Leu Gly Cys Asp Cys Phe Met Glu Pro	
155 160 165	
CCT AAA AGC GCT TTT GAT TTG ATT ATT AAC GCC ACT TCA GCG AGT TTG	642
Pro Lys Ser Ala Phe Asp Leu Ile Ile Asn Ala Thr Ser Ala Ser Leu	
170 175 180	
CAT AAC GAA TTG CCT TTG AAT AAA GAG GTT TTG AAA GGG TAT TTT AAA	690
His Asn Glu Leu Pro Leu Asn Lys Glu Val Leu Lys Gly Tyr Phe Lys	
185 190 195 200	
GAG GGC AAG CTC GCT TAT GAT TTG GCG TAT GGG TTT TTA ACG CCC TTT	738
Glu Gly Lys Leu Ala Tyr Asp Leu Ala Tyr Gly Phe Leu Thr Pro Phe	
205 210 215	
TTG TCT TTA GCC AAA GAG TTA AAA ACC CCT TTT CAA GAC GGA AAA GAC	786
Leu Ser Leu Ala Lys Glu Leu Lys Thr Pro Phe Gln Asp Gly Lys Asp	
220 225 230	
ATG CTC ATC TAT CAA GCT GCT TTA AGT TTT GAA AAA TTC AGC GCT TCT	834
Met Leu Ile Tyr Gln Ala Ala Leu Ser Phe Glu Lys Phe Ser Ala Ser	
235 240 245	
CAA ATC CCT TAT TCA AAA GCG TTT GAA GTC ATG CGA AGT GTT TTT TGATG	884
Gln Ile Pro Tyr Ser Lys Ala Phe Glu Val Met Arg Ser Val Phe	
250 255 260	
CAAGGGTTTT TAAGAAGCCT GTTTTTTGGG GTTAAAAAGA TCCCTAAACC ATTCGCTCCT	944
CTAGTAGAAA AGGGCGTTTT AAAAGAAGCG CTTGAATTGA AAAAGG	990

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(2) INFORMATION FOR SEQ ID NO:537:

(A) LENGTH: 990 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 91...879
(D) OTHER INFORMATION:

TCCAAAACGA	TTGGGCTGAA	ATTGAATTTT	CTCACGAAAC	AAAGGGCTAT	GTGTTTTTAA		60
AACTTTTAA	AAAGGCTGAA	TGAAAGAATA	ATG AAA TTA AAA TCT TTT GGG GTT				114
			Met Lys Leu Lys Ser Phe Gly Val				
			1		5		
TTT GGA AAT CCC ATT AAG CAT TCC AAA TCG CCC TTA ATC CAT AAC GCT							162
Phe Gly Asn Pro Ile Lys His Ser Lys Ser Pro Leu Ile His Asn Ala							
10			15			20	
TGT TTT TTA ACT TTT CAA AAA GAA TTA AGG TTT TTG GGG CAT TAC CAC							210
Cys Phe Leu Thr Phe Gln Lys Glu Leu Arg Phe Leu Gly His Tyr His							
25			30			35	40
CCC ATA TTA CTC CCT TTA GAA AGC CAC ATC AAA AGC GAG TTT TTG CAT							258
Pro Ile Leu Leu Pro Leu Glu Ser His Ile Lys Ser Glu Phe Leu His							
			45			50	55
TTG GGA TTG AGT GGG GCT AAT GTA ACC TTA CCC TTT AAA GAA AGG GCG							306
Leu Gly Leu Ser Gly Ala Asn Val Thr Leu Pro Phe Lys Glu Arg Ala							
			60			65	70

```

GGT TCA AGC GTT TTG ATA GAA GGG CGT TTG ACT TAT GAG AGT TGG ATG      354
Gly Ser Ser Val Leu Ile Glu Gly Arg Leu Thr Tyr Glu Ser Trp Met
70                               75                               80                               85

GAT CAA ACG GGC AAA AAA AAT TCC CGC CAC ACT ATC ACA GCG GAC TCG      402
Asp Gln Thr Gly Lys Lys Asn Ser Arg His Thr Ile Thr Ala Asp Ser
          90                               95                               100

TTG CAA TTT ATG GAT AAA AAG TCA GAC AAT CCC CAA GCA AAC GCT ATG      450
Leu Gln Phe Met Asp Lys Lys Ser Asp Asn Pro Gln Ala Asn Ala Met
          105                               110                               115

CAA GAT AGT ATA ATG CAT GAG AAT TCC AAC AAC GCT TAT CCC GCT AAT      498
Gln Asp Ser Ile Met His Glu Asn Ser Asn Asn Ala Tyr Pro Ala Asn
          120                               125                               130

CAT AAC GCT CCC AGC CAA GAT CCT TTT AAC CAA GCT TAT GCG CAA AAC      546
His Asn Ala Pro Ser Gln Asp Pro Phe Asn Gln Ala Tyr Ala Gln Asn
          135                               140                               145

GCT TAC GCT AAA GAG AAT TTA CAA GCA CAG CCG TCC AAG TAT CAA AAC      594
Ala Tyr Ala Lys Glu Asn Leu Gln Ala Gln Pro Ser Lys Tyr Gln Asn
          150                               155                               160                               165

AGC GTG CCT GAA ATC AAT ATT GAT GAA GAA GAA ATC CCC TTT TAAGGGTTA      645
Ser Val Pro Glu Ile Asn Ile Asp Glu Glu Glu Ile Pro Phe
          170                               175

AAATTAAGGA GACATTATGG AAAGAAAACG CTATTCAAAA CGCTATTGCA AATACACTGA      705
AGCTAAAATC AGCTT                                     720

```

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

```

Met Phe Asn Lys Val Ile Met Val Gly Arg Leu Thr Arg Asn Val Glu
 1                               5                               10                               15
Leu Lys Tyr Leu Pro Ser Gly Ser Ala Ala Thr Ile Gly Leu Ala
          20                               25                               30
Thr Ser Arg Arg Phe Lys Lys Gln Asp Gly Thr Leu Gly Glu Glu Val
          35                               40                               45
Cys Phe Ile Asp Ala Arg Leu Phe Gly Arg Thr Ala Glu Ile Ala Asn
          50                               55                               60
Gln Tyr Leu Ser Lys Gly Ser Ser Val Leu Ile Glu Gly Arg Leu Thr
          65                               70                               75                               80
Tyr Glu Ser Trp Met Asp Gln Thr Gly Lys Lys Asn Ser Arg His Thr

```

				740					745					750		
Val	Val	Glu	Gln	Gly	Asp	Ile	Lys	Glu	Met	Ile	Asp	Arg	Leu	Lys	Ser	
		755					760					765				
Lys	His	Glu	Arg	Leu	Leu	Ala	Met	Val	Phe	Lys	Lys	Glu	Asn	Glu	Arg	
	770					775					780					
Ile	Thr	Leu	Ala	Cys	Gly	Val	Lys	Asn	Ala	Pro	Ile	Lys	Ala	Asn	Val	
785					790					795					800	
Trp	Ala	Asn	Glu	Val	Ala	Gln	Ile	Leu	Gly	Gly	Lys	Gly	Gly	Gly	Arg	
			805						810					815		
Gly	Asp	Phe	Ala	Ser	Ala	Gly	Gly	Lys	Asp	Ile	Glu	Asn	Leu	Gln	Ala	
		820						825					830			
Ala	Leu	Asn	Leu	Ala	Lys	Asn	Thr	Ala	Leu	Lys	Ala	Leu	Glu	Gly		
		835					840					845				

(2) INFORMATION FOR SEO ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 100...636
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

TCGCACGCCA	AAGAAAAACA	CGAAAAAAC	GAACACACGC	ATTCTCACCA	CACAGAGGAA	60
GCAGAAAGCG	TAGGATCTCA	TAGCGAATAA	GGGCTTATC	ATG TTT AAT AAA	GTG	114
				Met Phe Asn Lys Val		
				1	5	
ATT ATG GTA	GGG CGT TTG	ACC AGG AAT	GTG GAG TTG	AAA TAT TTG	CCT	162
Ile Met Val	Gly Arg Leu	Thr Arg Asn	Val Glu Leu	Lys Tyr Leu	Pro	
	10		15		20	
AGC GGT TCG	GCT GCG GCT	ACA ATA GGT	TTA GCC ACA	AGC AGG CGT	TTT	210
Ser Gly Ser	Ala Ala Ala	Thr Ile Gly	Leu Ala Thr	Ser Arg Arg	Phe	
	25		30		35	
AAA AAA CAA	GAC GGC ACG	CTA GGC GAA	GAG GTG TGC	TTT ATA GAT	GCG	258
Lys Lys Gln	Asp Gly Thr	Leu Gly Glu	Glu Val Cys	Phe Ile Asp	Ala	
	40		45		50	
CGT TTG TTT	GGG CGA ACG	GCT GAA ATC	GCT AAC CAG	TAT TTG AGC	AAG	306
Arg Leu Phe	Gly Arg Thr	Ala Glu Ile	Ala Asn Gln	Tyr Leu Ser	Lys	
	55		60		65	

Arg His Gly Tyr Leu Met Gly Leu Lys Glu Ala Phe Leu Tyr Lys Val
 305 310 315 320
 Val Gly Val Val Cys Glu Gln Phe Ala Asn Thr His Ala Tyr Leu Lys
 325 330 335
 Glu Ser Lys Glu Met Val Val Lys Glu Cys Phe Glu Glu Glu Glu His
 340 345 350
 Phe Leu Glu Thr Leu Glu Ser Gly Met Glu Leu Phe Asn Leu Ser Leu
 355 360 365
 Lys His Leu Asn Glu Asn Lys Ile Phe Asp Gly Lys Ile Ala Phe Lys
 370 375 380
 Leu Tyr Asp Thr Phe Gly Phe Pro Leu Asp Leu Thr Asn Asp Met Leu
 385 390 395 400
 Arg Ser His Gly Ala Cys Ala Asp Met Gln Gly Phe Glu Leu Cys Met
 405 410 415
 Gln Glu Gln Val Lys Arg Ser Lys Ala Ser Trp Lys Gly Lys Gln Asn
 420 425 430
 Asn Ala Asp Phe Ser Ala Ile Leu Asn Ala Tyr Ala Pro Asn Val Phe
 435 440 445
 Val Gly Tyr Glu Thr Thr Glu Cys Ser Ala Lys Val Leu Gly Phe Phe
 450 455 460
 Asp Ser Asp Phe Lys Glu Ile Thr Asp Ala Asn Pro Asn Gln Glu Val
 465 470 475 480
 Trp Val Leu Leu Glu Lys Thr Pro Phe Tyr Ala Glu Gly Gly Gly Ala
 485 490 495
 Ile Gly Asp Arg Gly Ala Leu Phe Lys Asp Asn Gly Glu Val Ala Ile
 500 505 510
 Val Leu Asp Thr Lys Asn Phe Phe Gly Leu Asn Phe Ser Leu Leu Glu
 515 520 525
 Ile Lys Lys Ala Leu Lys Lys Gly Asp Gln Val Ile Ala Gln Val Ser
 530 535 540
 Asp Glu Arg Phe Glu Ile Ala Lys His His Ser Ala Thr His Leu Leu
 545 550 555 560
 Gln Ser Ala Leu Arg Glu Val Leu Gly Ser His Val Ser Gln Ala Gly
 565 570 575
 Ser Leu Val Glu Ser Lys Arg Leu Arg Phe Asp Phe Ser His Ala Lys
 580 585 590
 Ala Leu Asn Asp Glu Glu Leu Glu Lys Val Glu Asp Leu Val Asn Ala
 595 600 605
 Gln Ile Phe Lys His Leu Asn Ser Gln Val Glu His Met Pro Leu Asn
 610 615 620
 Gln Ala Lys Asp Lys Gly Ala Leu Ala Leu Phe Ser Glu Lys Tyr Ala
 625 630 635 640
 Glu Asn Val Arg Val Val Ser Phe Lys Glu Ala Ser Ile Glu Leu Cys
 645 650 655
 Gly Gly Ile His Val Glu Asn Thr Gly Leu Ile Gly Gly Phe Arg Ile
 660 665 670
 Val Lys Glu Ser Gly Val Ser Ser Gly Val Arg Arg Ile Glu Ala Val
 675 680 685
 Cys Gly Lys Ala Phe Tyr Gln Leu Ala Lys Glu Glu Asn Lys Glu Leu
 690 695 700
 Lys Asn Ala Lys Thr Leu Leu Lys Asn Asn Asp Val Ile Ala Gly Ile
 705 710 715 720
 Asn Lys Leu Lys Glu Ser Val Lys Asn Ser Gln Lys Ala Pro Val Ser
 725 730 735
 Met Asp Leu Pro Val Glu Lys Ile His Gly Val Asn Leu Val Val Gly

(2) INFORMATION FOR SEO ID NO:534:

(A) LENGTH: 847 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

Met 1	Asp	Ile	Arg	Asn 5	Glu	Phe	Leu	Gln	Phe 10	Gln	Asn	Lys	Gly 15	His	
Ala	Val	Tyr	Pro	Ser	Met	Pro	Leu	Val	Pro	Asn	Asp	Ala	Thr	Leu	Leu
			20					25					30		
Phe	Thr	Asn	Ala	Gly	Met	Val	Gln	Phe	Lys	Asp	Ile	Phe	Thr	Gly	Ile
		35					40					45			
Val	Pro	Arg	Pro	Ser	Ile	Pro	Arg	Ala	Ala	Ser	Ser	Gln	Leu	Cys	Met
	50					55					60				
Arg	Ala	Gly	Gly	Lys	His	Asn	Asp	Leu	Glu	Asn	Val	Gly	Tyr	Thr	Ala
65					70					75					80
Arg	His	His	Thr	Leu	Phe	Glu	Met	Leu	Gly	Asn	Phe	Ser	Phe	Gly	Asp
				85					90					95	
Tyr	Phe	Lys	Glu	Glu	Ala	Ile	Leu	Phe	Ala	Trp	Glu	Phe	Val	Thr	Lys
			100					105					110		
Asn	Leu	Gly	Phe	Lys	Pro	Lys	Asp	Leu	Tyr	Ile	Ser	Val	His	Glu	Lys
		115					120					125			
Asp	Asp	Glu	Ala	Val	Lys	Leu	Trp	Glu	Lys	Phe	Val	Pro	Val	Asp	Arg
	130					135					140				
Ile	Lys	Lys	Met	Gly	Asp	Lys	Asp	Asn	Phe	Trp	Gln	Met	Gly	Asp	Ser
145					150					155					160
Gly	Pro	Cys	Gly	Pro	Cys	Ser	Glu	Ile	Tyr	Ile	Asp	Gln	Gly	Glu	Lys
				165					170					175	
His	Phe	Lys	Gly	Ser	Glu	Asp	Tyr	Phe	Gly	Gly	Glu	Gly	Asp	Arg	Phe
			180					185					190		
Leu	Glu	Ile	Trp	Asn	Leu	Val	Phe	Met	Gln	Tyr	Glu	Arg	Ser	Asn	Asp
		195					200					205			
Gly	Val	Leu	Ser	Pro	Leu	Pro	Lys	Pro	Ser	Ile	Asp	Thr	Gly	Met	Gly
	210					215					220				
Leu	Glu	Arg	Val	Gln	Ala	Leu	Leu	Glu	His	Lys	Leu	Asn	Asn	Phe	Asp
225					230					235					240
Ser	Ser	Leu	Phe	Ala	Pro	Leu	Met	Glu	Glu	Ile	Ser	Glu	Leu	Thr	Ser
				245					250					255	
Leu	Asp	Tyr	Ala	Ser	Glu	Phe	Gln	Pro	Ser	Phe	Arg	Val	Val	Ala	Asp
			260					265					270		
His	Ala	Arg	Ala	Val	Ala	Phe	Leu	Leu	Ala	Gln	Gly	Val	His	Phe	Asn
		275					280					285			
Lys	Glu	Gly	Arg	Gly	Tyr	Val	Leu	Arg	Arg	Ile	Leu	Arg	Arg	Ala	Leu
	290					295					300				

GCC AAA GAT AAG GGA GCG TTA GCG TTA TTC AGT GAA AAA TAC GCT GAA	2038
Ala Lys Asp Lys Gly Ala Leu Ala Leu Phe Ser Glu Lys Tyr Ala Glu	
630 635 640	
AAT GTG CGG GTG GTG AGC TTT AAA GAA GCG TCC ATT GAA TTG TGT GGG	2086
Asn Val Arg Val Val Ser Phe Lys Glu Ala Ser Ile Glu Leu Cys Gly	
645 650 655	
GGC ATT CAT GTG GAA AAT ACT GGG CTT ATT GGG GGG TTT AGG ATT GTA	2134
Gly Ile His Val Glu Asn Thr Gly Leu Ile Gly Gly Phe Arg Ile Val	
660 665 670	
AAA GAA AGC GGG GTG AGT AGT GGG GTC AGA CGC ATT GAA GCG GTG TGC	2182
Lys Glu Ser Gly Val Ser Ser Gly Val Arg Arg Ile Glu Ala Val Cys	
675 680 685	
GGG AAA GCC TTT TAC CAA CTG GCT AAA GAA GAA AAT AAA GAG CTT AAA	2230
Gly Lys Ala Phe Tyr Gln Leu Ala Lys Glu Glu Asn Lys Glu Leu Lys	
690 695 700 705	
AAC GCT AAG ACT TTA TTG AAA AAT AAC GAT GTG ATC GCC GGT ATC AAT	2278
Asn Ala Lys Thr Leu Leu Lys Asn Asn Asp Val Ile Ala Gly Ile Asn	
710 715 720	
AAG CTT AAA GAG AGC GTG AAA AAC AGC CAA AAA GCC CCC GTT TCT ATG	2326
Lys Leu Lys Glu Ser Val Lys Asn Ser Gln Lys Ala Pro Val Ser Met	
725 730 735	
GAT TTA CCG GTT GAA AAA ATC CAT GGC GTG AAT TTG GTG GTG GGC GTA	2374
Asp Leu Pro Val Glu Lys Ile His Gly Val Asn Leu Val Val Gly Val	
740 745 750	
GTG GAA CAA GGC GAC ATT AAA GAA ATG ATT GAC CGA TTG AAA AGT AAG	2422
Val Glu Gln Gly Asp Ile Lys Glu Met Ile Asp Arg Leu Lys Ser Lys	
755 760 765	
CAT GAA AGA TTG CTC GCT ATG GTG TTT AAA AAA GAA AAT GAG CGA ATC	2470
His Glu Arg Leu Leu Ala Met Val Phe Lys Lys Glu Asn Glu Arg Ile	
770 775 780 785	
ACT CTC GCA TGC GGG GTG AAA AAC GCG CCC ATA AAA GCG AAT GTG TGG	2518
Thr Leu Ala Cys Gly Val Lys Asn Ala Pro Ile Lys Ala Asn Val Trp	
790 795 800	
GCT AAT GAA GTG GCG CAA ATT TTA GGG GGC AAA GGG GGC GGG AGA GGT	2566
Ala Asn Glu Val Ala Gln Ile Leu Gly Gly Lys Gly Gly Arg Gly	
805 810 815	
GAT TTT GCG AGC GCT GGA GGC AAG GAT ATT GAA AAT TTG CAA GCC GCA	2614
Asp Phe Ala Ser Ala Gly Gly Lys Asp Ile Glu Asn Leu Gln Ala Ala	
820 825 830	
CTC AAT TTA GCG AAA AAT ACC GCT CTT AAA GCT TTA GAG GGA TAGCATGGA	2665
Leu Asn Leu Ala Lys Asn Thr Ala Leu Lys Ala Leu Glu Gly	
835 840 845	

AGT CAT GGG GCG TGT GCG GAT ATG CAA GGC TTT GAA TTG TGC ATG CAA	1366
Ser His Gly Ala Cys Ala Asp Met Gln Gly Phe Glu Leu Cys Met Gln	
405 410 415	
GAG CAA GTG AAA CGC TCT AAA GCT TCA TGG AAA GGC AAA CAA AAC AAC	1414
Glu Gln Val Lys Arg Ser Lys Ala Ser Trp Lys Gly Lys Gln Asn Asn	
420 425 430	
GCC GAT TTT AGC GCT ATT TTA AAC GCT TAT GCA CCT AAT GTT TTT GTG	1462
Ala Asp Phe Ser Ala Ile Leu Asn Ala Tyr Ala Pro Asn Val Phe Val	
435 440 445	
GGG TAT GAA ACG ACA GAA TGT TCT GCT AAA GTT TTA GGG TTT TTT GAT	1510
Gly Tyr Glu Thr Thr Glu Cys Ser Ala Lys Val Leu Gly Phe Phe Asp	
450 455 460 465	
AGC GAT TTT AAA GAA ATA ACC GAT GCA AAT CCT AAC CAA GAA GTC TGG	1558
Ser Asp Phe Lys Glu Ile Thr Asp Ala Asn Pro Asn Gln Glu Val Trp	
470 475 480	
GTG TTG TTA GAA AAA ACC CCT TTT TAT GCA GAA GGT GGA GGG GCT ATA	1606
Val Leu Leu Glu Lys Thr Pro Phe Tyr Ala Glu Gly Gly Gly Ala Ile	
485 490 495	
GGC GAT AGG GGC GCG CTT TTT AAA GAC AAT GGA GAA GTG GCT ATC GTG	1654
Gly Asp Arg Gly Ala Leu Phe Lys Asp Asn Gly Glu Val Ala Ile Val	
500 505 510	
TTA GAT ACA AAA AAC TTT TTT GGG CTT AAT TTT TCA CTC CTT GAA ATC	1702
Leu Asp Thr Lys Asn Phe Phe Gly Leu Asn Phe Ser Leu Leu Glu Ile	
515 520 525	
AAA AAA GCG CTA AAA AAA GGC GAT CAA GTG ATC GCG CAA GTG AGC GAT	1750
Lys Lys Ala Leu Lys Lys Gly Asp Gln Val Ile Ala Gln Val Ser Asp	
530 535 540 545	
GAG CGC TTT GAA ATC GCC AAA CAC CAT AGT GCG ACT CAT TTA TTG CAG	1798
Glu Arg Phe Glu Ile Ala Lys His His Ser Ala Thr His Leu Leu Gln	
550 555 560	
AGC GCT TTA AGA GAA GTT TTA GGC TCG CAT GTG AGT CAA GCG GGG AGT	1846
Ser Ala Leu Arg Glu Val Leu Gly Ser His Val Ser Gln Ala Gly Ser	
565 570 575	
TTA GTG GAA TCC AAG CGA TTG CGC TTT GAT TTC TCG CAT GCT AAA GCG	1894
Leu Val Glu Ser Lys Arg Leu Arg Phe Asp Phe Ser His Ala Lys Ala	
580 585 590	
CTC AAT GAT GAA GAG CTA GAA AAA GTA GAA GAT TTA GTC AAC GCT CAA	1942
Leu Asn Asp Glu Glu Leu Glu Lys Val Glu Asp Leu Val Asn Ala Gln	
595 600 605	
ATT TTC AAG CAC CTA AAT AGC CAG GTG GAG CAT ATG CCT TTA AAC CAA	1990
Ile Phe Lys His Leu Asn Ser Gln Val Glu His Met Pro Leu Asn Gln	
610 615 620 625	

TTT AAG GGG AGC GAG GAT TAT TTT GGG GGC GAG GGC GAT AGG TTT TTA	694
Phe Lys Gly Ser Glu Asp Tyr Phe Gly Gly Glu Gly Asp Arg Phe Leu	
180 185 190	
GAA ATT TGG AAT CTG GTG TTC ATG CAA TAC GAA CGC TCT AAT GAT GGC	742
Glu Ile Trp Asn Leu Val Phe Met Gln Tyr Glu Arg Ser Asn Asp Gly	
195 200 205	
GTT TTA TCC CCC TTG CCA AAG CCT AGC ATT GAT ACA GGC ATG GGA TTA	790
Val Leu Ser Pro Leu Pro Lys Pro Ser Ile Asp Thr Gly Met Gly Leu	
210 215 220 225	
GAA AGG GTG CAA GCG CTA TTA GAA CAT AAG CTC AAT AAT TTT GAT TCT	838
Glu Arg Val Gln Ala Leu Leu Glu His Lys Leu Asn Asn Phe Asp Ser	
230 235 240	
TCA TTA TTT GCG CCC CTA ATG GAA GAA ATC AGC GAG CTT ACA AGC CTA	886
Ser Leu Phe Ala Pro Leu Met Glu Glu Ile Ser Glu Leu Thr Ser Leu	
245 250 255	
GAT TAT GCG AGC GAG TTC CAG CCA AGC TTT AGG GTA GTG GCC GAT CAC	934
Asp Tyr Ala Ser Glu Phe Gln Pro Ser Phe Arg Val Val Ala Asp His	
260 265 270	
GCA AGA GCG GTA GCA TTC TTG CTC GCT CAA GGG GTG CAT TTC AAT AAG	982
Ala Arg Ala Val Ala Phe Leu Leu Ala Gln Gly Val His Phe Asn Lys	
275 280 285	
GAA GGC CGT GGC TAT GTT TTA AGG CGC ATT TTA AGG CGA GCC TTA AGG	1030
Glu Gly Arg Gly Tyr Val Leu Arg Arg Ile Leu Arg Arg Ala Leu Arg	
290 295 300 305	
CAT GGG TAT TTA ATG GGC TTG AAA GAA GCG TTT TTA TAC AAA GTC GTG	1078
His Gly Tyr Leu Met Gly Leu Lys Glu Ala Phe Leu Tyr Lys Val Val	
310 315 320	
GGC GTG GTG TGC GAG CAA TTT GCT AAC ACG CAT GCG TAT TTG AAA GAG	1126
Gly Val Val Cys Glu Gln Phe Ala Asn Thr His Ala Tyr Leu Lys Glu	
325 330 335	
TCT AAA GAA ATG GTG GTA AAA GAA TGT TTT GAA GAA GAA GAG CAC TTT	1174
Ser Lys Glu Met Val Val Lys Glu Cys Phe Glu Glu Glu Glu His Phe	
340 345 350	
TTA GAG ACT TTG GAA TCG GGC ATG GAA TTG TTT AAC TTG TCT TTA AAG	1222
Leu Glu Thr Leu Glu Ser Gly Met Glu Leu Phe Asn Leu Ser Leu Lys	
355 360 365	
CAT TTG AAT GAA AAT AAA ATC TTT GAT GGC AAG ATC GCT TTC AAG CTT	1270
His Leu Asn Glu Asn Lys Ile Phe Asp Gly Lys Ile Ala Phe Lys Leu	
370 375 380 385	
TAT GAC ACT TTT GGT TTC CCT TTG GAT TTA ACA AAC GAC ATG TTA AGA	1318
Tyr Asp Thr Phe Gly Phe Pro Leu Asp Leu Thr Asn Asp Met Leu Arg	
390 395 400	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

TTCTCCTTTA ATTTTGGATG TTTAAAGTAT AATAAACTAT CTTTTTAAAA AAATAACTTA	60
AAAGAGCTAT AAAATAGCCT TAAAATACGC GATAAAACAA CAAAAAGGAA TACCC ATG	118
Met	
1	
GAT ATT CGC AAC GAA TTT TTA CAA TTT TTT CAA AAT AAA GGG CAT GCC	166
Asp Ile Arg Asn Glu Phe Leu Gln Phe Phe Gln Asn Lys Gly His Ala	
5 10 15	
GTT TAT CCT AGC ATG CCT TTA GTG CCT AAT GAC GCT ACC TTG CTT TTT	214
Val Tyr Pro Ser Met Pro Leu Val Pro Asn Asp Ala Thr Leu Leu Phe	
20 25 30	
ACC AAT GCC GGC ATG GTG CAA TTT AAA GAT ATT TTT ACC GGG ATT GTG	262
Thr Asn Ala Gly Met Val Gln Phe Lys Asp Ile Phe Thr Gly Ile Val	
35 40 45	
CCA CGC CCT AGC ATT CCT AGA GCG GCA AGC TCG CAA TTG TGC ATG CGC	310
Pro Arg Pro Ser Ile Pro Arg Ala Ala Ser Ser Gln Leu Cys Met Arg	
50 55 60 65	
GCA GGC GGC AAG CAT AAC GAT TTG GAA AAT GTC GGT TAT ACC GCA AGG	358
Ala Gly Gly Lys His Asn Asp Leu Glu Asn Val Gly Tyr Thr Ala Arg	
70 75 80	
CAC CAC ACG CTT TTT GAA ATG CTA GGG AAT TTC TCT TTT GGG GAT TAT	406
His His Thr Leu Phe Glu Met Leu Gly Asn Phe Ser Phe Gly Asp Tyr	
85 90 95	
TTC AAA GAA GAA GCG ATC TTG TTT GCG TGG GAA TTT GTA ACC AAG AAT	454
Phe Lys Glu Glu Ala Ile Leu Phe Ala Trp Glu Phe Val Thr Lys Asn	
100 105 110	
TTA GGG TTT AAG CCT AAA GAT TTA TAC ATC AGC GTG CAT GAA AAG GAC	502
Leu Gly Phe Lys Pro Lys Asp Leu Tyr Ile Ser Val His Glu Lys Asp	
115 120 125	
GAT GAA GCC GTT AAA TTA TGG GAA AAG TTT GTG CCT GTT GAT AGG ATT	550
Asp Glu Ala Val Lys Leu Trp Glu Lys Phe Val Pro Val Asp Arg Ile	
130 135 140 145	
AAA AAA ATG GGC GAT AAA GAT AAT TTT TGG CAA ATG GGC GAT AGC GGG	598
Lys Lys Met Gly Asp Lys Asp Asn Phe Trp Gln Met Gly Asp Ser Gly	
150 155 160	
CCT TGC GGG CCT TGC AGT GAA ATT TAC ATT GAT CAG GGC GAA AAA CAC	646
Pro Cys Gly Pro Cys Ser Glu Ile Tyr Ile Asp Gln Gly Glu Lys His	
165 170 175	

```

Lys Asp Asp Glu Ser Phe Phe Ser Cys Ala Gly Val Leu Ala Arg His
65          70          75          80
Tyr Asn Glu Phe Phe Ser Asn Ser Arg Ala Asp Phe Ser Leu Ser Ala
          85          90          95
Tyr Leu Lys Glu Arg Gly Val Leu Gly Val Cys Gly Val Asp Thr Arg
          100         105         110
Ser Leu Ile Lys Thr Leu Arg His His Gly Cys Leu Met Met Val Ala
          115         120         125
Ser Thr Ile Glu His Asp Lys Asn Lys Leu Glu Glu Ile Leu Lys Asn
          130         135         140
Ala Pro Lys Ile Ser His Ser Pro Leu Val Ser Ser Val Ser Thr Pro
          145         150         155         160
Lys Ile Thr Thr His Gln Arg Ala Thr Phe Asp Phe Lys Thr Leu Asp
          165         170         175
Tyr Lys Pro Phe Asp Glu Lys Thr Ser His Lys Ile Ile Ala Val Leu
          180         185         190
Asp Phe Gly Ala Lys Gly Asn Ile Leu Asn Glu Leu Gln Asn Val Gly
          195         200         205
Leu Lys Ala Leu Ile Tyr Pro His His Thr Lys Ala Ser Glu Leu Ile
          210         215         220
Lys Ala Tyr Glu Lys Lys Glu Ile Ser Gly Ile Phe Leu Ser Asn Gly
          225         230         235         240
Pro Gly Asp Pro Leu Ser Leu Gln Gln Glu Ile Gly Glu Ile Lys Gln
          245         250         255
Leu Ile Asn Ala Lys Ile Pro Met Leu Gly Ile Cys Leu Gly His Gln
          260         265         270
Leu Leu Ser Ile Ala Gln Gly Tyr Pro Thr Tyr Lys Leu Lys Phe Gly
          275         280         285
His His Gly Ser Asn His Pro Val Lys Asn Leu Lys Thr Asn Ala Val
          290         295         300
Glu Ile Thr Ala Gln Asn His Asn Tyr Cys Val Pro Glu Asp Ile Glu
          305         310         315         320
Glu Ile Ala Ile Ile Thr His Arg Asn Leu Phe Asp Asn Thr Ile Glu
          325         330         335
Gly Val Arg Tyr Lys Asn Ala Pro Ile Ile Ser Val Gln His His Pro
          340         345         350
Glu Ser Ser Pro Gly Pro Lys Glu Ser His Tyr Ile Phe Lys Glu Phe
          355         360         365
Val Glu Leu Leu Lys Asp Phe
          370         375

```

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 116...2656
- (D) OTHER INFORMATION:

```

ATT AAC GCT AAA ATC CCC ATG CTT GGC ATT TGC TTA GGG CAT CAA TTG      873
Ile Asn Ala Lys Ile Pro Met Leu Gly Ile Cys Leu Gly His Gln Leu
      260                      265                      270

CTC TCT ATC GCT CAA GGC TAC CCT ACT TAC AAG CTC AAA TTT GGT CAT      921
Leu Ser Ile Ala Gln Gly Tyr Pro Thr Tyr Lys Leu Lys Phe Gly His
      275                      280                      285

CAT GGG AGC AAC CAC CCC GTT AAA AAC CTA AAA ACA AAC GCC GTA GAA      969
His Gly Ser Asn His Pro Val Lys Asn Leu Lys Thr Asn Ala Val Glu
      290                      295                      300                      305

ATC ACC GCG CAA AAC CAC AAC TAT TGC GTC CCT GAA GAC ATT GAA GAA      1017
Ile Thr Ala Gln Asn His Asn Tyr Cys Val Pro Glu Asp Ile Glu Glu
      310                      315                      320

ATC GCC ATT ATC ACG CAC CGC AAT CTT TTT GAC AAC ACC ATT GAG GGC      1065
Ile Ala Ile Ile Thr His Arg Asn Leu Phe Asp Asn Thr Ile Glu Gly
      325                      330                      335

GTG CGT TAT AAA AAC GCT CCC ATT ATC TCT GTC CAG CAC CAC CCA GAA      1113
Val Arg Tyr Lys Asn Ala Pro Ile Ile Ser Val Gln His His Pro Glu
      340                      345                      350

AGT AGC CCA GGT CCT AAA GAG AGC CAC TAT ATT TTT AAA GAA TTT GTG      1161
Ser Ser Pro Gly Pro Lys Glu Ser His Tyr Ile Phe Lys Glu Phe Val
      355                      360                      365

GAA TTG TTA AAG GAT TTT TAGGGGTTTTT TAAAACAGCG CTTATAGAGA CTGAAAAG 1217
Glu Leu Leu Lys Asp Phe
      370                      375

CGCTTTTAAAA ATAGATTTAA ATCTTTTTTAT CAAAAAATCT CGC      1260

```

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

```

Met Val Ser Leu Tyr Leu Glu Asn Gly Leu Phe Leu Gln Ala Gln Ser
 1           5           10           15
Phe Gly Ala Ser Gly Thr Gln Ala Gly Glu Leu Val Phe Asn Thr Ser
      20           25           30
Met Ser Gly Tyr Gln Glu Val Ile Ser Asp Pro Ser Tyr Lys Gly Gln
      35           40           45
Phe Val Val Phe Ser Met Pro Glu Ile Gly Val Val Gly Ala Asn Ser
      50           55           60

```

AGC GGT TAT CAA GAA GTC ATT AGC GAC CCT AGC TAT AAG GGG CAA TTT	201
Ser Gly Tyr Gln Glu Val Ile Ser Asp Pro Ser Tyr Lys Gly Gln Phe	
35 40 45	
GTG GTT TTT AGC ATG CCT GAG ATT GGG GTT GTG GGT GCT AAT TCT AAA	249
Val Val Phe Ser Met Pro Glu Ile Gly Val Val Gly Ala Asn Ser Lys	
50 55 60 65	
GAT GAT GAA TCC TTT TTT TCA TGC GCA GGG GTT TTA GCG CGC CAT TAC	297
Asp Asp Glu Ser Phe Phe Ser Cys Ala Gly Val Leu Ala Arg His Tyr	
70 75 80	
AAC GAA TTT TTT TCT AAC TCA AGG GCG GAT TTT AGC TTG AGC GCT TAT	345
Asn Glu Phe Phe Ser Asn Ser Arg Ala Asp Phe Ser Leu Ser Ala Tyr	
85 90 95	
TTG AAA GAG CGT GGC GTT TTA GGG GTT TGT GGC GTT GAT ACT AGG AGT	393
Leu Lys Glu Arg Gly Val Leu Gly Val Cys Gly Val Asp Thr Arg Ser	
100 105 110	
TTG ATT AAA ACC TTA CGC CAT CAT GGG TGC TTA ATG ATG GTC GCT TCC	441
Leu Ile Lys Thr Leu Arg His His Gly Cys Leu Met Met Val Ala Ser	
115 120 125	
ACG ATA GAG CAT GAC AAA AAC AAG CTT GAA GAA ATT TTA AAA AAC GCT	489
Thr Ile Glu His Asp Lys Asn Lys Leu Glu Glu Ile Leu Lys Asn Ala	
130 135 140 145	
CCT AAA ATT TCT CAC TCC CCC CTA GTG TCT AGC GTT TCT ACG CCA AAA	537
Pro Lys Ile Ser His Ser Pro Leu Val Ser Ser Val Ser Thr Pro Lys	
150 155 160	
ATA ACC ACG CAC CAG CGT GCG ACT TTT GAT TTC AAA ACC CTA GAT TAC	585
Ile Thr Thr His Gln Arg Ala Thr Phe Asp Phe Lys Thr Leu Asp Tyr	
165 170 175	
AAG CCT TTT GAT GAA AAA ACC TCT CAT AAA ATT ATC GCG GTG TTA GAC	633
Lys Pro Phe Asp Glu Lys Thr Ser His Lys Ile Ile Ala Val Leu Asp	
180 185 190	
TTT GGG GCT AAG GGC AAT ATT TTA AAC GAG CTT CAA AAT GTG GGG TTA	681
Phe Gly Ala Lys Gly Asn Ile Leu Asn Glu Leu Gln Asn Val Gly Leu	
195 200 205	
AAA GCC CTT ATT TAC CCG CAC CAC ACT AAA GCT AGC GAG CTG ATT AAA	729
Lys Ala Leu Ile Tyr Pro His His Thr Lys Ala Ser Glu Leu Ile Lys	
210 215 220 225	
GCC TAT GAA AAA AAA GAA ATT AGC GGG ATT TTC CTC TCT AAC GGG CCG	777
Ala Tyr Glu Lys Lys Glu Ile Ser Gly Ile Phe Leu Ser Asn Gly Pro	
230 235 240	
GGC GAT CCT TTA AGC TTG CAG CAA GAA ATT GGC GAA ATC AAA CAA CTC	825
Gly Asp Pro Leu Ser Leu Gln Gln Glu Ile Gly Glu Ile Lys Gln Leu	
245 250 255	

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Gln	Cys	Gly	Glu	Arg	Asp	Phe	Arg	Gly	Leu	Phe	Phe	Gln	Ala	Ile	Arg
1				5					10					15	
Val	Ser	Asn	Tyr	Ala	Arg	Asn	Tyr	Gln	Val	Lys	His	Asn	Leu	Ala	Tyr
			20					25					30		
Trp	Gly	Ala	Lys	Asp	Tyr	Leu	Gly	Cys	Gly	Ala	Gly	Ala	Val	Gly	Cys
		35					40					45			
Val	Ala	Asn	Glu	Arg	Phe	Phe	Ala	Lys	Lys	Leu	Ile	Glu	Asn	Tyr	Ile
	50					55					60				
Lys	Asp	Pro	Leu	Gln	Arg	Gln	Val	Glu	Thr	Leu	Asn	Lys	Gln	Asp	Lys
65					70					75				80	
Arg	Leu	Glu	Lys	Leu	Phe	Leu	Gly	Leu	Arg	Cys	Val	Leu	Gly	Val	Glu
				85				90						95	
Leu	Ser	Phe	Leu	Asp	Glu	Asn	Lys	Val	Lys	Phe	Leu	Ile	Glu	Glu	Asn
			100				105						110		
Lys	Ala	Phe	Ile	Lys	Asn	Asn	Arg	Leu	Ile	Ala	Ser	Asp	Phe	Phe	Met
		115					120					125			
Ala	Asp	Glu	Met	Ala	Leu	Trp	Leu	Leu							
	130						135								

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...1179
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GTTGGTGT	TTT	GAAAGGCTCT	ATGAAGAAGA	ATTAAGGCGC	AAGGGTTTTT	TATA	ATG	57								
							Met									
							1									
GTC	TCT	CTC	TAT	TTA	GAA	AAC	GGG	CTT	TTT	TTG	CAA	GCG	CAA	AGT	TTT	105
Val	Ser	Leu	Tyr	Leu	Glu	Asn	Gly	Leu	Phe	Leu	Gln	Ala	Gln	Ser	Phe	
			5				10					15				
GGG	GCT	AGC	GGC	ACG	CAA	GCG	GGC	GAG	CTT	GTT	TTT	AAC	ACT	TCT	ATG	153
Gly	Ala	Ser	Gly	Thr	Gln	Ala	Gly	Glu	Leu	Val	Phe	Asn	Thr	Ser	Met	
		20					25					30				

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...411
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

CAA TGT GGT GAG AGA GAT TTT AGA GGG CTT TTC TTT CAA GCA ATA CGA	48
Gln Cys Gly Glu Arg Asp Phe Arg Gly Leu Phe Phe Gln Ala Ile Arg	
1 5 10 15	
GTG TCT AAT TAC GCT AGA AAT TAT CAA GTC AAA CAC AAC TTG GCT TAC	96
Val Ser Asn Tyr Ala Arg Asn Tyr Gln Val Lys His Asn Leu Ala Tyr	
20 25 30	
TGG GGG GCT AAA GAT TAT TTA GGG TGC GGG GCT GGG GCT GTG GGC TGC	144
Trp Gly Ala Lys Asp Tyr Leu Gly Cys Gly Ala Gly Ala Val Gly Cys	
35 40 45	
GTG GCG AAT GAG CGC TTT TTT GCA AAA AAA CTC ATA GAA AAC TAC ATC	192
Val Ala Asn Glu Arg Phe Phe Ala Lys Lys Leu Ile Glu Asn Tyr Ile	
50 55 60	
AAA GAC CCC CTA CAA CGC CAA GTT GAG ACG CTT AAT AAA CAA GAC AAA	240
Lys Asp Pro Leu Gln Arg Gln Val Glu Thr Leu Asn Lys Gln Asp Lys	
65 70 75 80	
CGC TTA GAA AAG CTG TTT TTA GGC TTG AGG TGC GTG CTT GGG GTT GAG	288
Arg Leu Glu Lys Leu Phe Leu Gly Leu Arg Cys Val Leu Gly Val Glu	
85 90 95	
CTT AGT TTC TTA GAT GAA AAT AAA GTA AAG TTT TTG ATT GAA GAG AAC	336
Leu Ser Phe Leu Asp Glu Asn Lys Val Lys Phe Leu Ile Glu Glu Asn	
100 105 110	
AAG GCT TTC ATT AAA AAT AAC CGC TTG ATA GCG AGC GAT TTT TTC ATG	384
Lys Ala Phe Ile Lys Asn Asn Arg Leu Ile Ala Ser Asp Phe Phe Met	
115 120 125	
GCC GAT GAA ATG GCT TTG TGG CTG TTA TGATTGTAGG CTTTGCTTCA ATCAAGC	438
Ala Asp Glu Met Ala Leu Trp Leu Leu	
130 135	
GTTAATAAAA CGCTAGAAAG CGTTTTTTTAA TGAATGCCTA CAAAATTTTT AGCCAAAAAC	498
CAACCAA	505

(2) INFORMATION FOR SEQ ID NO:530:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

TCATTCAAAA TATCGTATTT CATCACAAGC TTAGTGCCTT CATTGTCATA AGCGGCT 740

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:528:

Met	Phe	Leu	Gly	Asn	Pro	His	Ser	Ser	Ile	Leu	Arg	Leu	Gly	Pro	Thr
1				5					10					15	
Thr	Ile	Thr	Leu	Leu	Pro	Glu	Lys	Ser	Thr	Arg	Leu	Pro	Lys	Arg	Phe
			20					25					30		
Cys	Leu	Lys	Arg	Pro	Cys	Leu	Pro	Leu	Met	Ile	Ser	Leu	Ser	Asp	Phe
		35					40					45			
Lys	Gly	Arg	Leu	Leu	Ala	Pro	Leu	Thr	Ala	Leu	Val	Leu	Arg	Pro	Leu
	50				55					60					
Ser	Lys	Ser	Thr	Ser	Thr	Ala	Ser	Cys	Asn	Ile	Leu	Phe	Ser	Leu	Arg
65					70				75						80
Thr	Met	Ile	Ser	Gly	Ala	Pro	Ser	Ser	Ile	Lys	Arg	Phe	Lys	Arg	Trp
			85					90					95		
Leu	Arg	Leu	Met	Thr	Arg	Arg	Tyr	Asn	Ser	Phe	Thr	Ser	Leu	Thr	Ala
			100					105					110		
Asn	Phe	Pro	Pro	Ser	Ser	Ala	Thr	Lys	Gly	Leu	Lys	Ser	Gly	Gly	Asn
		115				120						125			
Thr	Gly	Lys	Thr	Val	Ser	Ile	Ile	His	Ser	Gly	Leu	Leu	Pro	Glu	Phe
	130					135					140				
Lys	Lys	Leu	Ser	Thr	Thr	Phe	Lys	Arg	Leu	Met	Ser	Phe	Phe	Phe	Phe
145					150					155					160
Ala	Ser	Glu	Leu	Val	Ser	Phe	Thr	Ser	Ser	Phe	Lys	Leu	Cys	Asn	Lys
			165					170					175		
Val	Ile	Lys	Ser	Ile	Ser	Ser	Asn	Lys	Ser	Leu	Ile	Ala	Ser	Pro	Pro
			180					185					190		
Ile	Cys	Ala	Thr	Lys	Pro	Leu	Ser	Ser	Tyr	Leu	Arg	Glu	Ile	Phe	
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

CTCTCTCTTC	AAGCTTGGAT	AACAAATGCG	TTTTGAAGAG	TTCTAACGCC	ATG	TTT	56
					Met	Phe	
					1		
TTA GGC AAC CCG CAT TCA TCC ATT TTG AGA TTA GGC CCA ACC ACA ATC	104						
Leu Gly Asn Pro His Ser Ser Ile Leu Arg Leu Gly Pro Thr Thr Ile							
5 10 15							
ACG CTT CTG CCT GAA AAA TCC ACG CGC TTA CCT AAA AGG TTT TGC CTG	152						
Thr Leu Leu Pro Glu Lys Ser Thr Arg Leu Pro Lys Arg Phe Cys Leu							
20 25 30							
AAA CGC CCC TGC TTG CCT TTA ATG ATT TCA CTG AGC GAT TTT AAA GGG	200						
Lys Arg Pro Cys Leu Pro Leu Met Ile Ser Leu Ser Asp Phe Lys Gly							
35 40 45 50							
CGT TTG TTA GCC CCT TTA ACC GCA TTA GTG CTG CGG CCG TTA TCA AAA	248						
Arg Leu Leu Ala Pro Leu Thr Ala Leu Val Leu Arg Pro Leu Ser Lys							
55 60 65							
AGC ACA TCC ACG GCT TCT TGC AAC ATC CTT TTT TCA TTG CGC ACA ATG	296						
Ser Thr Ser Thr Ala Ser Cys Asn Ile Leu Phe Ser Leu Arg Thr Met							
70 75 80							
ATT TCT GGC GCT CCA AGC TCC ATT AAG CGT TTC AAG CGT TGG TTA CGA	344						
Ile Ser Gly Ala Pro Ser Ser Ile Lys Arg Phe Lys Arg Trp Leu Arg							
85 90 95							
TTG ATG ACA CGA CGA TAC AAT TCA TTC ACA TCG CTG ACT GCA AAC TTC	392						
Leu Met Thr Arg Arg Tyr Asn Ser Phe Thr Ser Leu Thr Ala Asn Phe							
100 105 110							
CCG CCA TCT AGC GCG ACT AAA GGC CTT AAA TCC GGT GGC AAT ACC GGT	440						
Pro Pro Ser Ser Ala Thr Lys Gly Leu Lys Ser Gly Gly Asn Thr Gly							
115 120 125 130							
AAA ACC GTG AGC ATC ATC CAT TCA GGC CTA TTA CCA GAA TTT AAA AAG	488						
Lys Thr Val Ser Ile Ile His Ser Gly Leu Leu Pro Glu Phe Lys Lys							
135 140 145							
CTT TCT ACC ACT TTC AAA CGC TTA ATG AGT TTT TTC TTT TTC GCA TCA	536						
Leu Ser Thr Thr Phe Lys Arg Leu Met Ser Phe Phe Phe Phe Ala Ser							
150 155 160							
GAA TTG GTG TCT TTC ACT TCT TCT TTC AAA CTC TGC AAT AAG GTG ATC	584						
Glu Leu Val Ser Phe Thr Ser Ser Phe Lys Leu Cys Asn Lys Val Ile							
165 170 175							
AAA TCA ATT TCT TCT AAC AAA TCC TTG ATC GCT TCA CCG CCC ATT TGC	632						
Lys Ser Ile Ser Ser Asn Lys Ser Leu Ile Ala Ser Pro Pro Ile Cys							
180 185 190							
GCT ACA AAG CCC CTG TCT TCG TAT CTT CGT GAG ATA TTT TGATACTGCT CT	683						

CCT AGC AAT ATC GCT AAG GAA ATT GTA GAA AAG CGC AAA GGC TGATTTAAT 491
 Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly
 135 140

TATAACGCTC TCTTATTTTT AGGGGGTGTT ATAGGTGCTG TTTA 535

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

Met	Gln	Asn	Gly	Val	Leu	Ala	Gly	Tyr	Pro	Val	Val	Asp	Phe	Lys	Val
1				5					10					15	
Thr	Leu	Tyr	Asp	Gly	Ser	Tyr	His	Asp	Val	Asp	Ser	Ser	Glu	Met	Ala
			20					25					30		
Phe	Lys	Ile	Ala	Gly	Ser	Met	Ala	Phe	Lys	Glu	Ala	Ser	Arg	Ala	Ala
		35					40					45			
Asn	Pro	Val	Leu	Leu	Glu	Pro	Met	Met	Lys	Val	Glu	Val	Glu	Val	Pro
	50					55				60					
Glu	Glu	Tyr	Met	Gly	Asp	Val	Ile	Gly	Asp	Leu	Asn	Arg	Arg	Arg	Gly
65				70					75					80	
Gln	Ile	Asn	Ser	Met	Asp	Asp	Arg	Leu	Gly	Leu	Lys	Ile	Val	Asn	Ala
				85				90					95		
Phe	Val	Pro	Leu	Val	Glu	Met	Phe	Gly	Tyr	Ser	Thr	Asp	Leu	Arg	Ser
			100					105					110		
Ala	Thr	Gln	Gly	Arg	Gly	Thr	Tyr	Ser	Met	Glu	Phe	Asp	His	Tyr	Gly
		115				120						125			
Glu	Val	Pro	Ser	Asn	Ile	Ala	Lys	Glu	Ile	Val	Glu	Lys	Arg	Lys	Gly
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...671
- (D) OTHER INFORMATION:

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...482
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GTGATCCCTA AAGAATATAT CCTGCGGTGG ATAAGGGTAT CCAAGAAGCG	ATG CAA	56
	Met Gln	
	1	
AAT GGC GTT TTG GCA GGC TAT CCG GTG GTG GAT TTT AAA GTT ACC CTT		104
Asn Gly Val Leu Ala Gly Tyr Pro Val Val Asp Phe Lys Val Thr Leu		
5 10 15		
TAT GAT GGG AGC TAC CAT GAT GTG GAT TCT TCA GAA ATG GCG TTT AAA		152
Tyr Asp Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala Phe Lys		
20 25 30		
ATC GCT GGC TCT ATG GCG TTT AAA GAA GCG AGT CGC GCG GCT AAC CCG		200
Ile Ala Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro		
35 40 45 50		
GTT TTA CTA GAG CCT ATG ATG AAA GTG GAA GTG GAA GTC CCT GAA GAA		248
Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu		
55 60 65		
TAC ATG GGC GAT GTG ATT GGC GAT TTG AAT AGA AGA AGA GGG CAA ATC		296
Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile		
70 75 80		
AAT TCT ATG GAC GAT AGA TTA GGC TTG AAA ATC GTG AAC GCT TTT GTG		344
Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val		
85 90 95		
CCG TTG GTG GAA ATG TTT GGC TAT TCT ACG GAT TTA CGA TCA GCC ACC		392
Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr		
100 105 110		
CAA GGG CGT GGG ACT TAC TCT ATG GAG TTT GAT CAT TAT GGC GAA GTG		440
Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val		
115 120 125 130		

CTC TCA AAG CCT TTT GTT CGT TCA AAA AAT ATT TGC TGATGTTAAT AAAGAA 937
 Leu Ser Lys Pro Phe Val Arg Ser Lys Asn Ile Cys
 260 265

ATAGAAGCAG TTGCTAATAC TGAAAAGAAA GCAGAAAAAG MGGGTTATGG TTATAGTAAA 997
 AGGATGTAGG CATAAGAAAA TAAGAAC 1024

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met Lys Arg Val Arg Glu Leu Val Lys Lys His Pro Glu Lys Ser Ser
 1 5 10 15
 Val Ala Leu Val Val Leu Thr His Ala Ala Cys Lys Lys Ala Lys Glu
 20 25 30
 Leu Asp Asp Lys Val Gln Asp Lys Ser Lys Gln Ala Glu Lys Glu Asn
 35 40 45
 Gln Ile Asn Trp Trp Lys Tyr Ser Gly Leu Thr Ile Ala Thr Ser Leu
 50 55 60
 Leu Leu Ala Ala Cys Ser Val Gly Asp Ile Asp Lys Gln Ile Glu Leu
 65 70 75 80
 Glu Gln Glu Lys Lys Glu Ala Glu Asn Ala Arg Asp Arg Ala Asn Lys
 85 90 95
 Ser Gly Ile Glu Leu Glu Gln Glu Lys Gln Lys Thr Ile Lys Glu Gln
 100 105 110
 Lys Asp Leu Val Lys Lys Ala Glu Gln Asn Cys Gln Glu Asn His Gly
 115 120 125
 Gln Phe Phe Met Lys Lys Leu Gly Ile Lys Gly Gly Ile Ala Ile Glu
 130 135 140
 Val Glu Ala Glu Cys Lys Thr Pro Lys Pro Ala Lys Thr Asn Gln Thr
 145 150 155 160
 Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro His Ser Gln
 165 170 175
 Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln Lys Glu Leu
 180 185 190
 Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln Val Asn Phe
 195 200 205
 Tyr Arg Pro Ser Ser Val Ala Tyr Leu Glu Leu Asp Pro Arg Asp Phe
 210 215 220
 Lys Val Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile Arg Ser Lys
 225 230 235 240
 Ala Gln Ala Lys Met Leu Gly Asn Glu Lys Pro Thr Ser Pro Pro Phe
 245 250 255
 Asn Leu Ser Lys Pro Phe Val Arg Ser Lys Asn Ile Cys
 260 265

GAC	GAT	AAA	GTC	CAG	GAT	AAA	TCC	AAA	CAA	GCT	GAA	AAA	GAA	AAT	CAA	261
Asp	Asp	Lys	Val	Gln	Asp	Lys	Ser	Lys	Gln	Ala	Glu	Lys	Glu	Asn	Gln	
35						40					45					
ATC	AAT	TGG	TGG	AAA	TAT	TCA	GGA	TTA	ACA	ATA	GCG	ACA	AGT	TTA	TTA	309
Ile	Asn	Trp	Trp	Lys	Tyr	Ser	Gly	Leu	Thr	Ile	Ala	Thr	Ser	Leu	Leu	
50					55					60					65	
TTA	GCC	GCT	TGT	AGT	GTT	GGT	GAT	ATT	GAT	AAA	CAG	ATA	GAG	TTA	GAA	357
Leu	Ala	Ala	Cys	Ser	Val	Gly	Asp	Ile	Asp	Lys	Gln	Ile	Glu	Leu	Glu	
				70					75					80		
CAA	GAA	AAA	AAG	GAA	GCT	GAA	AAC	GCT	AGG	GAT	AGA	GCG	AAC	AAG	AGT	405
Gln	Glu	Lys	Lys	Glu	Ala	Glu	Asn	Ala	Arg	Asp	Arg	Ala	Asn	Lys	Ser	
			85					90					95			
GGG	ATA	GAA	CTG	GAA	CAG	GAA	AAA	CAA	AAG	ACC	ATT	AAA	GAA	CAA	AAA	453
Gly	Ile	Glu	Leu	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Ile	Lys	Glu	Gln	Lys	
	100						105					110				
GAT	TTA	GTT	AAA	AAA	GCA	GAA	CAA	AAT	TGC	CAA	GAA	AAT	CAT	GGC	CAA	501
Asp	Leu	Val	Lys	Lys	Ala	Glu	Gln	Asn	Cys	Gln	Glu	Asn	His	Gly	Gln	
	115					120					125					
TTC	TTT	ATG	AAA	AAA	TTA	GGA	ATT	AAG	GGT	GGC	ATT	GCT	ATA	GAA	GTA	549
Phe	Phe	Met	Lys	Lys	Leu	Gly	Ile	Lys	Gly	Gly	Ile	Ala	Ile	Glu	Val	
130					135					140					145	
GAA	GCT	GAA	TGC	AAA	ACC	CCT	AAA	CCT	GCA	AAA	ACC	AAT	CAA	ACC	CCT	597
Glu	Ala	Glu	Cys	Lys	Thr	Pro	Lys	Pro	Ala	Lys	Thr	Asn	Gln	Thr	Pro	
				150					155					160		
ATC	CAG	CCA	AAA	CAC	CTC	CCC	AAC	TCT	AAA	CAA	CCC	CAC	TCT	CAA	AGA	645
Ile	Gln	Pro	Lys	His	Leu	Pro	Asn	Ser	Lys	Gln	Pro	His	Ser	Gln	Arg	
			165					170					175			
GGA	TCA	AAA	GCG	CAA	GAG	CTT	ATC	GCT	TAT	TTG	CAA	AAA	GAG	TTA	GAA	693
Gly	Ser	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Tyr	Leu	Gln	Lys	Glu	Leu	Glu	
	180						185					190				
TCT	CTG	CCC	TAT	TCA	CAA	AAA	GCT	ATC	GCT	AAA	CAA	GTG	AAT	TTT	TAC	741
Ser	Leu	Pro	Tyr	Ser	Gln	Lys	Ala	Ile	Ala	Lys	Gln	Val	Asn	Phe	Tyr	
	195					200					205					
AGG	CCA	AGT	TCT	GTC	GCT	TAT	TTA	GAA	CTA	GAC	CCT	AGA	GAT	TTT	AAG	789
Arg	Pro	Ser	Ser	Val	Ala	Tyr	Leu	Glu	Leu	Asp	Pro	Arg	Asp	Phe	Lys	
210					215					220					225	
GTT	ACA	GAA	GAA	TGG	CAA	AAA	GAA	AAT	CTA	AAA	ATA	CGC	TCT	AAA	GCT	837
Val	Thr	Glu	Glu	Trp	Gln	Lys	Glu	Asn	Leu	Lys	Ile	Arg	Ser	Lys	Ala	
				230					235					240		
CAA	GCT	AAA	ATG	CTT	GGA	AAT	GAG	AAA	CCC	ACA	AGC	CCA	CCT	TTC	AAC	885
Gln	Ala	Lys	Met	Leu	Gly	Asn	Glu	Lys	Pro	Thr	Ser	Pro	Pro	Phe	Asn	
			245					250					255			

210	215	220
Ser Leu Val Ala Ile Val Val Trp Leu Lys Ile Glu Met Val Leu Gly		
225	230	235
Ala Phe Leu Ala Gly Leu Val Val Ser Thr Phe Phe Pro His Lys Ser		240
	245	250
Glu Leu Ile His Lys Leu Asn Asp Val Gly Phe Gly Phe Phe Val Pro		255
	260	265
Leu Phe Phe Ile His Val Gly Ser Thr Leu Asp Leu Lys Leu Val Phe		270
	275	280
Leu Asn Pro His Leu Ile Leu Gln Gly Ile Leu Ile Val Ile Ala Met		285
	290	295
Leu Ser Leu His Leu Ile Thr Ser Thr Leu Leu Trp Arg Lys Tyr Phe		300
305	310	315
Lys Glu Ala Lys His Leu Phe Ser Phe Ala Leu Gly Ala Ser Met Pro		320
	325	330
Leu Thr Phe Leu Val Thr Thr Ala Ala Val Gly Leu Lys Ala Gln Ala		335
	340	345
Ile Ser Gln Asn Thr Tyr Tyr Ala Leu Leu Met Ala Ala Ile Phe Glu		350
	355	360
Gly Val Leu Phe Thr Ile Ala Ile Lys Ile Leu Asn Lys Lys Ala		365
370	375	380

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1024 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 115...921
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

AGTTGGCAAA AACGCAGAGA CAGTAACGCA AAGGCAAATA AAGAGACTCA TTTTAAACAA	60
GCGAATGCCA TTACAAATAT AATCAGATCA GTTGGTGGGT TTTTACAAA GATT ATG	117
	Met
	1
AAG AGA GTT AGA GAA CTT GTA AAA AAA CAT CCC GAG AAA AGC AGT GTG	165
Lys Arg Val Arg Glu Leu Val Lys Lys His Pro Glu Lys Ser Ser Val	
5 10 15	
GCA TTA GTA GTA TTA ACC CAT GCT GCA TGC AAG AAA GCG AAA GAA TTG	213
Ala Leu Val Val Leu Thr His Ala Ala Cys Lys Lys Ala Lys Glu Leu	
20 25 30	

```

GCA GTA GGC TTA AAA GCG CAA GCG ATC TCA CAA AAC ACC TAC TAC GCA      1168
Ala Val Gly Leu Lys Ala Gln Ala Ile Ser Gln Asn Thr Tyr Tyr Ala
345                      350                      355                      360

TTG CTC ATG GCG GCT ATT TTT GAA GGG GTA TTA TTC ACG ATT GCG ATC      1216
Leu Leu Met Ala Ala Ile Phe Glu Gly Val Leu Phe Thr Ile Ala Ile
                      365                      370                      375

AAA ATA CTC AAC AAA AAA GCT TGAATGAAAG CTTAAGCGTC TAAATATTTA GCGT      1271
Lys Ile Leu Asn Lys Lys Ala
                      380

CGCTAAAGCT GTTCGCTTGA ACATTATTGA ACGCATTCTC TAAGCTATCA AAGAAACGAG      1331
GGTGCAAGTT TTGCATTCTT TTTAAGAAA
                      1360

```

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```

Met His Ala Glu Phe Phe Thr Phe Ala Leu Ile Met Leu Leu Ile Val
 1                      5                      10                      15
Met Ala Pro Tyr Met Ser Arg Ile Ser Arg Leu Pro Ile Thr Val Val
                20                      25                      30
Glu Ile Leu Phe Gly Ser Val Gly Ala Tyr Val Gly Phe Ile Glu Pro
 35                      40                      45
Thr Lys Gly Phe Glu Ile Met Ser Glu Ile Gly Phe Leu Phe Leu Met
 50                      55                      60
Phe Leu Cys Gly Leu Glu Val Glu Ile Tyr Leu Phe Lys Lys Leu Gly
 65                      70                      75                      80
Val Ser Leu Leu Lys Arg Ile Phe Ala Tyr Leu Leu Ile Leu Tyr Thr
                85                      90                      95
Leu Ser Phe Ile Leu Thr Phe Ser Leu Asn Leu Glu Pro Ile Phe Met
                100                      105                      110
Val Ile Phe Pro Ile Ile Ser Leu Gly Met Ile Met Thr Leu Val Lys
                115                      120                      125
Asp Tyr Arg Lys Glu Ile Leu Trp Leu Asp Leu Val Leu Lys Val Gly
 130                      135                      140
Val Ile Gly Glu Leu Leu Ser Ile Phe Gly Leu Val Val Val Asp Gly
 145                      150                      155                      160
Val Tyr Ser His Gly Leu Gly Met Asp Leu Ile Lys Asp Leu Gly Ile
                165                      170                      175
Leu Ile Val Phe Leu Ile Leu Ile Ile Val Ala Phe Gln Ile Phe Lys
                180                      185                      190
Thr Leu Phe Trp Trp Phe Pro His Leu Lys Leu Phe Val Met Pro Lys
                195                      200                      205
Ser Ser Gln Phe Asn Gln Asp Val Arg Phe Ser Leu Met Leu Phe Phe

```

GGC ATG ATC ATG ACT TTA GTC AAA GAT TAT CGT AAA GAG ATT TTG TGG	496
Gly Met Ile Met Thr Leu Val Lys Asp Tyr Arg Lys Glu Ile Leu Trp	
125 130 135	
CTT GAT TTG GTT TTG AAA GTG GGC GTT ATT GGG GAA TTG TTA AGC ATT	544
Leu Asp Leu Val Leu Lys Val Gly Val Ile Gly Glu Leu Leu Ser Ile	
140 145 150	
TTT GGT TTG GTG GTC GTG GAT GGG GTG TAT TCG CAT GGT TTG GGC ATG	592
Phe Gly Leu Val Val Val Asp Gly Val Tyr Ser His Gly Leu Gly Met	
155 160 165	
GAT TTG ATT AAA GAT TTA GGC ATT CTC ATT GTT TTT TTA ATC TTA ATT	640
Asp Leu Ile Lys Asp Leu Gly Ile Leu Ile Val Phe Leu Ile Leu Ile	
170 175 180	
ATC GTG GCG TTT CAA ATC TTT AAG ACT TTG TTT TGG TGG TTC CCG CAT	688
Ile Val Ala Phe Gln Ile Phe Lys Thr Leu Phe Trp Trp Phe Pro His	
185 190 195 200	
TTA AAG CTT TTT GTG ATG CCT AAA AGC AGT CAG TTT AAC CAA GAT GTG	736
Leu Lys Leu Phe Val Met Pro Lys Ser Ser Gln Phe Asn Gln Asp Val	
205 210 215	
CGT TTT TCG CTC ATG CTC TTT TTT TCC TTA GTT GCG ATC GTG GTG TGG	784
Arg Phe Ser Leu Met Leu Phe Phe Ser Leu Val Ala Ile Val Val Trp	
220 225 230	
CTC AAA ATA GAA ATG GTT TTA GGC GCG TTT CTA GCA GGG TTA GTC GTT	832
Leu Lys Ile Glu Met Val Leu Gly Ala Phe Leu Ala Gly Leu Val Val	
235 240 245	
TCT ACT TTT TTC CCT CAT AAA TCA GAA TTG ATC CAC AAG CTC AAT GAT	880
Ser Thr Phe Phe Pro His Lys Ser Glu Leu Ile His Lys Leu Asn Asp	
250 255 260	
GTG GGT TTT GGG TTT TTT GTG CCT TTG TTT TTC ATC CAT GTA GGC TCT	928
Val Gly Phe Gly Phe Phe Val Pro Leu Phe Phe Ile His Val Gly Ser	
265 270 275 280	
ACT TTA GAC TTA AAA TTA GTG TTT TTA AAC CCG CAT TTG ATT CTC CAA	976
Thr Leu Asp Leu Lys Leu Val Phe Leu Asn Pro His Leu Ile Leu Gln	
285 290 295	
GGG ATA TTG ATT GTC ATA GCG ATG TTG AGT TTG CAC TTG ATC ACT TCA	1024
Gly Ile Leu Ile Val Ile Ala Met Leu Ser Leu His Leu Ile Thr Ser	
300 305 310	
ACC TTA TTG TGG CGC AAA TAC TTT AAA GAG GCT AAG CAT TTA TTT TCA	1072
Thr Leu Leu Trp Arg Lys Tyr Phe Lys Glu Ala Lys His Leu Phe Ser	
315 320 325	
TTC GCT TTA GGG GCT TCT ATG CCT TTA ACT TTT TTA GTA ACC ACC GCA	1120
Phe Ala Leu Gly Ala Ser Met Pro Leu Thr Phe Leu Val Thr Thr Ala	
330 335 340	

435

440

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 89...1237
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

```

GAAATCAAAA AAGGGGTTTT TACCACTTAT AAAGAGAAAA ACCCTATCGC TTTGAAAAC 60
TAACCAATAA ATAAGGTAAA ATTAAGAC ATG CAT GCA GAA TTT TTC ACT TTC 112
                               Met His Ala Glu Phe Phe Thr Phe
                               1             5

GCG CTC ATC ATG CTT TTA ATT GTG ATG GCC CCT TAT ATG TCT AGA ATC 160
Ala Leu Ile Met Leu Leu Ile Val Met Ala Pro Tyr Met Ser Arg Ile
 10             15             20

TCT CGT TTG CCT ATC ACG GTT GTG GAG ATT TTA TTT GGA TCT GTT GGG 208
Ser Arg Leu Pro Ile Thr Val Val Glu Ile Leu Phe Gly Ser Val Gly
 25             30             35             40

GCG TAT GTG GGT TTT ATT GAG CCT ACT AAG GGC TTT GAA ATC ATG TCC 256
Ala Tyr Val Gly Phe Ile Glu Pro Thr Lys Gly Phe Glu Ile Met Ser
           45             50             55

GAA ATT GGC TTT TTG TTT TTA ATG TTT TTA TGC GGT TTG GAA GTG GAG 304
Glu Ile Gly Phe Leu Phe Leu Met Phe Leu Cys Gly Leu Glu Val Glu
           60             65             70

ATT TAT CTG TTC AAA AAA TTA GGG GTT TCT CTT TTA AAA CGC ATT TTT 352
Ile Tyr Leu Phe Lys Lys Leu Gly Val Ser Leu Leu Lys Arg Ile Phe
       75             80             85

GCT TAT CTG TTG ATT TTA TAC ACG CTT TCG TTT ATT CTT ACT TTT AGC 400
Ala Tyr Leu Leu Ile Leu Tyr Thr Leu Ser Phe Ile Leu Thr Phe Ser
  90             95             100

CTT AAT TTA GAG CCT ATT TTT ATG GTG ATT TTC CCT ATT ATT AGT TTG 448
Leu Asn Leu Glu Pro Ile Phe Met Val Ile Phe Pro Ile Ile Ser Leu
105             110             115             120

```

Met Phe Lys Lys Ile Phe Pro Leu Ala Leu Val Ser Ser Leu Arg Phe
 1 5 10 15
 Leu Gly Leu Phe Ile Val Leu Pro Val Ile Ser Leu Tyr Ala Asp Ser
 20 25 30
 Phe His Ser Ser Ser Pro Leu Leu Val Gly Leu Ala Val Gly Gly Ala
 35 40 45
 Tyr Leu Thr Gln Ile Val Phe Gln Thr Pro Met Gly Ile Leu Ser Asp
 50 55 60
 Lys Ile Gly Arg Lys Val Val Val Met Val Cys Leu Leu Leu Phe Leu
 65 70 75 80
 Ala Gly Ser Leu Val Cys Phe Ile Ala Asn Asp Ile Val Trp Leu Val
 85 90 95
 Ile Gly Arg Phe Ile Gln Gly Met Gly Ala Leu Gly Gly Val Ile Ser
 100 105 110
 Ala Met Val Ala Asp Glu Val Lys Glu Glu Glu Arg Thr Lys Ala Met
 115 120 125
 Ala Ile Met Gly Ala Phe Ile Phe Ile Ser Phe Thr Ile Ser Met Ala
 130 135 140
 Ile Gly Pro Gly Val Val Ala Phe Leu Gly Gly Ala Lys Trp Leu Phe
 145 150 155 160
 Leu Leu Thr Ala Ile Leu Thr Leu Leu Ser Leu Leu Met Leu Leu Lys
 165 170 175
 Val Lys Asp Ala Pro Lys Ile Ser Tyr Gln Ile Lys Asn Ile Lys Ala
 180 185 190
 Tyr Gln Pro Asn Ser Lys Ala Leu Tyr Leu Leu Tyr Leu Ser Ser Phe
 195 200 205
 Phe Glu Lys Ala Phe Met Thr Leu Ile Phe Val Leu Ile Pro Leu Ala
 210 215 220
 Leu Val Asn Glu Phe His Lys Asp Glu Ser Phe Leu Ile Leu Val Tyr
 225 230 235 240
 Val Pro Gly Ala Leu Leu Gly Val Leu Ser Met Gly Ile Ala Ser Val
 245 250 255
 Met Ala Glu Lys Tyr Asn Lys Pro Lys Gly Val Met Leu Ser Gly Val
 260 265 270
 Leu Leu Phe Ile Val Ser Tyr Leu Cys Leu Phe Leu Ala Asp Ser Ser
 275 280 285
 Phe Leu Gly Lys Tyr Leu Trp Leu Phe Ile Val Gly Val Ala Phe Phe
 290 295 300
 Phe Ile Gly Phe Ala Thr Leu Glu Pro Ile Met Gln Ser Leu Ala Ser
 305 310 315 320
 Lys Phe Ala Lys Val His Glu Lys Gly Lys Val Leu Gly Gln Phe Thr
 325 330 335
 Thr Phe Gly Tyr Leu Gly Ser Phe Val Gly Gly Val Ser Gly Gly Leu
 340 345 350
 Ser Tyr His His Leu Gly Val Ser Asn Thr Ser Leu Ile Val Val Ala
 355 360 365
 Leu Gly Leu Ile Trp Gly Leu Ser Leu Phe Leu Leu Asn Asn Pro Ser
 370 375 380
 Lys Gln Lys Asn Val Tyr Phe Pro Leu Asp Ala Tyr Asn Glu Glu Gln
 385 390 395 400
 Phe Glu Thr Leu Glu Asp Lys Ile Ile Glu Trp Tyr Val Asn Ile Ser
 405 410 415
 Glu Glu Ile Ile Ile Val Lys Tyr Asn Ser Asp His Ile Ser Glu Glu
 420 425 430
 Glu Ile Ile His Leu Ala Gln Asn Phe Arg Lys

TTA GCC GAC TCT AGC TTT TTA GGG AAA TAT TTA TGG CTT TTT ATT GTT	975
Leu Ala Asp Ser Ser Phe Leu Gly Lys Tyr Leu Trp Leu Phe Ile Val	
285 290 295	
GGG GTG GCG TTT TTC TTT ATT GGT TTT GCC ACC TTA GAG CCT ATC ATG	1023
Gly Val Ala Phe Phe Phe Ile Gly Phe Ala Thr Leu Glu Pro Ile Met	
300 305 310 315	
CAA TCT TTA GCG TCT AAA TTC GCC AAA GTG CAT GAA AAA GGC AAG GTT	1071
Gln Ser Leu Ala Ser Lys Phe Ala Lys Val His Glu Lys Gly Lys Val	
320 325 330	
TTA GGG CAA TTC ACT ACT TTT GGC TAT TTA GGG AGC TTT GTT GGG GGC	1119
Leu Gly Gln Phe Thr Thr Phe Gly Tyr Leu Gly Ser Phe Val Gly Gly	
335 340 345	
GTG AGC GGG GGG TTG AGC TAC CAT CAT TTA GGC GTT TCT AAC ACA AGC	1167
Val Ser Gly Gly Leu Ser Tyr His His Leu Gly Val Ser Asn Thr Ser	
350 355 360	
TTG ATC GTT GTA GCT TTA GGG CTT ATT TGG GGG CTA TCG CTC TTT TTA	1215
Leu Ile Val Val Ala Leu Gly Leu Ile Trp Gly Leu Ser Leu Phe Leu	
365 370 375	
CTC AAC AAC CCT TCC AAG CAA AAA AAT GTC TAT TTC CCC TTA GAC GCT	1263
Leu Asn Asn Pro Ser Lys Gln Lys Asn Val Tyr Phe Pro Leu Asp Ala	
380 385 390 395	
TAC AAT GAG GAA CAA TTT GAA ACT TTA GAG GAT AAA ATC ATT GAA TGG	1311
Tyr Asn Glu Glu Gln Phe Glu Thr Leu Glu Asp Lys Ile Ile Glu Trp	
400 405 410	
TAT GTT AAT ATT AGC GAA GAA ATC ATT ATT GTG AAA TAT AAT TCC GAT	1359
Tyr Val Asn Ile Ser Glu Glu Ile Ile Ile Val Lys Tyr Asn Ser Asp	
415 420 425	
CAC ATT AGC GAA GAA GAA ATC ATT CAC TTA GCG CAA AAC TTT AGA AAA T	1408
His Ile Ser Glu Glu Glu Ile Ile His Leu Ala Gln Asn Phe Arg Lys	
430 435 440	
AAAACAATTA AGGATCAAAA ATGGCCTATG AA	1440

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GGC	ATT	CTT	AGC	GAT	AAG	ATA	GGC	CGT	AAA	GTG	GTG	GTT	ATG	GTG	TGC	303
Gly	Ile	Leu	Ser	Asp	Lys	Ile	Gly	Arg	Lys	Val	Val	Val	Met	Val	Cys	
60					65					70					75	
TTG	CTG	TTG	TTT	TTA	GCC	GGC	TCG	TTA	GTG	TGC	TTT	ATA	GCG	AAT	GAT	351
Leu	Leu	Leu	Phe	Leu	Ala	Gly	Ser	Leu	Val	Cys	Phe	Ile	Ala	Asn	Asp	
				80					85						90	
ATT	GTT	TGG	CTC	GTT	ATA	GGG	CGC	TTC	ATT	CAA	GGC	ATG	GGG	GCT	TTA	399
Ile	Val	Trp	Leu	Val	Ile	Gly	Arg	Phe	Ile	Gln	Gly	Met	Gly	Ala	Leu	
			95					100						105		
GGG	GGG	GTT	ATT	AGT	GCG	ATG	GTG	GCG	GAT	GAA	GTG	AAA	GAA	GAA	GAG	447
Gly	Gly	Val	Ile	Ser	Ala	Met	Val	Ala	Asp	Glu	Val	Lys	Glu	Glu	Glu	
		110						115					120			
CGC	ACC	AAA	GCC	ATG	GCC	ATC	ATG	GGA	GCG	TTT	ATT	TTC	ATT	AGC	TTC	495
Arg	Thr	Lys	Ala	Met	Ala	Ile	Met	Gly	Ala	Phe	Ile	Phe	Ile	Ser	Phe	
		125					130					135				
ACT	ATA	AGC	ATG	GCG	ATT	GGC	CCT	GGG	GTT	GTA	GCG	TTT	TTG	GGG	GGG	543
Thr	Ile	Ser	Met	Ala	Ile	Gly	Pro	Gly	Val	Val	Ala	Phe	Leu	Gly	Gly	
140						145				150					155	
GCA	AAA	TGG	CTC	TTT	TTA	CTC	ACG	GCG	ATC	TTA	ACT	TTA	TTG	AGT	TTA	591
Ala	Lys	Trp	Leu	Phe	Leu	Leu	Thr	Ala	Ile	Leu	Thr	Leu	Leu	Ser	Leu	
				160						165					170	
TTG	ATG	CTT	TTA	AAA	GTC	AAA	GAC	GCC	CCT	AAA	ATT	TCT	TAC	CAG	ATC	639
Leu	Met	Leu	Leu	Lys	Val	Lys	Asp	Ala	Pro	Lys	Ile	Ser	Tyr	Gln	Ile	
				175					180					185		
AAA	AAC	ATA	AAA	GCT	TAC	CAA	CCC	AAC	TCT	AAA	GCC	TTG	TAT	CTT	TTG	687
Lys	Asn	Ile	Lys	Ala	Tyr	Gln	Pro	Asn	Ser	Lys	Ala	Leu	Tyr	Leu	Leu	
		190						195					200			
TAT	CTA	AGC	TCT	TTT	TTT	GAA	AAA	GCG	TTC	ATG	ACG	CTT	ATT	TTT	GTG	735
Tyr	Leu	Ser	Ser	Phe	Phe	Glu	Lys	Ala	Phe	Met	Thr	Leu	Ile	Phe	Val	
		205					210					215				
CTG	ATC	CCT	TTA	GCC	TTA	GTG	AAT	GAA	TTT	CAT	AAA	GAT	GAA	AGC	TTT	783
Leu	Ile	Pro	Leu	Ala	Leu	Val	Asn	Glu	Phe	His	Lys	Asp	Glu	Ser	Phe	
220						225				230					235	
TTA	ATC	TTG	GTG	TAT	GTG	CCT	GGA	GCC	TTA	TTA	GGG	GTC	TTA	AGC	ATG	831
Leu	Ile	Leu	Val	Tyr	Val	Pro	Gly	Ala	Leu	Leu	Gly	Val	Leu	Ser	Met	
				240						245					250	
GGA	ATA	GCG	AGC	GTT	ATG	GCT	GAA	AAA	TAC	AAC	AAG	CCT	AAA	GGA	GTG	879
Gly	Ile	Ala	Ser	Val	Met	Ala	Glu	Lys	Tyr	Asn	Lys	Pro	Lys	Gly	Val	
			255						260					265		
ATG	CTT	TCT	GGC	GTA	TTA	TTG	TTT	ATT	GTG	AGT	TAT	TTG	TGC	TTG	TTT	927
Met	Leu	Ser	Gly	Val	Leu	Leu	Phe	Ile	Val	Ser	Tyr	Leu	Cys	Leu	Phe	
			270					275						280		

```

Lys Val Gly Leu Lys Asp Ile Ile Met Ala Thr Gly Ala Ser Thr Asp
      100      105      110
Ser Lys Thr Asn Arg Val Arg Phe Leu Asn His Asp Leu Ser Ala Thr
      115      120      125
Pro Asp Phe Glu Leu Ser Leu Arg Ala Tyr Gln Thr Ala Lys Arg Leu
      130      135      140
Gly Ile Asp Leu Lys Val Gly Asn Val Phe Ser Ser Asp Phe Phe Tyr
      145      150      155      160
Ser Phe Glu Thr His Ala Phe Asp Leu Met Ala Lys Tyr Asn His Leu
      165      170      175
Ala Ile Glu Met Glu Ala Ala Gly Leu Tyr Ala Thr Ala Met Glu Leu
      180      185      190
Asn Ala Lys Ala Leu Cys Leu Cys Ser Val Ser Asp His Leu Ile Thr
      195      200      205
Lys Glu Ala Leu Ser Pro Lys Glu Arg Val Glu Ser Phe Asp Asn Met
      210      215      220
Ile Ile Leu Ala Leu Glu Met Met Ser
      225      230

```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...1407
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

```

TACATTAAAC TTTTATTATC AATCCTACTT CCTCAAATTG ATGACAAAAG TTGGGCATTT      60
TCTTGTAATA TAACCCGC ATG TTT AAG AAA ATT TTT CCA TTA GCG TTA GTG      111
      Met Phe Lys Lys Ile Phe Pro Leu Ala Leu Val
      1              5              10

TCA TCG TTG CGG TTT TTG GGG CTT TTT ATT GTT TTG CCG GTC ATT AGT      159
Ser Ser Leu Arg Phe Leu Gly Leu Phe Ile Val Leu Pro Val Ile Ser
      15              20              25

TTG TAT GCG GAT AGT TTC CAT TCA AGC AGT CCC TTA CTC GTG GGG TTG      207
Leu Tyr Ala Asp Ser Phe His Ser Ser Ser Pro Leu Leu Val Gly Leu
      30              35              40

GCT GTG GGC GGA GCG TAT CTT ACG CAA ATT GTT TTT CAA ACC CCC ATG      255
Ala Val Gly Gly Ala Tyr Leu Thr Gln Ile Val Phe Gln Thr Pro Met
      45              50              55

```



```

ACG CCT GAT TTT GAA TTG AGT TTA AGA GCG TAT CAA ACA GCA AAG CGT      494
Thr Pro Asp Phe Glu Leu Ser Leu Arg Ala Tyr Gln Thr Ala Lys Arg
      130                      135                      140

TTG GGT ATT GAT TTG AAA GTG GGC AAT GTT TTT TCA AGC GAT TTT TTC      542
Leu Gly Ile Asp Leu Lys Val Gly Asn Val Phe Ser Ser Asp Phe Phe
      145                      150                      155

TAT TCT TTT GAA ACG CAT GCC TTT GAT TTA ATG GCT AAA TAC AAC CAC      590
Tyr Ser Phe Glu Thr His Ala Phe Asp Leu Met Ala Lys Tyr Asn His
      160                      165                      170                      175

TTG GCT ATT GAA ATG GAA GCG GCG GGG TTA TAC GCC ACG GCG ATG GAA      638
Leu Ala Ile Glu Met Glu Ala Ala Gly Leu Tyr Ala Thr Ala Met Glu
      180                      185                      190

CTA AAC GCT AAG GCT TTA TGC TTA TGC TCA GTC TCA GAT CAC TTA ATC      686
Leu Asn Ala Lys Ala Leu Cys Leu Cys Ser Val Ser Asp His Leu Ile
      195                      200                      205

ACT AAA GAA GCC TTA AGC CCT AAA GAA AGG GTA GAA AGC TTT GAT AAC      734
Thr Lys Glu Ala Leu Ser Pro Lys Glu Arg Val Glu Ser Phe Asp Asn
      210                      215                      220

ATG ATA ATT TTG GCT TTG GAG ATG ATG AGT TAGCCTTTTT TGCCCCCATA AGT      787
Met Ile Ile Leu Ala Leu Glu Met Met Ser
      225                      230

TAAGGATAAA ATTTAAAGGA AAACCCTTAA AGCTAAAAGC CTTAAGGGAA CTTTGG      843

```

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

```

Met Thr Pro His Ile Asn Ala Lys Ile Gly Asp Phe Tyr Pro Gln Cys
 1           5           10           15
Leu Leu Cys Gly Asp Pro Leu Arg Val Ser Tyr Ile Ala Lys Lys Phe
      20           25           30
Leu Gln Asp Ala Lys Glu Ile Thr Asn Val Arg Asn Met Leu Gly Phe
      35           40           45
Ser Gly Lys Tyr Lys Gly Arg Gly Ile Ser Leu Met Gly His Gly Met
      50           55           60
Gly Ile Ala Ser Cys Thr Ile Tyr Val Thr Glu Leu Ile Lys Thr Tyr
      65           70           75           80
Gln Val Lys Glu Leu Leu Arg Ile Gly Thr Cys Gly Ala Ile Ser Pro
      85           90           95

```

435

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...764
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GCTCACTTTT TGGGATTAAG CCCCTAGAT TATGGCAAAA ACTTATTAAA CTTTAAAGGA	60
CAACC ATG ACC CCT CAC ATC AAC GCC AAA ATC GGC GAT TTT TAT CCT CAA	110
Met Thr Pro His Ile Asn Ala Lys Ile Gly Asp Phe Tyr Pro Gln	
1 5 10 15	
TGC CTT TTA TGC GGC GAT CCC TTA AGG GTG AGC TAC ATT GCA AAA AAA	158
Cys Leu Leu Cys Gly Asp Pro Leu Arg Val Ser Tyr Ile Ala Lys Lys	
20 25 30	
TTC TTA CAA GAC GCC AAA GAG ATC ACG AAT GTG CGT AAC ATG CTA GGC	206
Phe Leu Gln Asp Ala Lys Glu Ile Thr Asn Val Arg Asn Met Leu Gly	
35 40 45	
TTT AGC GGG AAG TAT AAG GGT AGG GGG ATT TCT TTA ATG GGG CAT GGC	254
Phe Ser Gly Lys Tyr Lys Gly Arg Gly Ile Ser Leu Met Gly His Gly	
50 55 60	
ATG GGC ATT GCG TCA TGC ACG ATT TAT GTA ACC GAA CTC ATT AAA ACC	302
Met Gly Ile Ala Ser Cys Thr Ile Tyr Val Thr Glu Leu Ile Lys Thr	
65 70 75	
TAT CAG GTT AAA GAG CTT TTA AGG ATT GGC ACT TGC GGG GCG ATT AGC	350
Tyr Gln Val Lys Glu Leu Leu Arg Ile Gly Thr Cys Gly Ala Ile Ser	
80 85 90 95	
CCA AAA GTT GGC CTG AAA GAC ATT ATC ATG GCG ACG GGG GCT TCA ACG	398
Pro Lys Val Gly Leu Lys Asp Ile Ile Met Ala Thr Gly Ala Ser Thr	
100 105 110	
GAT TCT AAA ACC AAT CGG GTG CGT TTT TTA AAC CAC GAT TTG AGC GCA	446
Asp Ser Lys Thr Asn Arg Val Arg Phe Leu Asn His Asp Leu Ser Ala	
115 120 125	

Met	Gly	Phe	Phe	Lys	Leu	Lys	Glu	His	Asn	Thr	Asn	Ile	Ala	Thr	Glu
1				5					10					15	
Phe	Arg	Ala	Gly	Leu	Thr	Thr	Phe	Ile	Thr	Met	Ile	Tyr	Ile	Val	Pro
			20					25					30		
Leu	Asn	Ala	Leu	Ile	Leu	Ser	Gln	Ala	Asn	Met	Pro	Tyr	Glu	Ala	Leu
		35					40					45			
Leu	Ser	Ala	Thr	Ala	Ile	Ile	Thr	Ile	Leu	Ser	Ser	Val	Phe	Asn	Gly
	50					55					60				
Leu	Trp	Ala	Asn	Thr	Pro	Ile	Ala	Met	Ser	Val	Gly	Leu	Gly	Leu	Ser
65					70					75					80
Ala	Tyr	Phe	Ser	Phe	Gly	Leu	Val	Gln	Gly	Leu	Lys	Leu	Pro	Trp	Gln
				85					90					95	
Ser	Ala	Leu	Gly	Ile	Val	Ala	Leu	Ser	Gly	Ala	Ile	Phe	Val	Ile	Leu
			100					105					110		
Ser	Phe	Thr	Lys	Phe	Arg	Ser	Trp	Val	Met	Arg	Ser	Ile	Pro	Ser	Asp
			115					120					125		
Leu	Arg	Arg	Ala	Val	Ser	Ala	Gly	Ile	Gly	Ala	Phe	Ile	Ala	Phe	Ile
	130						135						140		
Gly	Leu	Lys	Glu	Met	His	Ile	Val	Val	Thr	His	Xaa	Ala	Thr	Leu	Val
145					150					155					160
Thr	Leu	Gly	Asp	Phe	Gly	Asp	Pro	His	Val	Leu	Leu	Gly	Val	Val	Gly
				165					170					175	
Ile	Ile	Leu	Thr	Phe	Ala	Leu	Tyr	Thr	Leu	Lys	Ile	Arg	Gly	Ser	Phe
			180						185				190		
Ile	Ile	Ala	Val	Leu	Ile	Thr	Ser	Ile	Leu	Ala	Trp	Val	Leu	Lys	Leu
		195					200					205			
Ala	Pro	Tyr	Pro	Ser	Glu	Phe	Phe	Ser	Met	Pro	Ala	Ser	Ile	Gly	Pro
		210				215					220				
Ile	Ala	Phe	Gln	Leu	Asp	Phe	Lys	Gly	Ile	Phe	Phe	Asp	Ala	Ser	Gly
225					230					235					240
Ala	Phe	Thr	Leu	Ala	Leu	Val	Pro	Val	Ile	Ile	Thr	Phe	Phe	Val	Thr
				245					250					255	
Asp	Leu	Phe	Asp	Ser	Leu	Gly	Thr	Leu	Ala	Gly	Ile	Gly	His	Lys	Thr
			260					265					270		
Asp	Phe	Phe	Asn	Asp	Glu	Glu	Lys	Asn	Lys	Glu	Leu	Glu	Lys	Thr	Leu
		275					280					285			
Glu	Ala	Asp	Ala	Val	Ala	Ser	Leu	Gly	Ser	Ala	Val	Val	Gly	Val	Ser
	290					295					300				
Thr	Thr	Thr	Ala	Phe	Ile	Glu	Ser	Ala	Ser	Gly	Val	Glu	Glu	Gly	Gly
305					310					315					320
Arg	Thr	Gly	Leu	Thr	Ala	Val	Phe	Thr	Gly	Leu	Phe	Phe	Val	Leu	Thr
				325					330					335	
Leu	Phe	Cys	Leu	Pro	Leu	Leu	Lys	Ala	Ile	Pro	Ser	Asn	Ala	Ile	Tyr
			340					345					350		
Pro	Val	Leu	Val	Val	Val	Gly	Val	Leu	Met	Phe	Ser	Val	Leu	Glu	Gly
		355					360					365			
Val	Asn	Phe	Lys	Asp	Met	Ala	Ile	Ser	Val	Ser	Thr	Phe	Leu	Thr	Val
	370					375					380				
Val	Met	Met	Pro	Leu	Thr	Phe	Ser	Ile	Ala	Asp	Gly	Leu	Ala	Phe	Gly
385					390					395					400
Phe	Leu	Ser	Tyr	Ser	Ile	Ile	Lys	Leu	Val	Gln	Lys	Asp	Phe	Lys	Ala
				405					410					415	
Leu	Asn	Ser	Gly	Ile	Ile	Ile	Leu	Cys	Ile	Ile	Ser	Val	Ser	Val	Phe
			420					425					430		
Ile	Phe	Arg													

AAA AAC AAG GAA TTG GAA AAG ACT TTG GAA GCG GAT GCG GTG GCT TCT	918
Lys Asn Lys Glu Leu Glu Lys Thr Leu Glu Ala Asp Ala Val Ala Ser	
280 285 290 295	
TTA GGG AGC GCG GTG GTG GGC GTT TCT ACT ACG ACC GCT TTT ATA GAG	966
Leu Gly Ser Ala Val Val Gly Val Ser Thr Thr Ala Phe Ile Glu	
300 305 310	
AGC GCG AGT GGG GTT GAA GAG GGG GGC CGC ACA GGG CTT ACA GCG GTT	1014
Ser Ala Ser Gly Val Glu Glu Gly Gly Arg Thr Gly Leu Thr Ala Val	
315 320 325	
TTT ACC GGA TTA TTT TTT GTT TTA ACG CTC TTT TGC TTG CCT CTT TTA	1062
Phe Thr Gly Leu Phe Phe Val Leu Thr Leu Phe Cys Leu Pro Leu Leu	
330 335 340	
AAA GCT ATT CCT AGC AAT GCG ATT TAT CCG GTG CTG GTG GTA GTA GGG	1110
Lys Ala Ile Pro Ser Asn Ala Ile Tyr Pro Val Leu Val Val Val Gly	
345 350 355	
GTT TTG ATG TTT AGC GTG TTA GAG GGG GTG AAT TTT AAA GAC ATG GCC	1158
Val Leu Met Phe Ser Val Leu Glu Gly Val Asn Phe Lys Asp Met Ala	
360 365 370 375	
ATT AGC GTT TCC ACT TTT TTA ACC GTG GTG ATG ATG CCC TTA ACC TTC	1206
Ile Ser Val Ser Thr Phe Leu Thr Val Val Met Met Pro Leu Thr Phe	
380 385 390	
TCC ATT GCC GAT GGC TTA GCC TTT GGC TTT TTG TCT TAT AGT ATC ATC	1254
Ser Ile Ala Asp Gly Leu Ala Phe Gly Phe Leu Ser Tyr Ser Ile Ile	
395 400 405	
AAA TTG GTT CAA AAA GAC TTC AAA GCA CTC AAT TCA GGC ATT ATC ATT	1302
Lys Leu Val Gln Lys Asp Phe Lys Ala Leu Asn Ser Gly Ile Ile Ile	
410 415 420	
CTC TGC ATC ATT TCT GTT TCT GTA TTT ATC TTT CGT TAAGCTCTTT TTAAGG	1354
Leu Cys Ile Ile Ser Val Ser Val Phe Ile Phe Arg	
425 430 435	
GGCTTTGCAT TTTTACTCA TTTCATGCCT CTTTTCTTT ATTTAGACAG ATTATTATCT	1414
TAAAATAATT GTAATATCAT TATTAT	1440

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

ACT ATC TTA TCG AGC GTG TTT AAC GGA TTG TGG GCA AAC ACC CCT ATC	246
Thr Ile Leu Ser Ser Val Phe Asn Gly Leu Trp Ala Asn Thr Pro Ile	
60 65 70	
GCT ATG AGC GTG GGC TTA GGG CTG TCA GCT TAT TTT AGC TTC GGG TTG	294
Ala Met Ser Val Gly Leu Gly Leu Ser Ala Tyr Phe Ser Phe Gly Leu	
75 80 85	
GTT CAA GGG TTA AAA CTC CCT TGG CAG AGC GCT TTA GGC ATC GTA GCG	342
Val Gln Gly Leu Lys Leu Pro Trp Gln Ser Ala Leu Gly Ile Val Ala	
90 95 100	
CTC TCG GGA GCG ATT TTT GTG ATT TTG TCT TTC ACT AAA TTT AGA AGT	390
Leu Ser Gly Ala Ile Phe Val Ile Leu Ser Phe Thr Lys Phe Arg Ser	
105 110 115	
TGG GTC ATG CGA AGC ATT CCT AGC GAT TTA AGG CGT GCG GTG AGT GCG	438
Trp Val Met Arg Ser Ile Pro Ser Asp Leu Arg Arg Ala Val Ser Ala	
120 125 130 135	
GGG ATA GGG GCT TTT ATC GCG TTT ATT GGC CTT AAA GAA ATG CAT ATC	486
Gly Ile Gly Ala Phe Ile Ala Phe Ile Gly Leu Lys Glu Met His Ile	
140 145 150	
GTC GTT ACC CAT AAR GCT ACG CTT GTA ACC TTA GGC GAT TTT GGC GAT	534
Val Val Thr His Xaa Ala Thr Leu Val Thr Leu Gly Asp Phe Gly Asp	
155 160 165	
CCG CAT GTG TTA TTG GGG GTT GTG GGG ATC ATT CTA ACT TTC GCG CTC	582
Pro His Val Leu Leu Gly Val Val Gly Ile Ile Leu Thr Phe Ala Leu	
170 175 180	
TAC ACG CTC AAA ATC AGG GGT TCT TTC ATT ATA GCG GTC TTA ATC ACT	630
Tyr Thr Leu Lys Ile Arg Gly Ser Phe Ile Ile Ala Val Leu Ile Thr	
185 190 195	
TCC ATT CTC GCA TGG GTT TTA AAG CTA GCC CCT TAC CCT AGC GAG TTT	678
Ser Ile Leu Ala Trp Val Leu Lys Leu Ala Pro Tyr Pro Ser Glu Phe	
200 205 210 215	
TTT TCC ATG CCC GCT AGC ATT GGC CCT ATC GCC TTT CAA TTA GAC TTT	726
Phe Ser Met Pro Ala Ser Ile Gly Pro Ile Ala Phe Gln Leu Asp Phe	
220 225 230	
AAG GGC ATT TTT TTT GAT GCG AGT GGG GCT TTC ACT TTA GCG TTA GTG	774
Lys Gly Ile Phe Phe Asp Ala Ser Gly Ala Phe Thr Leu Ala Leu Val	
235 240 245	
CCA GTT ATT ATC ACT TTT TTT GTA ACC GAT TTG TTT GAT TCT TTA GGC	822
Pro Val Ile Ile Thr Phe Phe Val Thr Asp Leu Phe Asp Ser Leu Gly	
250 255 260	
ACG CTT GCA GGG ATT GGC CAC AAG ACT GAT TTT TTC AAT GAT GAA GAA	870
Thr Leu Ala Gly Ile Gly His Lys Thr Asp Phe Phe Asn Asp Glu Glu	
265 270 275	

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```

Ile Ser Ser Lys Arg Leu Glu Ile Ser Arg Leu Leu Glu Arg Lys Asn
 1           5           10           15
Glu Arg Ser Phe Leu Ala Glu Lys Tyr His Lys Ile Pro Thr Asn Lys
          20           25           30
Arg Lys Phe Lys Glu Arg Ser Ile Ile Ser Val Cys Glu Ile Ser Asn
          35           40           45
Pro Val Ala His Lys Gly Leu Lys Arg Ile Lys Asn Pro Asn Thr Ile
          50           55           60
Leu Thr Thr Asn Ile His Gln Leu Pro Lys Pro Ile Ala Thr Arg Leu
65           70           75           80
Phe Asn Ser Ser Ser Asn Thr Gly Ile Cys Ala Cys Asn Cys Ser Phe
          85           90           95
Ser Ala Cys Phe Ser Phe Cys Asn Cys Phe Ala Asn Ala Ser Asn Ser
          100           105           110

```

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1440 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 34...1338

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

```

TAATCTATAC CAAATAGTAA GGAGTTATCT AAC ATG GGG TTT TTC AAG CTT AAA      54
                               Met Gly Phe Phe Lys Leu Lys
                               1           5

GAA CAC AAC ACT AAC ATT GCC ACC GAG TTT AGA GCG GGT TTA ACG ACC      102
Glu His Asn Thr Asn Ile Ala Thr Glu Phe Arg Ala Gly Leu Thr Thr
          10           15           20

TTT ATC ACC ATG ATT TAC ATC GTG CCC TTA AAC GCT CTT ATC CTT TCT      150
Phe Ile Thr Met Ile Tyr Ile Val Pro Leu Asn Ala Leu Ile Leu Ser
          25           30           35

CAA GCC AAC ATG CCT TAT GAA GCC CTT TTA AGT GCA ACG GCC ATT ATC      198
Gln Ala Asn Met Pro Tyr Glu Ala Leu Leu Ser Ala Thr Ala Ile Ile
          40           45           50           55

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...336
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

ATC TCT TCT AAG CGT TTG GAG ATT TCA AGA CTT TTG GAG CGT AAA AAT	48
Ile Ser Ser Lys Arg Leu Glu Ile Ser Arg Leu Leu Glu Arg Lys Asn	
1 5 10 15	
GAA CGC AGT TTT TTA GCC GAA AAA TAC CAC AAA ATC CCC ACA AAT AAA	96
Glu Arg Ser Phe Leu Ala Glu Lys Tyr His Lys Ile Pro Thr Asn Lys	
20 25 30	
AGG AAA TTT AAA GAA CGC TCT ATA ATA TCT GTT TGT GAA ATA TCC AAT	144
Arg Lys Phe Lys Glu Arg Ser Ile Ile Ser Val Cys Glu Ile Ser Asn	
35 40 45	
CCA GTA GCG CAC AAA GGG CTT AAA AGG ATC AAA AAC CCT AAC ACC ATT	192
Pro Val Ala His Lys Gly Leu Lys Arg Ile Lys Asn Pro Asn Thr Ile	
50 55 60	
TTA ACT ACA AAC ATT CAT CAA CTC CCT AAA CCC ATA GCC ACA CGC TTG	240
Leu Thr Thr Asn Ile His Gln Leu Pro Lys Pro Ile Ala Thr Arg Leu	
65 70 75 80	
TTT AAC TCG TCT TCA AAT ACC GGC ATT TGC GCT TGC AAC TGC TCT TTT	288
Phe Asn Ser Ser Ser Asn Thr Gly Ile Cys Ala Cys Asn Cys Ser Phe	
85 90 95	
AGC GCT TGC TTT TCA TTT TGT AAT TGC TTC GCA AAC GCT TCA AAC TCT T	337
Ser Ala Cys Phe Ser Phe Cys Asn Cys Phe Ala Asn Ala Ser Asn Ser	
100 105 110	
GA	339

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

GTT TTA GGT TTT AGG GAA GTG AGC GAA GAA GAA ATT TTA GCT TCA CAC	543
Val Leu Gly Phe Arg Glu Val Ser Glu Glu Glu Ile Leu Ala Ser His	
145 150 155	
CAT GGC GGT GGG ACA GGT TGC TGT GGC GGT CAT GGG GGT CAT GGC GGA	591
His Gly Gly Thr Gly Cys Cys Gly Gly His Gly Gly His Gly Gly	
160 165 170	
AAG AAA GGT GGG GGT TGT GGT TGC TCA TGT TCG CAT GGG TAGTAAGGTA TA	642
Lys Lys Gly Gly Gly Cys Gly Cys Ser Cys Ser His Gly	
175 180 185	
GGAGTATTTA AAAGGCAAGG TCATGAATAG TTCTAATCTC AAAAATTGGC TATTCCCTAC	702
CATTTGCTTT TTTTAT	719

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

Met	Gln	Asn	His	Asp	Leu	Glu	Ser	Ile	Lys	Gln	Ala	Ala	Leu	Ile	Glu	1	5	10	15
Tyr	Glu	Val	Arg	Glu	Gln	Gly	Ser	Ser	Ile	Val	Leu	Asp	Ser	Asn	Ile	20	25	30	
Ser	Lys	Glu	Pro	Leu	Glu	Phe	Ile	Ile	Gly	Thr	Asn	Gln	Ile	Ile	Ala	35	40	45	
Gly	Leu	Glu	Lys	Ala	Val	Leu	Lys	Ala	Gln	Ile	Gly	Glu	Trp	Glu	Glu	50	55	60	
Val	Val	Ile	Ala	Pro	Glu	Glu	Ala	Tyr	Gly	Val	Tyr	Glu	Ser	Ser	Tyr	65	70	75	80
Leu	Gln	Glu	Val	Pro	Arg	Asp	Gln	Phe	Glu	Gly	Ile	Glu	Leu	Glu	Lys	85	90	95	
Gly	Met	Ser	Val	Phe	Gly	Gln	Thr	Glu	Asp	Asn	Gln	Thr	Ile	Gln	Ala	100	105	110	
Ile	Ile	Lys	Asp	Phe	Ser	Ala	Thr	His	Val	Met	Val	Asp	Tyr	Asn	His	115	120	125	
Pro	Leu	Ala	Gly	Lys	Thr	Leu	Ala	Phe	Arg	Phe	Lys	Val	Leu	Gly	Phe	130	135	140	
Arg	Glu	Val	Ser	Glu	Glu	Ile	Leu	Ala	Ser	His	His	Gly	Gly	Gly		145	150	155	160
Thr	Gly	Cys	Cys	Gly	Gly	His	Gly	Gly	His	Gly	Gly	Lys	Lys	Gly	Gly	165	170	175	
Gly	Cys	Gly	Cys	Ser	Cys	Ser	His	Gly								180	185		

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 76...630
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```

TGCAACACTT GTATCCTTCA AGCGAACAAG CTAAATGGC GCAAAAAATC TTAGAAAACA      60
AGGAGAAACA CCACC ATG CAA AAC CAT GAT TTA GAG TCA ATC AAA CAA GCC      111
      Met Gln Asn His Asp Leu Glu Ser Ile Lys Gln Ala
            1             5             10

GCT TTG ATT GAA TAT GAA GTG AGA GAA CAA GGC TCT AGT ATT GTG CTA      159
Ala Leu Ile Glu Tyr Glu Val Arg Glu Gln Gly Ser Ser Ile Val Leu
      15             20             25

GAC AGC AAT ATT TCC AAA GAG CCT TTA GAG TTT ATT ATA GGC ACT AAT      207
Asp Ser Asn Ile Ser Lys Glu Pro Leu Glu Phe Ile Ile Gly Thr Asn
      30             35             40

CAA ATC ATA GCA GGG TTA GAA AAG GCG GTA TTA AAG GCT CAA ATT GGC      255
Gln Ile Ile Ala Gly Leu Glu Lys Ala Val Leu Lys Ala Gln Ile Gly
      45             50             55             60

GAG TGG GAA GAG GTT GTC ATC GCC CCA GAG GAA GCT TAT GGG GTT TAT      303
Glu Trp Glu Glu Val Val Ile Ala Pro Glu Glu Ala Tyr Gly Val Tyr
            65             70             75

GAA AGC AGC TAT TTG CAA GAA GTC CCT AGA GAT CAA TTT GAA GGC ATT      351
Glu Ser Ser Tyr Leu Gln Glu Val Pro Arg Asp Gln Phe Glu Gly Ile
            80             85             90

GAA TTA GAA AAA GGC ATG AGC GTT TTT GGG CAA ACT GAA GAC AAT CAA      399
Glu Leu Glu Lys Gly Met Ser Val Phe Gly Gln Thr Glu Asp Asn Gln
            95             100             105

ACC ATT CAA GCC ATT ATC AAA GAC TTT AGC GCT ACG CAT GTG ATG GTG      447
Thr Ile Gln Ala Ile Ile Lys Asp Phe Ser Ala Thr His Val Met Val
      110             115             120

GAT TAT AAC CAC CCG TTA GCC GGG AAA ACT TTA GCG TTT CGT TTC AAG      495
Asp Tyr Asn His Pro Leu Ala Gly Lys Thr Leu Ala Phe Arg Phe Lys
      125             130             135             140

```

```

145          150          155          160
Pro Ala Ile Lys Leu Ala Glu Asn Gly Tyr Ala Ile Ser Gln Arg Gln
165          170          175
Ala Glu Thr Leu Lys Glu Ala Arg Glu Arg Phe Leu Lys Tyr Ser Ser
180          185          190
Ser Lys Lys Tyr Phe Phe Lys Lys Gly His Leu Asp Tyr Gln Glu Gly
195          200          205
Asp Leu Phe Val Gln Lys Asp Leu Ala Lys Thr Leu Asn Gln Ile Lys
210          215          220
Thr Leu Gly Ala Lys Gly Phe Tyr Gln Gly Gln Val Ala Glu Leu Ile
225          230          235          240
Glu Lys Asp Met Lys Lys Asn Gly Gly Ile Ile Thr Lys Glu Asp Leu
245          250          255
Ala Ser Tyr Asn Val Lys Trp Arg Lys Pro Val Val Gly Ser Tyr Arg
260          265          270
Gly Tyr Lys Ile Ile Ser Met Ser Pro Pro Ser Ser Gly Gly Thr His
275          280          285
Leu Ile Gln Ile Leu Asn Val Met Glu Asn Ala Asp Leu Ser Ala Leu
290          295          300
Gly Tyr Gly Ala Ser Lys Asn Ile His Ile Ala Ala Glu Ala Met Arg
305          310          315          320
Gln Ala Tyr Ala Asp Arg Ser Val Tyr Met Gly Asp Ala Asp Phe Val
325          330          335
Ser Val Pro Val Asp Lys Leu Ile Asn Lys Ala Tyr Ala Lys Lys Ile
340          345          350
Phe Asp Thr Ile Gln Pro Asp Thr Val Thr Pro Ser Ser Gln Ile Lys
355          360          365
Pro Gly Met Gly Gln Leu His Glu Gly Ser Asn Thr Thr His Tyr Ser
370          375          380
Val Ala Asp Arg Trp Gly Asn Ala Val Ser Val Thr Tyr Thr Ile Asn
385          390          395          400
Ala Ser Tyr Gly Ser Ala Ala Ser Ile Asp Gly Ala Gly Phe Leu Leu
405          410          415
Asn Asn Glu Met Asp Asp Phe Ser Ile Lys Pro Gly Asn Pro Asn Leu
420          425          430
Tyr Gly Leu Val Gly Gly Asp Ala Asn Ala Ile Glu Ala Asn Lys Arg
435          440          445
Pro Leu Ser Ser Met Ser Pro Thr Ile Val Leu Lys Asn Asn Lys Val
450          455          460
Phe Leu Val Val Gly Ser Pro Gly Gly Ser Arg Ile Ile Thr Thr Val
465          470          475          480
Leu Gln Val Ile Ser Asn Val Ile Asp Tyr Asn Met Asn Ile Ser Glu
485          490          495
Ala Val Ser Ala Pro Arg Phe His Met Gln Trp Leu Pro Asp Glu Leu
500          505          510
Arg Ile Glu Lys Phe Gly Met Pro Ala Asp Val Lys Asp Asn Leu Thr
515          520          525
Lys Met Gly Tyr Gln Ile Val Thr Lys Pro Val Met Gly Asp Val Asn
530          535          540
Ala Ile Gln Val Leu Pro Lys Thr Lys Gly Ser Val Phe Tyr Gly Ser
545          550          555          560
Thr Asp Pro Arg Lys Glu Phe
565

```

(2) INFORMATION FOR SEQ ID NO:511:

ATT GAT TAT AAT ATG AAT ATT TCT GAA GCG GTT TCA GCC CCA AGA TTT 1543
 Ile Asp Tyr Asn Met Asn Ile Ser Glu Ala Val Ser Ala Pro Arg Phe
 490 495 500

CAC ATG CAA TGG CTC CCT GAT GAA TTA AGG ATT GAA AAG TTT GGC ATG 1591
 His Met Gln Trp Leu Pro Asp Glu Leu Arg Ile Glu Lys Phe Gly Met
 505 510 515

CCC GCT GAT GTG AAA GAC AAC CTC ACT AAA ATG GGC TAT CAA ATC GTT 1639
 Pro Ala Asp Val Lys Asp Asn Leu Thr Lys Met Gly Tyr Gln Ile Val
 520 525 530 535

ACT AAG CCG GTC ATG GGT GAT GTG AAT GCG ATC CAA GTT TTG CCT AAA 1687
 Thr Lys Pro Val Met Gly Asp Val Asn Ala Ile Gln Val Leu Pro Lys
 540 545 550

ACT AAA GGG AGC GTT TTC TAT GGT TCA ACG GAT CCA AGG AAA GAA TTT T 1736
 Thr Lys Gly Ser Val Phe Tyr Gly Ser Thr Asp Pro Arg Lys Glu Phe
 555 560 565

AATTCCTTTGT CATATACAGG TTTTAAATCC TATTTAGCCT TATTTTTTTGG GATGGAGGGG 1796
 GGCTTTTGTAG CGAGAAAATC TTAAATTTAG TTTTAAATT CATA 1840

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

Met Arg Arg Ser Phe Leu Lys Thr Ile Gly Leu Gly Val Ile Ala Leu
 1 5 10 15
 Phe Leu Gly Leu Leu Asn Pro Leu Ser Ala Ala Ser Tyr Pro Pro Ile
 20 25 30
 Lys Asn Thr Lys Val Gly Leu Ala Leu Ser Ser His Pro Leu Ala Ser
 35 40 45
 Glu Ile Gly Gln Lys Val Leu Glu Glu Gly Gly Asn Ala Ile Asp Ala
 50 55 60
 Ala Val Ala Ile Gly Phe Ala Leu Ala Val Val His Pro Ala Ala Gly
 65 70 75 80
 Asn Ile Gly Gly Gly Phe Ala Val Ile His Leu Ala Asn Gly Glu
 85 90 95
 Asn Val Ala Leu Asp Phe Arg Glu Lys Ala Pro Leu Lys Ala Thr Lys
 100 105 110
 Asn Met Phe Leu Asp Lys Gln Gly Asn Val Val Pro Lys Leu Ser Glu
 115 120 125
 Asp Gly Tyr Leu Ala Ala Gly Val Pro Gly Thr Val Ala Gly Met Glu
 130 135 140
 Ala Met Leu Lys Lys Tyr Gly Thr Lys Lys Leu Ser Gln Leu Ile Asp

CGC AAA CCC GTG GTA GGG AGT TAT CGT GGG TAT AAG ATC ATT TCT ATG	871
Arg Lys Pro Val Val Gly Ser Tyr Arg Gly Tyr Lys Ile Ile Ser Met	
265 270 275	
TCG CCG CCA AGT TCG GGA GGC ACG CAT TTG ATC CAG ATT TTA AAT GTC	919
Ser Pro Pro Ser Ser Gly Gly Thr His Leu Ile Gln Ile Leu Asn Val	
280 285 290 295	
ATG GAA AAT GCG GAT TTA AGC GCC CTT GGG TAT GGG GCT TCT AAG AAT	967
Met Glu Asn Ala Asp Leu Ser Ala Leu Gly Tyr Gly Ala Ser Lys Asn	
300 305 310	
ATC CAT ATC GCT GCC GAA GCG ATG CGT CAG GCT TAT GCG GAT AGA TCG	1015
Ile His Ile Ala Ala Glu Ala Met Arg Gln Ala Tyr Ala Asp Arg Ser	
315 320 325	
GTT TAT ATG GGA GAC GCT GAT TTT GTT TCG GTG CCG GTG GAT AAA TTG	1063
Val Tyr Met Gly Asp Ala Asp Phe Val Ser Val Pro Val Asp Lys Leu	
330 335 340	
ATT AAT AAA GCG TAT GCC AAA AAG ATT TTT GAC ACT ATC CAG CCA GAT	1111
Ile Asn Lys Ala Tyr Ala Lys Lys Ile Phe Asp Thr Ile Gln Pro Asp	
345 350 355	
ACG GTT ACG CCA AGC TCT CAA ATC AAA CCA GGA ATG GGG CAG TTG CAT	1159
Thr Val Thr Pro Ser Ser Gln Ile Lys Pro Gly Met Gly Gln Leu His	
360 365 370 375	
GAG GGG AGC AAT ACC ACG CAT TAT TCT GTA GCG GAC AGG TGG GGG AAT	1207
Glu Gly Ser Asn Thr Thr His Tyr Ser Val Ala Asp Arg Trp Gly Asn	
380 385 390	
GCA GTC AGC GTT ACT TAC ACC ATT AAC GCT TCT TAT GGA AGC GCT GCC	1255
Ala Val Ser Val Thr Tyr Thr Ile Asn Ala Ser Tyr Gly Ser Ala Ala	
395 400 405	
AGT ATT GAT GGG GCA GGA TTT TTA TTG AAC AAT GAA ATG GAT GAT TTT	1303
Ser Ile Asp Gly Ala Gly Phe Leu Leu Asn Asn Glu Met Asp Asp Phe	
410 415 420	
TCC ATC AAG CCA GGG AAT CCC AAT CTC TAT GGT TTA GTA GGG GGC GAT	1351
Ser Ile Lys Pro Gly Asn Pro Asn Leu Tyr Gly Leu Val Gly Gly Asp	
425 430 435	
GCG AAT GCG ATT GAA GCC AAT AAG CGC CCT TTA AGC TCC ATG TCG CCT	1399
Ala Asn Ala Ile Glu Ala Asn Lys Arg Pro Leu Ser Ser Met Ser Pro	
440 445 450 455	
ACG ATT GTG TTG AAA AAC AAT AAG GTT TTT TTG GTG GTG GGA AGC CCT	1447
Thr Ile Val Leu Lys Asn Asn Lys Val Phe Leu Val Val Gly Ser Pro	
460 465 470	
GGA GGG TCT AGG ATT ATC ACT ACG GTG CTG CAA GTG ATT TCT AAT GTC	1495
Gly Gly Ser Arg Ile Ile Thr Thr Val Leu Gln Val Ile Ser Asn Val	
475 480 485	

GCC CTT TCT AGC CAC CCG CTA GCT AGT GAG ATC GGG CAA AAG GTT TTA	199
Ala Leu Ser Ser His Pro Leu Ala Ser Glu Ile Gly Gln Lys Val Leu	
40 45 50 55	
GAA GAG GGA GGT AAT GCG ATT GAT GCG GCT GTA GCG ATA GGT TTT GCT	247
Glu Glu Gly Gly Asn Ala Ile Asp Ala Ala Val Ala Ile Gly Phe Ala	
60 65 70	
CTT GCG GTT GTC CAT CCG GCA GCA GGC AAT ATT GGT GGA GGC GGT TTT	295
Leu Ala Val Val His Pro Ala Ala Gly Asn Ile Gly Gly Gly Gly Phe	
75 80 85	
GCG GTT ATC CAT TTG GCT AAT GGT GAA AAT GTT GCG TTA GAT TTT AGA	343
Ala Val Ile His Leu Ala Asn Gly Glu Asn Val Ala Leu Asp Phe Arg	
90 95 100	
GAA AAA GCC CCC TTA AAA GCC ACT AAA AAC ATG TTT TTA GAC AAG CAA	391
Glu Lys Ala Pro Leu Lys Ala Thr Lys Asn Met Phe Leu Asp Lys Gln	
105 110 115	
GGC AAT GTA GTC CCT AAA CTC AGC GAA GAT GGC TAT TTG GCG GCC GGG	439
Gly Asn Val Val Pro Lys Leu Ser Glu Asp Gly Tyr Leu Ala Ala Gly	
120 125 130 135	
GTT CCT GGA ACG GTG GCA GGC ATG GAA GCG ATG CTG AAA AAA TAC GGC	487
Val Pro Gly Thr Val Ala Gly Met Glu Ala Met Leu Lys Lys Tyr Gly	
140 145 150	
ACT AAA AAA CTA TCG CAA CTC ATT GAT CCT GCC ATT AAA TTG GCT GAA	535
Thr Lys Lys Leu Ser Gln Leu Ile Asp Pro Ala Ile Lys Leu Ala Glu	
155 160 165	
AAT GGT TAT GCG ATT TCA CAA AGA CAA GCA GAA ACC CTA AAG GAA GCA	583
Asn Gly Tyr Ala Ile Ser Gln Arg Gln Ala Glu Thr Leu Lys Glu Ala	
170 175 180	
AGG GAG CGG TTT TTA AAA TAC AGT TCT AGC AAA AAG TAT TTT TTT AAA	631
Arg Glu Arg Phe Leu Lys Tyr Ser Ser Ser Lys Lys Tyr Phe Phe Lys	
185 190 195	
AAA GGC CAT CTT GAT TAT CAA GAA GGG GAT TTG TTT GTC CAA AAA GAT	679
Lys Gly His Leu Asp Tyr Gln Glu Gly Asp Leu Phe Val Gln Lys Asp	
200 205 210 215	
TTA GCC AAG ACT TTG AAT CAA ATC AAA ACG CTA GGC GCT AAA GGC TTT	727
Leu Ala Lys Thr Leu Asn Gln Ile Lys Thr Leu Gly Ala Lys Gly Phe	
220 225 230	
TAT CAA GGG CAA GTC GCT GAG CTT ATT GAG AAA GAC ATG AAA AAA AAT	775
Tyr Gln Gly Gln Val Ala Glu Leu Ile Glu Lys Asp Met Lys Lys Asn	
235 240 245	
GGA GGG ATT ATC ACT AAA GAA GAT TTA GCC AGT TAC AAT GTG AAA TGG	823
Gly Gly Ile Ile Thr Lys Glu Asp Leu Ala Ser Tyr Asn Val Lys Trp	
250 255 260	

			100				105				110					
Trp	Val	Gly	Lys	His	Glu	Glu	Thr	Lys	Trp	Phe	Gly	Phe	Arg	Trp	Gly	
		115				120				125						
Leu	Phe	Tyr	Asp	Leu	Ser	Ala	Ser	Leu	Tyr	Gly	Gln	Lys	Glu	Ser	Gln	
	130				135				140							
Ser	Val	Ile	Ile	Ser	Thr	Tyr	Gly	Thr	Tyr	Met	Asp	Leu	Leu	Leu	Asn	
145					150				155						160	
Ala	Tyr	Asn	Gly	Asp	Lys	Phe	Phe	Ala	Gly	Phe	Asn	Leu	Gly	Ile	Ala	
			165				170				175					
Phe	Ala	Gly	Val	Tyr	Asp	Lys	Val	Ser	Asp	Ala	Leu	Leu	Tyr	Gln	Ala	
		180				185				190						
Leu	Leu	Leu	Asp	Thr	Phe	Gly	Gly	Lys	Val	Asp	Pro	Asn	Gly	Phe	Gln	
	195				200				205							
Phe	Leu	Val	Asn	Leu	Gly	Val	Arg	Leu	Gly	Asn	Lys	His	Asn	Gln	Phe	
	210				215				220							
Gly	Phe	Gly	Ile	Lys	Ile	Pro	Thr	Tyr	Tyr	Phe	Asn	His	Tyr	Tyr	Ser	
225				230				235							240	
Met	Asn	Asn	Ile	Ser	Asn	Asn	Ser	Glu	Asp	Val	Leu	Lys	Val	Leu	Arg	
			245				250				255					
Phe	Leu	Glu	Tyr	Gly	Ile	Asn	Ser	Leu	Leu	Tyr	Gln	Val	Asp	Phe	Arg	
	260				265				270							
Arg	Asn	Tyr	Ser	Val	Tyr	Phe	Asn	Tyr	Thr	Tyr	Ile	Phe				
	275				280				285							

(2) INFORMATION FOR SEO ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1840 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 35...1735
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

AAATTTTAAG	CGTAACTGAT	TGAAAGGAAA	ACAG	ATG	AGA	CGG	AGT	TTT	TTG	AAA	55					
				Met	Arg	Arg	Ser	Phe	Leu	Lys						
				1				5								
ACG	ATT	GGC	TTG	GGT	GTG	ATA	GCA	CTC	TTT	TTG	GGT	TTG	TTA	AAC	CCT	103
Thr	Ile	Gly	Leu	Gly	Val	Ile	Ala	Leu	Phe	Leu	Gly	Leu	Leu	Asn	Pro	
		10					15					20				
TTG	AGT	GCG	GCG	AGT	TAC	CCC	CCC	ATT	AAA	AAC	ACT	AAA	GTA	GGC	TTA	151
Leu	Ser	Ala	Ala	Ser	Tyr	Pro	Pro	Ile	Lys	Asn	Thr	Lys	Val	Gly	Leu	
		25				30					35					

180	185	190	
CTT CTT TTA GAC ACT TTT GGC GGG AAA GTG GAT CCA AAT GGC TTC CAG			624
Leu Leu Leu Asp Thr Phe Gly Gly Lys Val Asp Pro Asn Gly Phe Gln			
195	200	205	
TTT TTG GTA AAT TTA GGG GTT CGT TTA GGG AAT AAG CAC AAC CAA TTT			672
Phe Leu Val Asn Leu Gly Val Arg Leu Gly Asn Lys His Asn Gln Phe			
210	215	220	
GGC TTT GGG ATT AAA ATC CCT ACT TAT TAT TTT AAC CAT TAT TAT TCC			720
Gly Phe Gly Ile Lys Ile Pro Thr Tyr Tyr Phe Asn His Tyr Tyr Ser			
225	230	235	240
ATG AAT AAC ATT AGC AAT AAT AGT GAA GAT GTC CTC AAA GTT TTA CGA			768
Met Asn Asn Ile Ser Asn Asn Ser Glu Asp Val Leu Lys Val Leu Arg			
245	250	255	
TTT TTA GAA TAC GGG ATC AAC AGC TTG TTA TAC CAA GTT GAT TTC AGG			816
Phe Leu Glu Tyr Gly Ile Asn Ser Leu Leu Tyr Gln Val Asp Phe Arg			
260	265	270	
CGC AAT TAC TCG GTT TAT TTC AAC TAC ACT TAT ATT TTT TAAGCGATAG CG			867
Arg Asn Tyr Ser Val Tyr Phe Asn Tyr Thr Tyr Ile Phe			
275	280	285	
TTTAAAGCGT TCTTAATTGA GCGATTTTCGT CTCTCAAACG CATCGCTTCT TCAAAATCCA			927
AATTCTTCGT GCATTCTCGC A			948

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

Lys Ile Glu Val Leu Arg Gly Phe Leu Lys Arg Ala Leu Tyr Leu Ile
 1 5 10 15
 Leu Gly Leu Phe Tyr Thr Leu Asn Ala Glu Ser Phe Lys Asp Val Leu
 20 25 30
 Thr Lys Val Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile
 35 40 45
 Lys Arg Tyr Ala Asp Arg Ser Ala Phe Tyr Leu Gly Leu Gly Tyr Gln
 50 55 60
 Leu Gly Ser Ile Gln His Asn Ser Ser Asn Leu Asn Leu Ser Gln Gln
 65 70 75 80
 Phe Asn Lys Ser Gln Ile Ile Phe Ser Asp Ser Leu Ser Pro Val Phe
 85 90 95
 Lys Asn Ser Tyr Val Ser Asn Gly Leu Gly Val Gln Val Gly Tyr Lys

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...855
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

AAA ATT GAA GTT TTA AGG GGT TTT TTG AAA CGA GCG TTA TAC TTA ATT	48
Lys Ile Glu Val Leu Arg Gly Phe Leu Lys Arg Ala Leu Tyr Leu Ile	
1 5 10 15	
TTA GGG CTT TTT TAC ACG CTT AAT GCA GAG AGC TTT AAA GAT GTT TTG	96
Leu Gly Leu Phe Tyr Thr Leu Asn Ala Glu Ser Phe Lys Asp Val Leu	
20 25 30	
ACT AAA GTG GAT TAC ACT TTT TTT AAT AAA AAG GTG GTT TCG CCC ATC	144
Thr Lys Val Asp Tyr Thr Phe Phe Asn Lys Lys Val Val Ser Pro Ile	
35 40 45	
AAA CGC TAT GCG GAT AGA TCG GCG TTT TAT CTG GGG CTT GGG TAT CAA	192
Lys Arg Tyr Ala Asp Arg Ser Ala Phe Tyr Leu Gly Leu Gly Tyr Gln	
50 55 60	
TTA GGG AGC ATT CAG CAC AAC TCT AGC AAC TTG AAT TTA TCC CAG CAA	240
Leu Gly Ser Ile Gln His Asn Ser Ser Asn Leu Asn Leu Ser Gln Gln	
65 70 75 80	
TTC AAT AAG AGT CAG ATT ATT TTC AGC GAT AGT CTA AGC CCT GTT TTT	288
Phe Asn Lys Ser Gln Ile Ile Phe Ser Asp Ser Leu Ser Pro Val Phe	
85 90 95	
AAA AAT TCG TAT GTG TCT AAT GGC CTT GGC GTG CAA GTG GGC TAT AAG	336
Lys Asn Ser Tyr Val Ser Asn Gly Leu Gly Val Gln Val Gly Tyr Lys	
100 105 110	
TGG GTG GGT AAG CAT GAA GAG ACG AAA TGG TTT GGC TTC AGG TGG GGG	384
Trp Val Gly Lys His Glu Glu Thr Lys Trp Phe Gly Phe Arg Trp Gly	
115 120 125	
CTG TTT TAT GAT TTG AGC GCC TCT CTT TAT GGC CAA AAA GAA TCA CAG	432
Leu Phe Tyr Asp Leu Ser Ala Ser Leu Tyr Gly Gln Lys Glu Ser Gln	
130 135 140	
TCT GTC ATC ATT TCC ACT TAC GGC ACT TAT ATG GAT TTA TTA TTG AAC	480
Ser Val Ile Ile Ser Thr Tyr Gly Thr Tyr Met Asp Leu Leu Leu Asn	
145 150 155 160	
GCT TAT AAT GGG GAT AAG TTT TTT GCT GGG TTC AAT CTG GGG ATT GCT	528
Ala Tyr Asn Gly Asp Lys Phe Phe Ala Gly Phe Asn Leu Gly Ile Ala	
165 170 175	
TTT GCT GGA GTG TAT GAC AAA GTG AGC GAT GCG TTA TTG TAT CAA GCC	576
Phe Ala Gly Val Tyr Asp Lys Val Ser Asp Ala Leu Leu Tyr Gln Ala	

65					70					75					80
Arg	Val	Ser	Thr	Ala	Thr	Ser	Ser	Gln	Gly	Leu	Ala	Leu	Met	Val	Glu
				85					90					95	
Val	Leu	Tyr	Gln	Ala	Ser	Gly	Met	Arg	Leu	Pro	Ile	Val	Leu	Asn	Leu
			100					105					110		
Val	Asn	Arg	Ala	Leu	Ala	Ala	Pro	Leu	Asn	Ile	His	Gly	Asp	His	Ser
		115					120					125			
Asp	Met	Tyr	Leu	Ser	Arg	Asp	Ser	Gly	Trp	Ile	Ser	Leu	Cys	Thr	Cys
	130					135					140				
Asn	Pro	Gln	Glu	Ala	Tyr	Asp	Phe	Thr	Leu	Met	Ala	Phe	Arg	Ile	Ala
145					150				155					160	
Glu	His	Gln	Lys	Val	Arg	Val	Pro	Thr	Ile	Val	Asn	Gln	Asp	Gly	Phe
			165						170					175	
Leu	Cys	Ser	His	Thr	Val	Gln	Asn	Val	Arg	Pro	Leu	Ser	Asp	Ala	Val
			180					185					190		
Ala	Tyr	Gln	Phe	Val	Gly	Glu	Tyr	Gln	Thr	Lys	His	Ser	Leu	Leu	Asp
	195						200					205			
Phe	Asp	Lys	Pro	Val	Ser	Tyr	Gly	Ala	Gln	Ala	Glu	Glu	Glu	Trp	His
	210					215					220				
Tyr	Glu	His	Lys	Ala	Gln	Leu	His	His	Ala	Ile	Met	Ser	Ala	Ser	Ser
225					230				235					240	
Val	Ile	Glu	Glu	Val	Phe	Asn	Asp	Phe	Ala	Lys	Leu	Thr	Gly	Arg	Gln
			245					250					255		
Tyr	His	Leu	Thr	Lys	Thr	Phe	Gln	Leu	Glu	Asp	Ala	Glu	Ile	Ala	Ile
		260					265					270			
Phe	Ala	Leu	Gly	Thr	Thr	Tyr	Glu	Ser	Ala	Ile	Val	Ala	Ala	Lys	Glu
	275					280					285				
Met	Arg	Lys	Lys	Gly	Ile	Lys	Ala	Gly	Val	Ala	Thr	Ile	His	Ser	Leu
	290				295						300				
Arg	Pro	Phe	Pro	Tyr	Glu	Arg	Leu	Gly	Gln	Asp	Leu	Lys	Asn	Leu	Lys
305					310				315					320	
Ala	Leu	Ala	Ile	Leu	Asp	Lys	Ser	Ser	Pro	Ala	Gly	Thr	Met	Gly	Ala
			325					330					335		
Met	Phe	Asn	Glu	Val	Thr	Ser	Ala	Val	Tyr	Gln	Thr	Gln	Gly	Thr	Lys
		340					345					350			
His	Pro	Val	Val	Ser	Asn	Tyr	Ile	Tyr	Gly	Leu	Gly	Glu	Arg	Asp	Met
	355					360					365				
Thr	Ile	Ala	His	Leu	Cys	Glu	Ile	Phe	Glu	Glu	Ile	Asn	Glu	Asp	Ala
	370				375				380						
Leu	Lys	Gly	Thr	Leu	Thr	His	Pro	Thr	Gln	Gln	Phe	Val	Gly	Leu	His
385				390				395					400		
Gly	Pro	Lys	Met	Ser	Phe	Phe									
				405											

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

Val Ala Ala Lys Glu Met Arg Lys Lys Gly Ile Lys Ala Gly Val Ala
 285 290 295

ACC ATC CAT TCC TTG CGC CCC TTC CCT TAT GAA AGA TTA GGG CAG GAT 1022
 Thr Ile His Ser Leu Arg Pro Phe Pro Tyr Glu Arg Leu Gly Gln Asp
 300 305 310 315

TTG AAA AAT CTT AAA GCT TTA GCG ATT TTA GAC AAG AGC TCT CCA GCG 1070
 Leu Lys Asn Leu Lys Ala Leu Ala Ile Leu Asp Lys Ser Ser Pro Ala
 320 325 330

GGC ACT ATG GGG GCG ATG TTT AAT GAA GTA ACG AGC GCG GTG TAT CAA 1118
 Gly Thr Met Gly Ala Met Phe Asn Glu Val Thr Ser Ala Val Tyr Gln
 335 340 345

ACG CAA GGG ACT AAA CAC CCC GTG GTG TCT AAC TAC ATT TAT GGT TTA 1166
 Thr Gln Gly Thr Lys His Pro Val Val Ser Asn Tyr Ile Tyr Gly Leu
 350 355 360

GGC GAA AGG GAT ATG ACG ATC GCG CAT TTA TGC GAA ATT TTT GAA GAA 1214
 Gly Glu Arg Asp Met Thr Ile Ala His Leu Cys Glu Ile Phe Glu Glu
 365 370 375

ATC AAT GAA GAC GCT CTT AAA GGC ACG CTC ACG CAC CCT ACC CAA CAA 1262
 Ile Asn Glu Asp Ala Leu Lys Gly Thr Leu Thr His Pro Thr Gln Gln
 380 385 390 395

TTC GTA GGC TTG CAC GGC CCT AAA ATG AGC TTT TTT TAAAAAGGAA ATATCA 1314
 Phe Val Gly Leu His Gly Pro Lys Met Ser Phe Phe
 400 405

TGGTAAAAGA AGTCAAAACA CTCAAAGGTT TTAGC 1349

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Met Ala Lys Ser Ile Glu Leu Gln Glu Ile Glu Val Trp Asp Gly Asn
 1 5 10 15
 Thr Ala Ser Ser Asn Ala Leu Arg Gln Ala Gln Ile Asp Val Ile Ala
 20 25 30
 Ala Tyr Pro Ile Thr Pro Ser Thr Pro Ile Val Gln Asn Tyr Gly Ser
 35 40 45
 Phe Lys Asp Asn Gly Tyr Val Asp Gly Glu Phe Val Leu Val Glu Ser
 50 55 60
 Glu His Ala Ala Met Ser Ala Cys Val Gly Ala Ala Ala Ala Gly Gly

60	65	70	75	
GCC GCA GCT GGA GGG AGA GTC AGC ACT GCG ACT AGC TCT CAA GGT TTG				350
Ala Ala Ala Gly Gly Arg Val Ser Thr Ala Thr Ser Ser Gln Gly Leu	80	85	90	
GCG TTA ATG GTA GAG GTT TTA TAC CAG GCT TCT GGA ATG CGT TTG CCT				398
Ala Leu Met Val Glu Val Leu Tyr Gln Ala Ser Gly Met Arg Leu Pro	95	100	105	
ATC GTT TTG AAT TTA GTC AAT CGT GCT TTA GCA GCC CCT TTG AAT ATC				446
Ile Val Leu Asn Leu Val Asn Arg Ala Leu Ala Ala Pro Leu Asn Ile	110	115	120	
CAT GGC GAT CAT TCT GAT ATG TAT TTA AGC AGG GAT TCT GGT TGG ATA				494
His Gly Asp His Ser Asp Met Tyr Leu Ser Arg Asp Ser Gly Trp Ile	125	130	135	
AGT TTA TGC ACA TGC AAC CCC CAA GAA GCT TAT GAT TTC ACT TTA ATG				542
Ser Leu Cys Thr Cys Asn Pro Gln Glu Ala Tyr Asp Phe Thr Leu Met	140	145	150	155
GCG TTT AGA ATC GCA GAG CAT CAA AAG GTG CGC GTG CCT ACT ATT GTC				590
Ala Phe Arg Ile Ala Glu His Gln Lys Val Arg Val Pro Thr Ile Val	160	165	170	
AAT CAA GAC GGG TTT TTA TGC TCG CAC ACC GTG CAA AAT GTC CGC CCT				638
Asn Gln Asp Gly Phe Leu Cys Ser His Thr Val Gln Asn Val Arg Pro	175	180	185	
TTG AGC GAT GCA GTG GCT TAC CAA TTC GTG GGC GAA TAC CAA ACC AAG				686
Leu Ser Asp Ala Val Ala Tyr Gln Phe Val Gly Glu Tyr Gln Thr Lys	190	195	200	
CAT TCC CTT TTG GAT TTT GAT AAA CCG GTA AGC TAT GGC GCG CAA GCT				734
His Ser Leu Leu Asp Phe Asp Lys Pro Val Ser Tyr Gly Ala Gln Ala	205	210	215	
GAA GAA GAA TGG CAT TAT GAG CAT AAA GCC CAA CTC CAC CAT GCC ATC				782
Glu Glu Glu Trp His Tyr Glu His Lys Ala Gln Leu His His Ala Ile	220	225	230	235
ATG AGC GCG TCT TCT GTG ATT GAA GAA GTG TTC AAT GAT TTC GCT AAA				830
Met Ser Ala Ser Ser Val Ile Glu Glu Val Phe Asn Asp Phe Ala Lys	240	245	250	
CTC ACA GGC AGG CAA TAC CAT TTA ACC AAA ACT TTC CAG CTA GAA GAC				878
Leu Thr Gly Arg Gln Tyr His Leu Thr Lys Thr Phe Gln Leu Glu Asp	255	260	265	
GCT GAA ATC GCT ATC TTT GCG TTA GGC ACT ACT TAT GAA TCA GCG ATC				926
Ala Glu Ile Ala Ile Phe Ala Leu Gly Thr Thr Tyr Glu Ser Ala Ile	270	275	280	
GTA GCG GCT AAA GAA ATG CGT AAA AAA GGC ATT AAG GCC GGC GTG GCT				974

```

      115              120              125
Lys Lys Glu His Tyr Lys Pro Ile Lys Asn Ile Arg Lys Ser Lys Trp
      130              135              140
Tyr Ala Tyr Leu Glu Ala Leu Gly Leu Glu Lys Phe Phe Gln Tyr Thr
145              150              155              160
Trp Asp Thr Lys Lys Asn Asn Lys Lys Lys Leu Ile Ile Asp Asp
      165              170              175
Lys Asp Gly Asp Glu Ile Glu Ile Lys Asp Gln Tyr Lys Gly Asp Tyr
      180              185              190
Glu Glu Leu Lys Lys Val Leu Asp Leu Asn Ser Lys Ser Leu Ile Pro
      195              200              205
Leu Lys Asn Phe Leu Gly Gln Phe Ala Glu Asn Asn Gln Lys Thr Asn
      210              215              220
Pro Lys Ile Phe
225

```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 78...1298
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```

AAGAACAAAT TGAGCCTGCT ACCGCTCTCA CTCAATGGCC GCAAAAACAA GAAAAGAAAA      60
AATCATAAGG AAAAAAT ATG GCA AAA AGT ATT GAA TTG CAA GAG ATA GAA      110
      Met Ala Lys Ser Ile Glu Leu Gln Glu Ile Glu
              1              5              10

GTG TGG GAT GGC AAT ACC GCT AGT TCT AAC GCT TTA AGA CAG GCT CAA      158
Val Trp Asp Gly Asn Thr Ala Ser Ser Asn Ala Leu Arg Gln Ala Gln
      15              20              25

ATT GAT GTC ATC GCA GCC TAT CCT ATC ACC CCA TCA ACG CCC ATT GTG      206
Ile Asp Val Ile Ala Ala Tyr Pro Ile Thr Pro Ser Thr Pro Ile Val
      30              35              40

CAA AAT TAT GGC TCG TTT AAG GAT AAT GGC TAT GTT GAT GGC GAA TTC      254
Gln Asn Tyr Gly Ser Phe Lys Asp Asn Gly Tyr Val Asp Gly Glu Phe
      45              50              55

GTT TTA GTG GAA TCT GAG CAT GCC GCC ATG AGC GCA TGC GTG GGA GCT      302
Val Leu Val Glu Ser Glu His Ala Ala Met Ser Ala Cys Val Gly Ala

```

```

AAA AAC ATA AGA AAA AGT AAG TGG TAT GCC TAT TTA GAA GCG CTT GGA      486
Lys Asn Ile Arg Lys Ser Lys Trp Tyr Ala Tyr Leu Glu Ala Leu Gly
      140                      145                      150

TTA GAA AAA TTT TTC CAA TAC ACA TGG GAC ACA AAG AAA AAG AAT AAT      534
Leu Glu Lys Phe Phe Gln Tyr Thr Trp Asp Thr Lys Lys Lys Asn Asn
      155                      160                      165

AAA AAA AAG CTT ATC ATT GAC GAT AAA GAT GGA GAT GAG ATT GAG ATA      582
Lys Lys Lys Leu Ile Ile Asp Asp Lys Asp Gly Asp Glu Ile Glu Ile
      170                      175                      180

AAA GAT CAA TAT AAA GGA GAT TAT GAA GAA CTA AAA AAA GTT CTT GAT      630
Lys Asp Gln Tyr Lys Gly Asp Tyr Glu Glu Leu Lys Lys Val Leu Asp
      185                      190                      195                      200

CTT AAC TCA AAA TCT CTT ATT CCC CTT AAA AAT TTT TTA GGG CAA TTT      678
Leu Asn Ser Lys Ser Leu Ile Pro Leu Lys Asn Phe Leu Gly Gln Phe
      205                      210                      215

GCA GAA AAT AAT CAA AAA ACA AAT CCT AAA ATT TTC TAATTTAACA AAATAT      730
Ala Glu Asn Asn Gln Lys Thr Asn Pro Lys Ile Phe
      220                      225

ATTACAATTA CCAAAAAAGT ATTATTTTTC TTAAAAGGTG CGCTGTGAAA TTGTGGTTTC      790
CTTATTTTTT AGCGATTGTG TTCTTGCATG CATTGGGTTT      830

```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

```

Met Ala Asp Lys Glu Ile Leu Ile Phe Val Glu Gly Pro Ser Asp Lys
 1           5           10           15
Val Phe Leu Glu Val Tyr Leu Tyr Phe Leu Glu Arg Phe Pro Ile Lys
      20           25           30
Asn Phe Lys Val Gln Asn Val Asp Gly Lys Asp Asn Leu Ser Lys Arg
      35           40           45
Leu Leu Glu Ile Glu Lys Tyr Asp Lys Thr Leu Ile Ile Phe Asp Ala
      50           55           60
Asp Lys Asp Tyr Glu Ser Asn Lys Lys Glu Ile Leu Lys Ile Val Ser
      65           70           75           80
Glu Ser Lys Gln Thr Ile Ser Glu Glu Gln Ile Phe Leu Phe Pro Asn
      85           90           95
Asn Gln Asp Asp Gly Asp Leu Glu Thr Leu Leu Leu Lys Ile Ala Asn
      100          105          110
His Lys Glu Phe Ile Asn Cys Phe Glu Ser Tyr Leu Asp Cys Ile Lys

```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...714
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```

AAAGCACTAT ATTAAGATTA GGATCATTTA  ATG GCA GAT AAA GAA ATA CTG ATT      54
                               Met Ala Asp Lys Glu Ile Leu Ile
                               1             5

TTT GTA GAA GGT CCA AGC GAT AAG GTG TTT TTA GAA GTT TAT CTG TAT      102
Phe Val Glu Gly Pro Ser Asp Lys Val Phe Leu Glu Val Tyr Leu Tyr
 10             15             20

TTT CTA GAA AGA TTT CCA ATC AAA AAC TTT AAA GTG CAA AAT GTA GAT      150
Phe Leu Glu Arg Phe Pro Ile Lys Asn Phe Lys Val Gln Asn Val Asp
25             30             35             40

GGA AAA GAT AAC CTG TCT AAA CGA TTG CTT GAA ATT GAA AAA TAC GAT      198
Gly Lys Asp Asn Leu Ser Lys Arg Leu Leu Glu Ile Glu Lys Tyr Asp
              45             50             55

AAA ACA CTT ATC ATT TTT GAT GCG GAT AAA GAC TAT GAG AGT AAT AAA      246
Lys Thr Leu Ile Ile Phe Asp Ala Asp Lys Asp Tyr Glu Ser Asn Lys
              60             65             70

AAA GAG ATT TTA AAA ATT GTA TCA GAA TCG AAA CAA ACT ATT TCA GAA      294
Lys Glu Ile Leu Lys Ile Val Ser Glu Ser Lys Gln Thr Ile Ser Glu
 75             80             85

GAA CAA ATT TTT TTA TTT CCT AAT AAT CAA GAT GAT GGC GAT TTA GAA      342
Glu Gln Ile Phe Leu Phe Pro Asn Asn Gln Asp Asp Gly Asp Leu Glu
 90             95             100

ACC CTA TTA TTA AAG ATT GCT AAC CAC AAA GAG TTC ATA AAT TGT TTT      390
Thr Leu Leu Leu Lys Ile Ala Asn His Lys Glu Phe Ile Asn Cys Phe
105             110             115             120

GAA AGC TAT TTG GAT TGT ATT AAA AAG AAA GAA CAT TAC AAA CCG ATT      438
Glu Ser Tyr Leu Asp Cys Ile Lys Lys Lys Glu His Tyr Lys Pro Ile
              125             130             135

```

```

Thr Tyr Phe Arg Ala Ile Gly Lys Phe Gly Val Gln Phe Arg Thr Ile
      140                      145                      150

GTT TTG TAT CAT AAG GTG GAT GTA GAA ATT GGC ATG AAA ATC TTT CTA      534
Val Leu Tyr His Lys Val Asp Val Glu Ile Gly Met Lys Ile Phe Leu
      155                      160                      165

ACT CCT GAA AGG CGC AGT TTG TTT GAA AGG AGC TTT TTG TTT TTT GTT      582
Thr Pro Glu Arg Arg Ser Leu Phe Glu Arg Ser Phe Leu Phe Phe Val
      170                      175                      180

TCG CAT TCG TGG CAT TTT TAAATGGCGG AGAGAGAGGG ATTCTGAACCC TCGAAGGC      638
Ser His Ser Trp His Phe
185                      190

TTGCACCTTA CACGCGT
                                         655

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```

Met Ser Phe Leu Asn Ile Leu Asn Ala Glu Asn Leu Ser Tyr Met Ser
  1              5              10              15
Ser Ser Tyr Gln Ile Gly Thr Val Phe Met Arg Pro Leu Asn Thr Asn
      20              25              30
Lys Leu Leu Gln Gly Ala Ser Ile Leu Gln Gly Tyr Glu Val Asn Pro
      35              40              45
Lys Asn Asp Trp Ala Tyr Ser Arg Tyr Tyr Phe Phe Ile Asp Tyr Gly
      50              55              60
Asn Val Leu Phe Asn Asn Asp Ser Thr Leu Gln Ala Asn Met Phe Thr
      65              70              75              80
Tyr Gly Val Gly Gly Asp Phe Met Val Ala Tyr Ala Lys Asn Pro Ile
      85              90              95
Asn Arg Trp Ala Phe Phe Phe Gly Leu Gln Leu Ala Ala Asn Thr Trp
      100             105             110
Ile Leu Asn Asn Lys Val Lys Asp Leu Val Val Asn Thr Trp Asp Ser
      115             120             125
Leu Lys Asp Phe Asn Phe His Asn Thr Tyr Phe Arg Ala Ile Gly Lys
      130             135             140
Phe Gly Val Gln Phe Arg Thr Ile Val Leu Tyr His Lys Val Asp Val
      145             150             155             160
Glu Ile Gly Met Lys Ile Phe Leu Thr Pro Glu Arg Arg Ser Leu Phe
      165             170             175
Glu Arg Ser Phe Leu Phe Phe Val Ser His Ser Trp His Phe
      180             185             190

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...600
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GTGCATTATT TAAGAATTTT AATACTGAGT	ATG AGT TTT TTA AAT ATT TTA AAT	54
	Met Ser Phe Leu Asn Ile Leu Asn	
	1 5	
GCT GAA AAT TTG AGT TAT ATG TCT TCT TCT TAT CAA ATA GGC ACG GTG		102
Ala Glu Asn Leu Ser Tyr Met Ser Ser Ser Tyr Gln Ile Gly Thr Val		
10 15 20		
TTT ATG CGC CCT TTA AAC ACC AAC AAG CTT TTA CAA GGG GCT TCA ATC		150
Phe Met Arg Pro Leu Asn Thr Asn Lys Leu Leu Gln Gly Ala Ser Ile		
25 30 35 40		
CTT CAA GGC TAT GAA GTG AAT CCT AAA AAC GAT TGG GCT TAT TCT AGG		198
Leu Gln Gly Tyr Glu Val Asn Pro Lys Asn Asp Trp Ala Tyr Ser Arg		
45 50 55		
TAT TAT TTC TTT ATA GAT TAT GGC AAT GTG CTT TTT AAT AAT GAC TCT		246
Tyr Tyr Phe Phe Ile Asp Tyr Gly Asn Val Leu Phe Asn Asn Asp Ser		
60 65 70		
ACT TTA CAA GCG AAC ATG TTC ACT TAT GGG GTG GGA GGG GAT TTT ATG		294
Thr Leu Gln Ala Asn Met Phe Thr Tyr Gly Val Gly Gly Asp Phe Met		
75 80 85		
GTC GCC TAC GCT AAA AAC CCT ATC AAC CGC TGG GCT TTT TTC TTT GGC		342
Val Ala Tyr Ala Lys Asn Pro Ile Asn Arg Trp Ala Phe Phe Phe Gly		
90 95 100		
TTG CAA CTG GCC GCT AAC ACA TGG ATA CTC AAC AAT AAA GTC AAA GAT		390
Leu Gln Leu Ala Ala Asn Thr Trp Ile Leu Asn Asn Lys Val Lys Asp		
105 110 115 120		
TTG GTG GTG AAT ACT TGG GAT TCA TTA AAA GAT TTC AAT TTT CAC AAC		438
Leu Val Val Asn Thr Trp Asp Ser Leu Lys Asp Phe Asn Phe His Asn		
125 130 135		
ACT TAT TTC AGG GCT ATT GGG AAG TTT GGG GTG CAG TTT CGC ACG ATC		486

AAT AAC ACC AAA GAG AAT ACA AAG AGC GAG TCG TAGTTGAAAG AATTTGATTT 889
 Asn Asn Thr Lys Glu Asn Thr Lys Ser Glu Ser
 245 250

AGAAAGCTAT GATTATTATT TGCCTAAGGA ATTGATCGCA AGCTACCCCG TTTTGCCCAA 949
 AGAAAAGGCT AAATTACTCG TCTATGAAAG GCGTTCGCAA 989

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

Met	Phe	Glu	Asp	Leu	Lys	Pro	His	Leu	Gln	Glu	Leu	Arg	Lys	Arg	Leu
1				5					10					15	
Met	Val	Ser	Val	Gly	Thr	Ile	Leu	Val	Ala	Phe	Leu	Gly	Cys	Phe	His
			20					25					30		
Phe	Trp	Lys	Ser	Ile	Phe	Glu	Phe	Val	Lys	Asn	Ser	Tyr	Lys	Gly	Thr
		35					40					45			
Leu	Ile	Gln	Leu	Ser	Pro	Ile	Glu	Gly	Val	Met	Val	Ala	Val	Lys	Ile
	50					55				60					
Ser	Phe	Ser	Ala	Ala	Ile	Val	Ile	Ser	Met	Pro	Ile	Ile	Phe	Trp	Gln
65					70					75				80	
Leu	Trp	Leu	Phe	Ile	Ala	Pro	Gly	Leu	Tyr	Lys	Asn	Glu	Lys	Lys	Val
				85					90					95	
Ile	Leu	Pro	Phe	Val	Phe	Phe	Gly	Ser	Gly	Met	Phe	Leu	Ile	Gly	Ala
			100					105					110		
Ala	Phe	Ser	Tyr	Tyr	Val	Val	Phe	Pro	Phe	Ile	Ile	Glu	Tyr	Leu	Ala
		115					120					125			
Thr	Phe	Gly	Ser	Asp	Val	Phe	Ala	Ala	Asn	Ile	Ser	Ala	Ser	Ser	Tyr
	130					135					140				
Val	Ser	Phe	Phe	Thr	Arg	Leu	Ile	Leu	Gly	Phe	Gly	Val	Ala	Phe	Glu
145					150					155				160	
Leu	Pro	Val	Leu	Ala	Tyr	Phe	Leu	Ala	Lys	Val	Gly	Leu	Ile	Thr	Asp
			165						170					175	
Ala	Ser	Leu	Lys	Ala	Tyr	Phe	Lys	Tyr	Ala	Ile	Val	Val	Ile	Phe	Ile
		180						185					190		
Val	Ala	Ala	Ile	Ile	Thr	Pro	Pro	Asp	Val	Val	Ser	Gln	Ile	Phe	Met
		195					200					205			
Ala	Leu	Pro	Leu	Val	Gly	Leu	Tyr	Gly	Leu	Ser	Ile	Leu	Ile	Ala	Lys
	210					215					220				
Met	Val	Asn	Pro	Ala	Pro	Lys	Asp	Asn	Glu	Asn	Asn	Glu	Asn	Asn	
225					230					235					240
Asn	Glu	Asn	Asn	Thr	Lys	Glu	Asn	Thr	Lys	Ser	Glu	Ser			
				245						250					

(2) INFORMATION FOR SEQ ID NO:501:

TCT	GTA	GGA	ACG	ATT	CTA	GTG	GCG	TTT	TTG	GGG	TGC	TTT	CAT	TTT	TGG	212
Ser	Val	Gly	Thr	Ile	Leu	Val	Ala	Phe	Leu	Gly	Cys	Phe	His	Phe	Trp	
20						25					30					
AAA	AGT	ATT	TTT	GAA	TTT	GTT	AAA	AAT	TCC	TAT	AAA	GGC	ACG	CTC	ATT	260
Lys	Ser	Ile	Phe	Glu	Phe	Val	Lys	Asn	Ser	Tyr	Lys	Gly	Thr	Leu	Ile	
35				40						45				50		
CAG	CTC	TCC	CCT	ATT	GAA	GGG	GTC	ATG	GTA	GCG	GTT	AAA	ATC	AGT	TTT	308
Gln	Leu	Ser	Pro	Ile	Glu	Gly	Val	Met	Val	Ala	Val	Lys	Ile	Ser	Phe	
				55					60					65		
TCA	GCC	GCT	ATC	GTC	ATT	TCC	ATG	CCC	ATT	ATT	TTT	TGG	CAA	TTA	TGG	356
Ser	Ala	Ala	Ile	Val	Ile	Ser	Met	Pro	Ile	Ile	Phe	Trp	Gln	Leu	Trp	
			70					75					80			
CTC	TTT	ATC	GCT	CCA	GGG	CTT	TAC	AAG	AAT	GAA	AAA	AAA	GTG	ATT	TTG	404
Leu	Phe	Ile	Ala	Pro	Gly	Leu	Tyr	Lys	Asn	Glu	Lys	Lys	Val	Ile	Leu	
	85						90					95				
CCT	TTT	GTG	TTT	TTT	GGG	AGT	GGG	ATG	TTT	TTG	ATT	GGG	GCG	GCG	TTT	452
Pro	Phe	Val	Phe	Phe	Gly	Ser	Gly	Met	Phe	Leu	Ile	Gly	Ala	Ala	Phe	
100						105					110					
TCT	TAT	TAT	GTG	GTG	TTC	CCT	TTC	ATT	ATT	GAA	TAC	TTA	GCC	ACT	TTT	500
Ser	Tyr	Tyr	Val	Val	Phe	Pro	Phe	Ile	Ile	Glu	Tyr	Leu	Ala	Thr	Phe	
115					120					125				130		
GGG	AGC	GAT	GTG	TTT	GCG	GCT	AAT	ATT	TCT	GCG	TCC	AGT	TAC	GTG	AGC	548
Gly	Ser	Asp	Val	Phe	Ala	Ala	Asn	Ile	Ser	Ala	Ser	Ser	Tyr	Val	Ser	
				135					140					145		
TTT	TTC	ACG	CGC	TTG	ATT	TTA	GGC	TTT	GGC	GTG	GCG	TTT	GAA	TTG	CCT	596
Phe	Phe	Thr	Arg	Leu	Ile	Leu	Gly	Phe	Gly	Val	Ala	Phe	Glu	Leu	Pro	
			150					155					160			
GTT	TTG	GCG	TAT	TTT	TTG	GCT	AAA	GTG	GGC	TTG	ATT	ACT	GAT	GCG	AGC	644
Val	Leu	Ala	Tyr	Phe	Leu	Ala	Lys	Val	Gly	Leu	Ile	Thr	Asp	Ala	Ser	
		165					170					175				
TTG	AAA	GCG	TAT	TTT	AAA	TAC	GCT	ATT	GTA	GTG	ATT	TTT	ATT	GTA	GCA	692
Leu	Lys	Ala	Tyr	Phe	Lys	Tyr	Ala	Ile	Val	Val	Ile	Phe	Ile	Val	Ala	
	180					185					190					
GCC	ATT	ATC	ACT	CCC	CCT	GAT	GTG	GTG	AGT	CAA	ATC	TTT	ATG	GCG	TTG	740
Ala	Ile	Ile	Thr	Pro	Pro	Asp	Val	Val	Ser	Gln	Ile	Phe	Met	Ala	Leu	
195				200						205				210		
CCC	TTA	GTG	GGG	CTT	TAT	GGG	CTT	TCT	ATT	TTA	ATC	GCC	AAA	ATG	GTC	788
Pro	Leu	Val	Gly	Leu	Tyr	Gly	Leu	Ser	Ile	Leu	Ile	Ala	Lys	Met	Val	
				215					220					225		
AAT	CCG	GCT	CCC	AAA	GAT	AAC	GAA	AAT	AAC	AAC	GAA	AAT	AAT	AAC	GAA	836
Asn	Pro	Ala	Pro	Lys	Asp	Asn	Glu	Asn	Asn	Asn	Glu	Asn	Asn	Asn	Glu	
			230					235						240		

130	135	140
Thr Ile Lys Ile Asp Leu Pro Pro Phe Thr Leu Ile Gly Ala Thr Thr		
145	150	155
Arg Ala Gly Met Leu Ser Asn Pro Leu Arg Asp Arg Phe Gly Met Ser		160
	165	170
Phe Arg Met Gln Phe Tyr Asn Pro Ser Glu Leu Ala Leu Ile Ile Lys		175
	180	185
Lys Ala Ala Val Lys Leu Asn Gln Asp Ile Lys Gln Glu Ser Ala Asp		190
	195	200
Glu Ile Ala Lys Arg Ser Arg Gly Thr Pro Arg Ile Ala Leu Arg Leu		205
	210	215
Leu Lys Arg Val Arg Asp Phe Ala Leu Val Lys Asn Ser Ser Leu Met		220
225	230	235
Asp Leu Asn Ile Thr Leu His Ala Leu Asn Glu Leu Gly Val Asn Glu		240
	245	250
Leu Gly Phe Asp Glu Ala Asp Leu Ala Tyr Leu Ser Leu Leu Ala Asn		255
	260	265
Ala Gln Gly Lys Pro Val Gly Leu Asn Thr Ile Ala Ala Ser Met Arg		270
	275	280
Glu Asp Glu Gly Thr Ile Glu Asp Val Ile Glu Pro Phe Leu Leu Ala		285
	290	295
Asn Gly Tyr Leu Glu Arg Thr Ala Lys Gly Arg Ile Ala Thr Pro Lys		300
305	310	315
Thr His Glu Leu Leu Lys Ile Pro Thr Leu Asn Pro Gln Thr Leu Phe		320
	325	330
		335

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 111...869
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

AGTTTCCAAT GAAGAAGCCT TAAACAAAGA AGTTTCAAGC GATGAATCCC CTAAAGAAGT	60
CCAATTAGCA ACCGATAACA ACACCAAAGA ACACGACAAA GAAAAAGAGA ATG TTT	116
	Met Phe
	1
GAA GAT TTA AAA CCG CAT TTA CAG GAA TTA AGA AAG CGT TTG ATG GTT	164
Glu Asp Leu Lys Pro His Leu Gln Glu Leu Arg Lys Arg Leu Met Val	
5 10 15	

```

Leu Asn Glu Leu Gly Val Asn Glu Leu Gly Phe Asp Glu Ala Asp Leu
250                               255                               260

GCG TAT TTA TCT TTG TTG GCT AAC GCT CAA GGA AAG CCG GTG GGT TTG      928
Ala Tyr Leu Ser Leu Leu Ala Asn Ala Gln Gly Lys Pro Val Gly Leu
265                               270                               275                               280

AAC ACG ATT GCA GCA TCT ATG AGA GAA GAT GAA GGC ACG ATT GAA GAC      976
Asn Thr Ile Ala Ala Ser Met Arg Glu Asp Glu Gly Thr Ile Glu Asp
                285                               290                               295

GTG ATT GAG CCT TTT TTA CTC GCT AAT GGT TAT TTA GAG CGC ACC GCT      1024
Val Ile Glu Pro Phe Leu Leu Ala Asn Gly Tyr Leu Glu Arg Thr Ala
                300                               305                               310

AAA GGC AGA ATC GCC ACG CCT AAA ACC CAT GAG CTC TTA AAA ATC CCC      1072
Lys Gly Arg Ile Ala Thr Pro Lys Thr His Glu Leu Leu Lys Ile Pro
                315                               320                               325

ACT TTA AAC CCC CAA ACT TTA TTT TAATCTTGTT TAGAAAGAAA ATTACACTAC      1126
Thr Leu Asn Pro Gln Thr Leu Phe
                330                               335

AATAACGATA AAATTTTAAA GGGTGTAATA GTAGATTGTT ATGTT      1171

```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```

Met Lys Glu Arg Ile Val Asn Leu Glu Thr Leu Asp Phe Glu Ile Ser
1           5           10           15
Gln Glu Val Ser Leu Arg Pro Ser Leu Trp Glu Asp Phe Ile Gly Gln
20           25           30
Glu Lys Ile Lys Ser Asn Leu Gln Ile Ser Ile Cys Ala Ala Lys Lys
35           40           45
Arg Gln Glu Ser Leu Asp His Met Leu Phe Phe Gly Pro Pro Gly Leu
50           55           60
Gly Lys Thr Ser Ile Ser His Ile Ile Ala Lys Glu Met Glu Thr Asn
65           70           75           80
Ile Lys Ile Thr Ala Ala Pro Met Ile Glu Lys Ser Gly Asp Leu Ala
85           90           95
Ala Ile Leu Thr Asn Leu Gln Ala Lys Asp Ile Leu Phe Ile Asp Glu
100          105          110
Ile His Arg Leu Ser Pro Ala Ile Glu Glu Val Leu Tyr Pro Ala Met
115          120          125
Glu Asp Phe Arg Leu Asp Ile Ile Ile Gly Ser Gly Pro Ala Ala Gln

```

25	30	35	40	
ATT TCT ATT TGC GCG GCT AAA AAA CGC CAA GAA AGT TTG GAT CAC ATG				256
Ile Ser Ile Cys Ala Ala Lys Lys Arg Gln Glu Ser Leu Asp His Met	45	50	55	
CTT TTT TTT GGC CCG CCC GGT TTG GGT AAA ACT TCA ATC AGC CAT ATC				304
Leu Phe Phe Gly Pro Pro Gly Leu Gly Lys Thr Ser Ile Ser His Ile	60	65	70	
ATC GCT AAA GAA ATG GAA ACC AAT ATC AAG ATC ACC GCC GCT CCC ATG				352
Ile Ala Lys Glu Met Glu Thr Asn Ile Lys Ile Thr Ala Ala Pro Met	75	80	85	
ATA GAA AAA AGC GGT GAT TTA GCC GCC ATT TTG ACC AAT TTG CAA GCT				400
Ile Glu Lys Ser Gly Asp Leu Ala Ala Ile Leu Thr Asn Leu Gln Ala	90	95	100	
AAA GAC ATT CTT TTT ATT GAT GAA ATC CAC CGG CTC AGC CCA GCG ATT				448
Lys Asp Ile Leu Phe Ile Asp Glu Ile His Arg Leu Ser Pro Ala Ile	105	110	115	120
GAA GAG GTT TTA TAC CCG GCG ATG GAA GAT TTT AGG TTG GAT ATT ATC				496
Glu Glu Val Leu Tyr Pro Ala Met Glu Asp Phe Arg Leu Asp Ile Ile	125	130	135	
ATA GGC TCA GGC CCA GCG GCT CAA ACC ATT AAA ATT GAT TTA CCC CCT				544
Ile Gly Ser Gly Pro Ala Ala Gln Thr Ile Lys Ile Asp Leu Pro Pro	140	145	150	
TTC ACT CTC ATC GGC GCT ACC ACC AGA GCC GGA ATG CTC TCT AAC CCC				592
Phe Thr Leu Ile Gly Ala Thr Thr Arg Ala Gly Met Leu Ser Asn Pro	155	160	165	
TTA AGA GAC AGA TTT GGC ATG AGT TTT AGA ATG CAA TTT TAT AAC CCT				640
Leu Arg Asp Arg Phe Gly Met Ser Phe Arg Met Gln Phe Tyr Asn Pro	170	175	180	
AGC GAA CTG GCC CTC ATC ATT AAA AAA GCT GCC GTT AAA CTC AAC CAA				688
Ser Glu Leu Ala Leu Ile Ile Lys Lys Ala Ala Val Lys Leu Asn Gln	185	190	195	200
GAC ATC AAA CAA GAA AGT GCT GAT GAA ATC GCT AAA AGG AGT AGA GGC				736
Asp Ile Lys Gln Glu Ser Ala Asp Glu Ile Ala Lys Arg Ser Arg Gly	205	210	215	
ACG CCA AGG ATC GCT TTA AGG CTT TTA AAA AGG GTG CGC GAT TTT GCG				784
Thr Pro Arg Ile Ala Leu Arg Leu Leu Lys Arg Val Arg Asp Phe Ala	220	225	230	
CTA GTC AAA AAT TCA AGC TTG ATG GAT TTA AAC ATC ACT TTG CAT GCT				832
Leu Val Lys Asn Ser Ser Leu Met Asp Leu Asn Ile Thr Leu His Ala	235	240	245	
TTG AAT GAA TTA GGC GTG AAT GAA TTA GGC TTT GAT GAA GCG GAT TTG				880

```

      50              55              60
Met Val Arg Thr Asn Ser Ser Ser Ile Thr Gly Asn Ile Leu Asn Tyr
65              70              75              80
Leu Phe Ala Tyr Gly Leu Arg Phe Gly Tyr Gln Thr Phe Arg Pro Ser
      85              90              95
Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly Arg Arg Ile Tyr
      100              105              110
Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly Phe Gly Asp Val
      115              120              125
Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu Leu Asp Phe Pro
      130              135              140
Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly Tyr Met Gly Leu
145              150              155              160
Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr Ala Glu Trp Gly
      165              170              175
Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu Glu Lys Asn Arg
      180              185              190
Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro Phe Leu Gln Ser
      195              200              205
Asn Ser Ser Lys Glu Thr Trp Trp Gly Ala Met Ala Asn Ile Gly Tyr
      210              215              220
Gln Tyr Val Phe
225

```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 89...1096
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```

GGAAAGAATT GATTCAAAC GCTATCAAAC AATACGCTGA TGATGTGAAA AAGGGAAACT      60
TCCCTAACGA ATTAGAAAGT TATCATTA ATG AAA GAA CGG ATA GTC AAT TTA      112
              Met Lys Glu Arg Ile Val Asn Leu
              1              5

GAA ACT TTG GAT TTT GAA ATT TCT CAA GAA GTG AGT TTG CGC CCT AGT      160
Glu Thr Leu Asp Phe Glu Ile Ser Gln Glu Val Ser Leu Arg Pro Ser
      10              15              20

CTT TGG GAA GAT TTT ATC GGT CAA GAA AAG ATT AAA AGC AAT TTG CAA      208
Leu Trp Glu Asp Phe Ile Gly Gln Glu Lys Ile Lys Ser Asn Leu Gln

```

AGG CGC ATT TAT ATC CAA TAT TAT GGA GGA GCT CCT AAA AAA GCG GGC	447
Arg Arg Ile Tyr Ile Gln Tyr Tyr Gly Gly Ala Pro Lys Lys Ala Gly	
110 115 120	
TTT GGG GAT GTA GGG TTT CAA TCG GTT ATG CTG AAT GGG GAT TTT TTA	495
Phe Gly Asp Val Gly Phe Gln Ser Val Met Leu Asn Gly Asp Phe Leu	
125 130 135 140	
TTG GAT TTT CCT TTG CCT TTT GTG GGG AAA TAC CTT TAT ATG GGG GGT	543
Leu Asp Phe Pro Leu Pro Phe Val Gly Lys Tyr Leu Tyr Met Gly Gly	
145 150 155	
TAT ATG GGT TTA GGT TTG GGG GTT GTA GCG CAT GGG GTG AAT TAC ACG	591
Tyr Met Gly Leu Gly Leu Gly Val Val Ala His Gly Val Asn Tyr Thr	
160 165 170	
GCG GAA TGG GGG ATG TCT TTT AAC GCA GGA TTG GCT CTA ACG GTA TTA	639
Ala Glu Trp Gly Met Ser Phe Asn Ala Gly Leu Ala Leu Thr Val Leu	
175 180 185	
GAA AAA AAC CGC ATT GAA TTT GGA TTT AAA ATT TTG AAT AAT TTC CCT	687
Glu Lys Asn Arg Ile Glu Phe Gly Phe Lys Ile Leu Asn Asn Phe Pro	
190 195 200	
TTT TTG CAA TCT AAT TCT TCA AAA GAG ACT TGG TGG GGA GCT ATG GCA	735
Phe Leu Gln Ser Asn Ser Ser Lys Glu Thr Trp Trp Gly Ala Met Ala	
205 210 215 220	
AAC ATT GGG TAT CAA TAT GTG TTC TAAAAAATA AGAAATCTCA TTTTATGCTT	789
Asn Ile Gly Tyr Gln Tyr Val Phe	
225	
TGGTTTTATG TTGGGCTTGC ACGCTGAAGA AAATACGACT GAAGGAAATA TGACTGAAGA	849
AAATATCTCT AAAGACGCTC	869

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Met Gly Phe Tyr Ala Gly Leu Asn Ala Leu Asp Tyr Asp Thr Ile Asp	
1 5 10 15	
Pro Lys Tyr Tyr Lys Tyr Ile Lys Tyr Tyr Lys Ala Tyr Glu Asp Lys	
20 25 30	
Glu Val Glu Glu Leu Ile Arg Asp Leu Lys Arg Ala Asn Ala Lys Ser	
35 40 45	
Gly Leu Ile Leu Gly Ile Asn Thr Gly Phe Phe Tyr Asn His Glu Ile	

```

His Asp Tyr Asn Gly Tyr Val Lys Gln Asp Tyr Leu Glu Lys Pro Leu
      355                      360                      365
Asp Leu Val Ser Ser Gln Gly Ile Gly Phe Glu Lys Thr Leu Leu Glu
      370                      375                      380
Trp Leu Asp Lys Ile Arg Asn
385                      390

```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 76...759
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

```

AAGAACTTT TAACAAACAA TTCAAGGGAT TTGGCGATTT TGGGTCTTAA AAAATATGCT      60
ATTTTATGGT CTTTA ATG GGG TTT TAT GCA GGA TTG AAC GCG CTT GAT TAT      111
      Met Gly Phe Tyr Ala Gly Leu Asn Ala Leu Asp Tyr
              1              5              10

GAC ACC ATA GAC CCA AAA TAC TAC AAG TAT ATC AAG TAT TAT AAA GCC      159
Asp Thr Ile Asp Pro Lys Tyr Tyr Lys Tyr Ile Lys Tyr Tyr Lys Ala
      15              20              25

TAT GAG GAT AAA GAA GTT GAA GAA TTG ATC AGA GAC TTA AAA AGG GCG      207
Tyr Glu Asp Lys Glu Val Glu Glu Leu Ile Arg Asp Leu Lys Arg Ala
      30              35              40

AAC GCT AAA AGC GGG CTT ATT TTA GGG ATC AAT ACC GGG TTT TTT TAC      255
Asn Ala Lys Ser Gly Leu Ile Leu Gly Ile Asn Thr Gly Phe Phe Tyr
      45              50              55              60

AAT CAT GAA ATC ATG GTT AGA ACT AAT AGC TCT AGC ATC ACG GGG AAT      303
Asn His Glu Ile Met Val Arg Thr Asn Ser Ser Ser Ile Thr Gly Asn
      65              70              75

ATT TTA AAT TAT TTG TTC GCT TAC GGC TTG CGT TTT GGC TAT CAA ACT      351
Ile Leu Asn Tyr Leu Phe Ala Tyr Gly Leu Arg Phe Gly Tyr Gln Thr
      80              85              90

TTC AGG CCG TCG TTT TTT GCG CGC TTG GTC AAG CCA AAT ATC ATT GGC      399
Phe Arg Pro Ser Phe Phe Ala Arg Leu Val Lys Pro Asn Ile Ile Gly
      95              100              105

```


(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

```

Met Ser Leu Thr Ser Leu Leu Asn Pro Lys Ser Leu Glu Asp Phe Leu
 1           5           10          15
Gly Gln Glu His Leu Val Gly Lys Asp Ala Pro Leu Phe Lys Ala Leu
          20          25          30
Gln Ser Lys His Phe Pro His Ala Phe Phe Tyr Gly Pro Pro Gly Val
          35          40          45
Gly Lys Thr Ser Leu Ala Gln Ile Ile Ala Tyr Met Leu Glu Arg Pro
          50          55          60
Ile Leu Leu Phe Asn Ala Thr Asp Phe Lys Leu Glu Asp Leu Arg Leu
65          70          75          80
Lys Leu Lys Asn Tyr Gln Asn Thr Leu Leu Lys Pro Val Val Phe Ile
          85          90          95
Asp Glu Thr His Arg Leu Asn Lys Thr Gln Gln Glu Phe Leu Leu Pro
          100         105         110
Ile Met Glu Lys Asp His Ala Leu Ile Leu Gly Ala Ser Thr Gln Asp
          115         120         125
Pro Asn Tyr Ser Leu Ser His Ala Ile Arg Ser Arg Ser Phe Ile Phe
          130         135         140
Glu Leu Thr Pro Leu Asn Lys Ser Asp Leu Asp Arg Leu Cys Ala Lys
145         150         155         160
Ala Leu Thr Leu Leu Lys Lys Gln Ile Glu Pro Gly Ala Lys Thr Tyr
          165         170         175
Leu Leu Asn Asn Ser Ala Gly Asp Ala Arg Ala Leu Leu Asn Leu Leu
          180         185         190
Asp Leu Ser Ala Lys Ile Glu Asp Pro Ile Thr Leu Lys Thr Leu Gln
          195         200         205
Ser Leu Arg Pro His Ser Leu Asn Asp Gly Ser Tyr Ser Asp Asp Thr
          210         215         220
His Tyr Asn Leu Thr Ser Ala Leu Ile Lys Ser Leu Arg Gly Ser Asp
225         230         235         240
Glu Asn Ala Ser Ile Tyr Tyr Leu Ala Arg Leu Ile Ala Gly Gly Glu
          245         250         255
Asn Pro Glu Phe Ile Ala Arg Arg Leu Val Ile Phe Ala Ser Glu Asp
          260         265         270
Ile Gly Asn Ala Asn Pro Asn Ala Leu Asn Leu Ala Ala Ser Cys Leu
          275         280         285
Phe Ala Val Lys Gln Ile Gly Tyr Pro Glu Ala Arg Ile Ile Leu Ser
          290         295         300
Gln Cys Val Ile Tyr Leu Ala Cys Ser Pro Lys Ser Asn Thr Ala Tyr
305         310         315         320
Arg Ala Ile Asn Gln Ala Leu Asp Cys Val Gln Lys Gly Ser Leu Tyr
          325         330         335
Pro Ile Pro Lys His Leu Leu Pro Asn Ala Lys Asp Tyr Leu Tyr Pro
          340         345         350

```

AGC GCT AAA ATA GAA GAT CCT ATC ACT TTA AAA ACG CTA CAA TCC TTA	742
Ser Ala Lys Ile Glu Asp Pro Ile Thr Leu Lys Thr Leu Gln Ser Leu	
195 200 205 210	
CGG CCT CAT AGC CTA AAT GAT GGA TCT TAT AGC GAT GAT ACG CAT TAT	790
Arg Pro His Ser Leu Asn Asp Gly Ser Tyr Ser Asp Asp Thr His Tyr	
215 220 225	
AAC CTT ACT AGC GCG TTA ATC AAA TCT TTA AGA GGG AGC GAT GAA AAC	838
Asn Leu Thr Ser Ala Leu Ile Lys Ser Leu Arg Gly Ser Asp Glu Asn	
230 235 240	
GCT TCC ATC TAT TAT CTG GCG CGC TTG ATT GCT GGC GGG GAA AAC CCG	886
Ala Ser Ile Tyr Tyr Leu Ala Arg Leu Ile Ala Gly Gly Glu Asn Pro	
245 250 255	
GAA TTT ATC GCC AGA AGG CTG GTG ATT TTT GCG AGC GAA GAT ATT GGT	934
Glu Phe Ile Ala Arg Arg Leu Val Ile Phe Ala Ser Glu Asp Ile Gly	
260 265 270	
AAC GCT AAC CCG AAC GCC CTT AAT TTA GCC GCT TCT TGT TTG TTT GCA	982
Asn Ala Asn Pro Asn Ala Leu Asn Leu Ala Ala Ser Cys Leu Phe Ala	
275 280 285 290	
GTC AAA CAA ATC GGC TAC CCT GAA GCG CGC ATC ATT TTA AGC CAA TGC	1030
Val Lys Gln Ile Gly Tyr Pro Glu Ala Arg Ile Ile Leu Ser Gln Cys	
295 300 305	
GTG ATT TAT CTG GCT TGT TCG CCC AAG TCT AAC ACG GCT TAT AGA GCG	1078
Val Ile Tyr Leu Ala Cys Ser Pro Lys Ser Asn Thr Ala Tyr Arg Ala	
310 315 320	
ATC AAT CAG GCT TTG GAT TGC GTT CAA AAA GGC TCA CTC TAC CCT ATT	1126
Ile Asn Gln Ala Leu Asp Cys Val Gln Lys Gly Ser Leu Tyr Pro Ile	
325 330 335	
CCT AAA CAC CTG CTG CCT AAC GCT AAA GAT TAC CTT TAC CCG CAT GAT	1174
Pro Lys His Leu Leu Pro Asn Ala Lys Asp Tyr Leu Tyr Pro His Asp	
340 345 350	
TAT AAC GGC TAT GTC AAA CAA GAT TAT TTG GAA AAA CCC CTA GAT TTG	1222
Tyr Asn Gly Tyr Val Lys Gln Asp Tyr Leu Glu Lys Pro Leu Asp Leu	
355 360 365 370	
GTT TCT TCT CAA GGC ATA GGA TTT GAA AAA ACC CTT TTA GAA TGG CTT	1270
Val Ser Ser Gln Gly Ile Gly Phe Glu Lys Thr Leu Leu Glu Trp Leu	
375 380 385	
GAT AAG ATA AGA AAT TGATCTTATA AGTTACATTA AAATGCGACA ATGGTAATAA A	1326
Asp Lys Ile Arg Asn	
390	
AAATCAATAT TTTTGGATTG AATT	1350

(2) INFORMATION FOR SEQ ID NO:494:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

ACCTGAATAA AGAGTTGCAA GACGCTCTGC ACAAACACTC TAAAAATACC AAAACCCCAA	60
CGAAAAATTT AAACACCCTT ACGAATTTTT ACGAATTGAT TTTATTTAAA AA ATG AGC	118
Met Ser	
1	
CTG ACT TCG CTT TTA AAC CCA AAA AGC CTA GAA GAT TTT TTA GGC CAA	166
Leu Thr Ser Leu Leu Asn Pro Lys Ser Leu Glu Asp Phe Leu Gly Gln	
5 10 15	
GAG CAT TTA GTA GGG AAA GAC GCC CCC TTA TTT AAA GCC CTA CAA TCC	214
Glu His Leu Val Gly Lys Asp Ala Pro Leu Phe Lys Ala Leu Gln Ser	
20 25 30	
AAA CAC TTC CCC CAT GCC TTT TTC TAT GGC CCT CCT GGC GTG GGT AAA	262
Lys His Phe Pro His Ala Phe Phe Tyr Gly Pro Pro Gly Val Gly Lys	
35 40 45 50	
ACA AGC CTG GCT CAA ATC ATC GCC TAT ATG CTA GAG CGC CCC ATT CTT	310
Thr Ser Leu Ala Gln Ile Ile Ala Tyr Met Leu Glu Arg Pro Ile Leu	
55 60 65	
TTA TTC AAT GCG ACG GAT TTT AAA TTA GAG GAT TTG CGC CTT AAG CTT	358
Leu Phe Asn Ala Thr Asp Phe Lys Leu Glu Asp Leu Arg Leu Lys Leu	
70 75 80	
AAA AAT TAC CAA AAT ACC CTT TTA AAA CCC GTT GTT TTT ATT GAT GAA	406
Lys Asn Tyr Gln Asn Thr Leu Leu Lys Pro Val Val Phe Ile Asp Glu	
85 90 95	
ACC CAC AGA TTG AAT AAA ACC CAA CAA GAA TTT TTA CTC CCC ATT ATG	454
Thr His Arg Leu Asn Lys Thr Gln Gln Glu Phe Leu Leu Pro Ile Met	
100 105 110	
GAA AAA GAT CAC GCT TTA ATT TTA GGG GCT AGC ACG CAA GAT CCT AAT	502
Glu Lys Asp His Ala Leu Ile Leu Gly Ala Ser Thr Gln Asp Pro Asn	
115 120 125 130	
TAC AGC CTA AGC CAT GCG ATC CGA TCA AGA AGT TTT ATT TTT GAA TTA	550
Tyr Ser Leu Ser His Ala Ile Arg Ser Arg Ser Phe Ile Phe Glu Leu	
135 140 145	
ACC CCC CTA AAC AAG AGC GAT TTA GAC AGG CTT TGC GCT AAA GCT TTA	598
Thr Pro Leu Asn Lys Ser Asp Leu Asp Arg Leu Cys Ala Lys Ala Leu	
150 155 160	
ACA TTG CTC AAA AAA CAA ATA GAG CCT GGC GCT AAA ACC TAT CTT TTA	646
Thr Leu Leu Lys Lys Gln Ile Glu Pro Gly Ala Lys Thr Tyr Leu Leu	
165 170 175	
AAC AAC AGC GCT GGC GAC GCT AGA GCG TTA TTA AAC CTT TTA GAT TTG	694
Asn Asn Ser Ala Gly Asp Ala Arg Ala Leu Leu Asn Leu Leu Asp Leu	
180 185 190	

```

Met Ser Lys Ser Leu Tyr Gln Thr Leu Asn Val Ser Glu Asn Ala Ser
 1           5           10           15
Gln Asp Glu Ile Lys Lys Ser Tyr Arg Arg Leu Ala Arg Gln Tyr His
          20           25           30
Pro Asp Leu Asn Lys Thr Lys Glu Ala Glu Glu Lys Phe Lys Glu Ile
          35           40           45
Asn Ala Ala Tyr Glu Ile Leu Ser Asp Glu Glu Lys Arg Arg Gln Tyr
          50           55           60
Asp Gln Phe Gly Asp Asn Met Phe Gly Gly Gln Asn Phe Ser Asp Phe
65           70           75           80
Ala Arg Ser Arg Gly Pro Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser
          85           90           95
Ile Phe Gly Lys Gly Gly Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln
          100          105          110
Gly Phe Ser Gly Phe Asn Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp
          115          120          125
Ile Thr Ala Ala Leu Asn Val Ser Val Leu Asp Thr Leu Leu Gly Asn
          130          135          140
Lys Lys Gln Val Ser Ile Asn Asn Glu Thr Phe Ser Leu Lys Ile Pro
145           150           155           160
Ile Gly Val Glu Glu Gly Glu Lys Ile Arg Val Arg Asn Lys Gly Lys
          165          170          175
Thr Gly Arg Thr Thr Arg Gly Asp Leu Leu Leu Glu Ile His Ile Glu
          180          185          190
Glu Asp Glu Met Tyr Arg Arg Glu Lys Asp Asp Ile Thr Gln Ile Phe
          195          200          205
Asp Leu Pro Leu Lys Thr Ala Leu Phe Gly Gly Lys Ile Glu Ile Ala
          210          215          220
Thr Trp His Lys Thr Leu Thr Leu Thr Ile Pro Pro Asn Thr Lys Ala
225           230           235           240
Met Gln Lys Phe Arg Ile Lys Glu Lys Gly Ile Lys Asn Arg Lys Thr
          245          250          255
Ser His Val Gly Asp Leu Tyr Leu Gln Ala Arg Leu Ile Leu Pro Lys
          260          265          270
Thr Glu Thr Leu Ser Asn Glu Leu Lys Ala Leu Leu Glu Lys Glu Leu
          275          280          285

```

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 113...1285
- (D) OTHER INFORMATION:

GTC TCT GTT TTA GAC ACC CTT TTA GGC AAT AAA AAA CAA GTG AGC ATC	488
Val Ser Val Leu Asp Thr Leu Leu Gly Asn Lys Lys Gln Val Ser Ile	
135 140 145 150	
AAT AAT GAG ACT TTT AGC CTT AAA ATC CCT ATT GGC GTG GAA GAG GGC	536
Asn Asn Glu Thr Phe Ser Leu Lys Ile Pro Ile Gly Val Glu Glu Gly	
155 160 165	
GAA AAG ATT AGG GTT CGC AAC AAG GGG AAA ACG GGG CGA ACG ACT AGG	584
Glu Lys Ile Arg Val Arg Asn Lys Gly Lys Thr Gly Arg Thr Thr Arg	
170 175 180	
GGC GAT TTG CTC TTA GAG ATC CAT ATT GAA GAA GAT GAA ATG TAT AGG	632
Gly Asp Leu Leu Leu Glu Ile His Ile Glu Glu Asp Glu Met Tyr Arg	
185 190 195	
CGC GAG AAA GAT GAT ATT ACC CAA ATC TTT GAT TTA CCC TTA AAA ACG	680
Arg Glu Lys Asp Asp Ile Thr Gln Ile Phe Asp Leu Pro Leu Lys Thr	
200 205 210	
GCT CTT TTT GGA GGG AAA ATT GAA ATC GCT ACT TGG CAT AAA ACC TTA	728
Ala Leu Phe Gly Gly Lys Ile Glu Ile Ala Thr Trp His Lys Thr Leu	
215 220 225 230	
ACC CTA ACC ATT CCC CCT AAC ACC AAA GCG ATG CAA AAA TTC CGC ATT	776
Thr Leu Thr Ile Pro Pro Asn Thr Lys Ala Met Gln Lys Phe Arg Ile	
235 240 245	
AAA GAA AAA GGG ATC AAA AAC AGA AAA ACT TCG CAT GTG GGG GAT TTG	824
Lys Glu Lys Gly Ile Lys Asn Arg Lys Thr Ser His Val Gly Asp Leu	
250 255 260	
TAT TTG CAG GCT CGT TTG ATT TTG CCT AAA ACT GAA ACG CTT TCT AAT	872
Tyr Leu Gln Ala Arg Leu Ile Leu Pro Lys Thr Glu Thr Leu Ser Asn	
265 270 275	
GAG TTG AAA GCG TTA TTA GAA AAA GAA TTG TAAGGAGGAA TCGTGTGCGA TTA	925
Glu Leu Lys Ala Leu Leu Glu Lys Glu Leu	
280 285	
TGATGAACCG CTTTATTATA TCAGCGTCGT GGCTAAAATC TTAGGCGTGC ACCCTCAAAC	985
CTTGC	990

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...902
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

ATGATAGTAT TCTAATAAAA CTATTTTAAA GGTGATCC ATG AGT AAG AGT TTA TAC	56
Met Ser Lys Ser Leu Tyr	
1 5	
CAA ACT TTA AAT GTG AGC GAA AAC GCC AGC CAA GAT GAA ATC AAA AAA	104
Gln Thr Leu Asn Val Ser Glu Asn Ala Ser Gln Asp Glu Ile Lys Lys	
10 15 20	
TCC TAC CGC CGT TTA GCC CGA CAA TAC CAC CCG GAT TTG AAT AAA ACC	152
Ser Tyr Arg Arg Leu Ala Arg Gln Tyr His Pro Asp Leu Asn Lys Thr	
25 30 35	
AAA GAA GCC GAA GAG AAA TTC AAA GAA ATC AAC GCC GCT TAT GAA ATT	200
Lys Glu Ala Glu Glu Lys Phe Lys Glu Ile Asn Ala Ala Tyr Glu Ile	
40 45 50	
TTG AGC GAT GAA GAA AAA CGC CGC CAA TAC GAT CAG TTT GGC GAT AAC	248
Leu Ser Asp Glu Glu Lys Arg Arg Gln Tyr Asp Gln Phe Gly Asp Asn	
55 60 65 70	
ATG TTT GGC GGG CAG AAT TTC AGC GAT TTT GCC AGA AGC CGT GGT CCT	296
Met Phe Gly Gly Gln Asn Phe Ser Asp Phe Ala Arg Ser Arg Gly Pro	
75 80 85	
AGT GAA GAT TTA GAC GAT ATT TTA AGC TCT ATT TTT GGG AAA GGA GGC	344
Ser Glu Asp Leu Asp Asp Ile Leu Ser Ser Ile Phe Gly Lys Gly Gly	
90 95 100	
TTT TCG CAA AGA TTT TCT CAA AAC TCG CAA GGC TTT TCT GGC TTT AAT	392
Phe Ser Gln Arg Phe Ser Gln Asn Ser Gln Gly Phe Ser Gly Phe Asn	
105 110 115	
TTT TCC AAT TTC GCC CCT GAA AAT TTA GAC ATA ACC GCC GCT TTA AAT	440
Phe Ser Asn Phe Ala Pro Glu Asn Leu Asp Ile Thr Ala Ala Leu Asn	
120 125 130	

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

```

Met Ile Pro Lys Glu Arg Met Glu Arg Ala Leu Gly Ser Gly Val Ile
 1           5           10           15
Ile Ser Lys Asp Gly Tyr Ile Val Thr Asn Asn His Val Ile Asp Gly
          20           25           30
Ala Asp Lys Ile Lys Val Thr Ile Pro Gly Ser Asn Lys Glu Tyr Ser
          35           40           45
Ala Thr Leu Val Gly Thr Asp Ser Glu Ser Asp Leu Ala Val Ile Arg
          50           55           60
Ile Thr Lys Asp Asn Leu Pro Thr Ile Lys Phe Ser Asp Ser Asn Asp
65           70           75           80
Ile Ser Val Gly Asp Leu Val Phe Ala Ile Gly Asn Pro Phe Gly Val
          85           90           95
Gly Glu Ser Val Thr Gln Gly Ile Val Ser Ala Leu Asn Lys Ser Gly
          100          105          110
Ile Gly Ile Asn Ser Tyr Glu Asn Phe Ile Gln Thr Asp Ala Ser Ile
          115          120          125
Asn Pro Gly Asn Ser Gly Gly Ala Leu Ile Asp Ser Arg Gly Gly Leu
          130          135          140
Val Gly Ile Asn Thr Ala Ile Ile Ser Lys Thr Gly Gly Asn His Gly
145          150          155          160
Ile Gly Phe Ala Ile Pro Ser Asn Met Val Lys Asp Thr Val Thr Gln
          165          170          175
Leu Ile Lys Thr Gly Lys Ile Glu Arg Gly Tyr Leu Gly Val Gly Leu
          180          185          190
Gln Asp Leu Ser Gly Asp Leu Gln Asn Ser Tyr Asp Asn Lys Glu Gly
          195          200          205
Ala Val Val Ile Ser Val Glu Lys Asp Ser Pro Ala Lys Lys Ala Gly
          210          215          220
Ile Leu Val Trp Asp Leu Ile Thr Glu Val Asn Gly Lys Lys Val Lys
225          230          235          240
Asn Thr Asn Glu Leu Arg Asn Leu Ile Gly Ser Met Leu Pro Asn Gln
          245          250          255
Arg Val Thr Leu Lys Val Ile Arg Asp Lys Lys Glu Arg Ala Phe Thr
          260          265          270
Leu Thr Leu Ala Glu Arg Lys Asn Pro Asn Lys Lys Glu Thr Ile Ser
          275          280          285
Ala Gln Asn Gly Ala Gln Gly Gln Leu Asn Gly Leu Gln Val Glu Asp
          290          295          300
Leu Thr Gln Glu Thr Lys Arg Ser Met Arg Leu Ser Asp Asp Val Gln
305          310          315          320
Gly Val Leu Val Ser Gln Val Asn Glu Asn Ser Pro Ala Glu Gln Ala
          325          330          335
Gly Phe Arg Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val
          340          345          350
Lys Ser Val Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys
          355          360          365
Pro Lys Arg Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile
          370          375          380
Leu Val Lys
385

```

ATT AGC GTA GAA AAA GAC TCT CCG GCT AAA AAA GCA GGG ATT TTG GTG	910
Ile Ser Val Glu Lys Asp Ser Pro Ala Lys Lys Ala Gly Ile Leu Val	
215 220 225	
TGG GAT TTG ATC ACC GAA GTC AAT GGG AAA AAG GTT AAA AAC ACG AAT	958
Trp Asp Leu Ile Thr Glu Val Asn Gly Lys Lys Val Lys Asn Thr Asn	
230 235 240	
GAG TTA AGA AAT CTA ATC GGC TCC ATG CTA CCC AAT CAA AGA GTA ACC	1006
Glu Leu Arg Asn Leu Ile Gly Ser Met Leu Pro Asn Gln Arg Val Thr	
245 250 255	
TTA AAA GTC ATT AGA GAC AAA AAA GAA CGC GCT TTC ACC CTC ACT CTA	1054
Leu Lys Val Ile Arg Asp Lys Lys Glu Arg Ala Phe Thr Leu Thr Leu	
260 265 270 275	
GCT GAA AGG AAA AAC CCT AAC AAA AAA GAA ACC ATT TCT GCT CAA AAC	1102
Ala Glu Arg Lys Asn Pro Asn Lys Lys Glu Thr Ile Ser Ala Gln Asn	
280 285 290	
GGC GCG CAA GGC CAA TTG AAC GGG CTT CAA GTA GAA GAT TTA ACT CAA	1150
Gly Ala Gln Gly Gln Leu Asn Gly Leu Gln Val Glu Asp Leu Thr Gln	
295 300 305	
GAA ACC AAA AGG TCT ATG CGT TTG AGC GAT GAT GTT CAA GGG GTT TTA	1198
Glu Thr Lys Arg Ser Met Arg Leu Ser Asp Asp Val Gln Gly Val Leu	
310 315 320	
GTC TCT CAA GTG AAT GAA AAT TCC CCA GCA GAG CAA GCC GGA TTT AGG	1246
Val Ser Gln Val Asn Glu Asn Ser Pro Ala Glu Gln Ala Gly Phe Arg	
325 330 335	
CAA GGT AAC ATT ATC ACA AAA ATT GAA GAG GTT GAA GTT AAA AGC GTT	1294
Gln Gly Asn Ile Ile Thr Lys Ile Glu Glu Val Glu Val Lys Ser Val	
340 345 350 355	
GCG GAT TTT AAC CAT GCT TTA GAA AAG TAT AAA GGC AAA CCC AAA CGA	1342
Ala Asp Phe Asn His Ala Leu Glu Lys Tyr Lys Gly Lys Pro Lys Arg	
360 365 370	
TTC TTA GTT TTA GAC TTG AAT CAA GGT TAT AGG ATC ATT TTG GTG AAA T	1391
Phe Leu Val Leu Asp Leu Asn Gln Gly Tyr Arg Ile Ile Leu Val Lys	
375 380 385	
GATAGGGGTG GGTCGTTAGT CGCATGTCTT TGATTAGAGT GAATGGGGAA GCTTTTAAAC	1451
TCTCTTTAGA AAGTTTAGAA GAAGACCCTT TTGAAACTAA AGAAACGCTA GAAACGCTTA	1511
TCAAACAAAC GAGCGTTG	1529

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Met Ile Pro
1

AAA GAA AGA ATG GAA AGG GCT TTA GGC AGC GGC GTA ATC ATT TCT AAA	286
Lys Glu Arg Met Glu Arg Ala Leu Gly Ser Gly Val Ile Ile Ser Lys	
5 10 15	
GAC GGC TAT ATT GTA ACT AAT AAC CAT GTG ATT GAT GGC GCG GAT AAG	334
Asp Gly Tyr Ile Val Thr Asn Asn His Val Ile Asp Gly Ala Asp Lys	
20 25 30 35	
ATT AAA GTT ACC ATT CCA GGG AGC AAT AAA GAA TAT TCC GCC ACT CTA	382
Ile Lys Val Thr Ile Pro Gly Ser Asn Lys Glu Tyr Ser Ala Thr Leu	
40 45 50	
GTA GGC ACC GAT TCT GAA AGC GAT TTA GCG GTG ATT CGC ATC ACT AAA	430
Val Gly Thr Asp Ser Glu Ser Asp Leu Ala Val Ile Arg Ile Thr Lys	
55 60 65	
GAC AAT CTG CCC ACG ATC AAA TTC TCT GAT TCT AAT GAT ATT TCA GTG	478
Asp Asn Leu Pro Thr Ile Lys Phe Ser Asp Ser Asn Asp Ile Ser Val	
70 75 80	
GGC GAT TTG GTT TTT GCG ATT GGT AAC CCT TTT GGC GTG GGC GAA AGC	526
Gly Asp Leu Val Phe Ala Ile Gly Asn Pro Phe Gly Val Gly Glu Ser	
85 90 95	
GTT ACG CAA GGC ATT GTT TCA GCG CTC AAT AAA AGC GGG ATT GGG ATC	574
Val Thr Gln Gly Ile Val Ser Ala Leu Asn Lys Ser Gly Ile Gly Ile	
100 105 110 115	
AAC AGC TAT GAG AAT TTC ATT CAA ACA GAC GCT TCC ATC AAT CCT GGA	622
Asn Ser Tyr Glu Asn Phe Ile Gln Thr Asp Ala Ser Ile Asn Pro Gly	
120 125 130	
AAT TCC GGC GGC GCT TTA ATT GAT AGC CGT GGA GGG TTA GTG GGG ATT	670
Asn Ser Gly Gly Ala Leu Ile Asp Ser Arg Gly Gly Leu Val Gly Ile	
135 140 145	
AAT ACC GCT ATT ATC TCT AAA ACT GGG GGC AAC CAC GGC ATT GGC TTT	718
Asn Thr Ala Ile Ile Ser Lys Thr Gly Gly Asn His Gly Ile Gly Phe	
150 155 160	
GCC ATC CCT TCT AAC ATG GTT AAA GAT ACT GTA ACC CAA CTC ATC AAA	766
Ala Ile Pro Ser Asn Met Val Lys Asp Thr Val Thr Gln Leu Ile Lys	
165 170 175	
ACC GGT AAG ATT GAA AGA GGT TAC TTG GGC GTG GGC TTG CAA GAT TTG	814
Thr Gly Lys Ile Glu Arg Gly Tyr Leu Gly Val Gly Leu Gln Asp Leu	
180 185 190 195	
AGT GGC GAT TTG CAA AAT TCT TAT GAC AAC AAA GAA GGG GCG GTA GTC	862
Ser Gly Asp Leu Gln Asn Ser Tyr Asp Asn Lys Glu Gly Ala Val Val	
200 205 210	

```

Lys Ala Thr Leu Trp Arg Ile Val Phe Phe Phe Leu Gly Ser Val Phe
 290                               295                               300
Val Ile Ser Val Phe Leu Pro Met Asn Asp Ser Ser Ile Thr Gln Ser
305                               310                               315                               320
Pro Phe Val Ser Val Leu Glu Arg Ile Asn Leu Pro Phe Ile Gly Met
                               325                               330                               335
Gly Ile Pro Tyr Val Ala Asp Ile Met Asn Ala Val Ile Ile Thr Ala
                               340                               345                               350
Met Phe Ser Thr Ala Asn Ser Gly Leu Tyr Gly Ala Ser Arg Met Ile
                               355                               360                               365
Tyr Gly Leu Ser Lys Gln Lys Met Phe Phe Lys Val Phe Ser Gln Leu
                               370                               375                               380
Asn Arg Gln Gly Thr Pro Thr Tyr Ala Met Phe Phe Ser Leu Ser Phe
385                               390                               395                               400
Ser Leu Ile Gly Leu Leu Val Gln Ile Tyr Ala Lys Glu Asn Val Val
                               405                               410                               415
Glu Ala Leu Ile Asn Val Ile Ser Phe Thr Val Ile Ile Val Trp Val
                               420                               425                               430
Ser Val Ser Val Ser Gln Tyr Ser Phe Arg Lys Gln Tyr Leu Lys Ala
                               435                               440                               445
Gly His Ser Leu Glu Asp Leu Pro Tyr Lys Ala Pro Phe Leu Pro Phe
                               450                               455                               460
Leu Gln Leu Ile Gly Ile Thr Gly Cys Ala Ile Gly Val Ile Gly Ser
465                               470                               475                               480
Ala Met Asp Lys Asp Gln Arg Ile Gly Met Ile Leu Thr Ile Val Phe
                               485                               490                               495
Ala Val Ile Cys Tyr Ile Gly Tyr Tyr Phe Thr Gln Lys Ala Asn Glu
                               500                               505                               510
Asn Asn Lys Lys Asp Leu Ile
                               515

```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 230...1390
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```

TTAAGCTTGA ATGCGGGCAA TATCCAAATC CAGAGCATGC CCAAAGTTAA AGAGCGAGTG      60
AGTGTCCCCT CTAAAGACGA TACGGATCTA TTCTTACCAC GATTCTATTA AGGACTCTAT      120
TAAGGCGGTG GTGAATATCT CCACTGAAAA GAAGATTAAA AACAATTTTA TAGGTGGCGG      180
TGTGTTTAAT GACCCCTTTT TCCAACAATT TTTTGGGGAT TTGGGTGGC ATG ATT CCT      238

```

AAT GAA AAT AAC AAA AAA GAT TTG ATA TAATCTTTTC TTAATTTTGA AGTTTAG 1651
 Asn Glu Asn Asn Lys Lys Asp Leu Ile
 515

CAAATTTTAA GGAAGTAACC ATGATGAAAA AAACCCTTTT TATCTCTTTG GCTTTAGC 1709

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

Met	Leu	Leu	Ile	Val	Phe	Phe	Lys	Phe	Tyr	Phe	Gln	Tyr	Ser	Ile	Lys	1	5	10	15
Lys	Lys	Ser	Phe	Tyr	Phe	Ile	Phe	Val	Ile	Ile	Gln	Ala	Ile	Phe	Ile	20	25	30	
Phe	Asn	Leu	Arg	Arg	Cys	Arg	Met	Asp	Asn	Gln	Lys	Ile	Thr	His	Gln	35	40	45	
Asn	Ile	Thr	Gln	Lys	Gln	Gly	Glu	Leu	Lys	Arg	Asp	Met	Lys	Met	Arg	50	55	60	
His	Leu	Leu	Met	Ile	Ala	Phe	Gly	Gly	Ala	Ile	Gly	Thr	Gly	Leu	Phe	65	70	75	80
Val	Gly	Thr	Gly	Gly	Asn	Ile	Ala	Ser	Ala	Gly	Pro	Leu	Gly	Thr	Leu	85	90	95	
Ile	Ala	Tyr	Cys	Phe	Gly	Gly	Leu	Val	Val	Tyr	Cys	Ile	Met	Leu	Ser	100	105	110	
Leu	Gly	Glu	Leu	Ala	Ser	Val	Tyr	Pro	Thr	Thr	Gly	Ser	Phe	Gly	Asp	115	120	125	
Tyr	Ala	Ala	Lys	Phe	Ile	Gly	Pro	Gly	Thr	Gly	Tyr	Met	Val	Phe	Trp	130	135	140	
Met	Tyr	Trp	Leu	Gly	Trp	Val	Ile	Thr	Val	Ala	Leu	Glu	Tyr	Ile	Ala	145	150	155	160
Ile	Gly	Met	Leu	Met	Gln	Arg	Trp	Phe	Ala	Asp	Ile	Pro	Ile	His	Tyr	165	170	175	
Trp	Val	Ile	Leu	Cys	Ile	Ala	Leu	Val	Phe	Leu	Leu	Asn	Phe	Phe	Ser	180	185	190	
Val	Lys	Ile	Phe	Ala	Glu	Gly	Glu	Phe	Phe	Phe	Ser	Leu	Ile	Lys	Val	195	200	205	
Leu	Ala	Val	Ile	Ala	Phe	Ile	Gly	Ile	Gly	Ala	Ile	Gly	Ile	Ile	Tyr	210	215	220	
Gln	Ile	Tyr	Ser	His	Gly	Phe	Gly	Ser	Ile	Phe	Asp	Asn	Phe	His	Phe	225	230	235	240
Gly	Asp	Lys	Gly	Phe	Phe	Pro	Asn	Gly	Ser	Ala	Ala	Val	Phe	Ser	Ala	245	250	255	
Met	Leu	Ala	Val	Ile	Phe	Ala	Phe	Thr	Gly	Thr	Glu	Val	Ile	Gly	Val	260	265	270	
Ala	Val	Gly	Glu	Thr	Lys	Asn	Ala	Ser	Glu	Val	Met	Pro	Lys	Ala	Ile	275	280	285	

GCG ATT AAA GCG ACC TTG TGG CGG ATT GTC TTT TTC TTT TTA GGC TCT	973
Ala Ile Lys Ala Thr Leu Trp Arg Ile Val Phe Phe Phe Leu Gly Ser	
290 295 300	
GTG TTT GTC ATT TCT GTT TTT TTA CCC ATG AAT GAT TCT TCT ATC ACG	1021
Val Phe Val Ile Ser Val Phe Leu Pro Met Asn Asp Ser Ser Ile Thr	
305 310 315	
CAA AGC CCT TTT GTG AGC GTT TTA GAA CGC ATT AAT TTG CCC TTT ATT	1069
Gln Ser Pro Phe Val Ser Val Leu Glu Arg Ile Asn Leu Pro Phe Ile	
320 325 330	
GGC ATG GGT ATC CCT TAT GTG GCT GAT ATA ATG AAC GCT GTT ATC ATT	1117
Gly Met Gly Ile Pro Tyr Val Ala Asp Ile Met Asn Ala Val Ile Ile	
335 340 345 350	
ACG GCG ATG TTT TCT ACC GCT AAT TCA GGG CTT TAT GGA GCG AGC CGC	1165
Thr Ala Met Phe Ser Thr Ala Asn Ser Gly Leu Tyr Gly Ala Ser Arg	
355 360 365	
ATG ATT TAT GGG CTG TCC AAA CAA AAG ATG TTT TTT AAG GTT TTT TCC	1213
Met Ile Tyr Gly Leu Ser Lys Gln Lys Met Phe Phe Lys Val Phe Ser	
370 375 380	
CAA CTC AAC CGA CAA GGC ACG CCC ACT TAT GCG ATG TTT TTT TCC CTT	1261
Gln Leu Asn Arg Gln Gly Thr Pro Thr Tyr Ala Met Phe Phe Ser Leu	
385 390 395	
TCT TTT TCT CTC ATA GGG CTT TTA GTC CAA ATT TAT GCC AAA GAA AAT	1309
Ser Phe Ser Leu Ile Gly Leu Leu Val Gln Ile Tyr Ala Lys Glu Asn	
400 405 410	
GTC GTG GAA GCT TTG ATT AAT GTG ATC AGT TTC ACG GTG ATT ATT GTG	1357
Val Val Glu Ala Leu Ile Asn Val Ile Ser Phe Thr Val Ile Ile Val	
415 420 425 430	
TGG GTT AGC GTG TCT GTT TCG CAA TAT TCT TTC CGC AAG CAA TAC TTA	1405
Trp Val Ser Val Ser Val Ser Gln Tyr Ser Phe Arg Lys Gln Tyr Leu	
435 440 445	
AAA GCC GGG CAT TCT TTA GAG GAT TTG CCT TAT AAA GCC CCC TTT CTA	1453
Lys Ala Gly His Ser Leu Glu Asp Leu Pro Tyr Lys Ala Pro Phe Leu	
450 455 460	
CCC TTT TTG CAA CTC ATA GGG ATC ACT GGG TGT GCC ATC GGC GTG ATT	1501
Pro Phe Leu Gln Leu Ile Gly Ile Thr Gly Cys Ala Ile Gly Val Ile	
465 470 475	
GGT TCG GCT ATG GAT AAG GAT CAA CGC ATT GGG ATG ATT TTA ACG ATT	1549
Gly Ser Ala Met Asp Lys Asp Gln Arg Ile Gly Met Ile Leu Thr Ile	
480 485 490	
GTT TTC GCT GTT ATT TGT TAC ATT GGA TAC TAT TTT ACA CAA AAA GCT	1597
Val Phe Ala Val Ile Cys Tyr Ile Gly Tyr Tyr Phe Thr Gln Lys Ala	
495 500 505 510	

ATG CGC CAT CTC TTA ATG ATT GCA TTT GGA GGA GCG ATC GGC ACA GGG	301
Met Arg His Leu Leu Met Ile Ala Phe Gly Gly Ala Ile Gly Thr Gly	
65 70 75	
CTT TTT GTA GGC ACT GGG GGT AAT ATT GCG AGC GCT GGC CCT TTA GGG	349
Leu Phe Val Gly Thr Gly Gly Asn Ile Ala Ser Ala Gly Pro Leu Gly	
80 85 90	
ACC TTG ATC GCT TAT TGT TTT GGA GGG CTT GTG GTC TAT TGT ATC ATG	397
Thr Leu Ile Ala Tyr Cys Phe Gly Gly Leu Val Val Tyr Cys Ile Met	
95 100 105 110	
CTC TCT TTA GGC GAA TTG GCT AGC GTT TAT CCC ACT ACA GGA AGT TTT	445
Leu Ser Leu Gly Glu Leu Ala Ser Val Tyr Pro Thr Thr Gly Ser Phe	
115 120 125	
GGG GAT TAT GCG GCT AAA TTC ATA GGC CCT GGC ACG GGC TAT ATG GTT	493
Gly Asp Tyr Ala Ala Lys Phe Ile Gly Pro Gly Thr Gly Tyr Met Val	
130 135 140	
TTT TGG ATG TAT TGG CTT GGC TGG GTG ATC ACG GTG GCG TTA GAA TAC	541
Phe Trp Met Tyr Trp Leu Gly Trp Val Ile Thr Val Ala Leu Glu Tyr	
145 150 155	
ATC GCT ATA GGC ATG CTC ATG CAA CGC TGG TTT GCG GAT ATT CCC ATC	589
Ile Ala Ile Gly Met Leu Met Gln Arg Trp Phe Ala Asp Ile Pro Ile	
160 165 170	
CAT TAT TGG GTT ATT TTA TGC ATT GCG TTA GTT TTT TTA TTG AAC TTT	637
His Tyr Trp Val Ile Leu Cys Ile Ala Leu Val Phe Leu Leu Asn Phe	
175 180 185 190	
TTT TCG GTT AAA ATT TTT GCC GAG GGC GAG TTT TTC TTT AGC CTG ATT	685
Phe Ser Val Lys Ile Phe Ala Glu Gly Glu Phe Phe Phe Ser Leu Ile	
195 200 205	
AAA GTT TTA GCG GTG ATC GCT TTT ATA GGC ATT GGC GCG ATT GGG ATT	733
Lys Val Leu Ala Val Ile Ala Phe Ile Gly Ile Gly Ala Ile Gly Ile	
210 215 220	
ATT TAT CAA ATC TAT TCG CAT GGG TTT GGT TCT ATT TTT GAT AAT TTC	781
Ile Tyr Gln Ile Tyr Ser His Gly Phe Gly Ser Ile Phe Asp Asn Phe	
225 230 235	
CAT TTT GGC GAT AAG GGG TTT TTC CCT AAT GGG AGC GCA GCG GTT TTT	829
His Phe Gly Asp Lys Gly Phe Phe Pro Asn Gly Ser Ala Ala Val Phe	
240 245 250	
AGC GCG ATG CTC GCT GTT ATT TTT GCT TTC ACT GGC ACA GAG GTG ATT	877
Ser Ala Met Leu Ala Val Ile Phe Ala Phe Thr Gly Thr Glu Val Ile	
255 260 265 270	
GGG GTG GCT GTG GGA GAG ACT AAA AAC GCT AGC GAA GTG ATG CCC AAA	925
Gly Val Ala Val Gly Glu Thr Lys Asn Ala Ser Glu Val Met Pro Lys	
275 280 285	

```

Glu Val Pro Asn Ile Lys Ala Ile Lys Glu Ala Ser Gly Ser Leu Lys
                      165                      170                      175
Arg Val Thr Glu Leu His Tyr Tyr Glu Lys Asp Phe Lys Ile Phe Ser
                      180                      185                      190
Gly Glu Asp Ser Leu Asn His Ser Ile Met Phe Ser Gly Gly Cys Gly
                      195                      200                      205
Val Ile Ser Val Thr Gly Asn Leu Met Pro Asn Leu Ile Ser Gln Met
                      210                      215                      220
Val Asn Cys Ala Leu Lys Gln Lys Tyr Gln Gln Ala Leu Glu Ile Gln
225                      230                      235                      240
Asn Lys Leu Phe Cys Leu His Gln Ala Leu Phe Val Glu Thr Asn Pro
                      245                      250                      255
Ile Pro Ile Lys Met Ala Met His Leu Ala Gly Leu Ile Glu Asn Pro
                      260                      265                      270
Ser Tyr Arg Leu Pro Leu Val Ala Pro Ser Lys Glu Thr Ile Gln Leu
                      275                      280                      285
Leu Glu Lys Thr Leu Gln Gln Tyr Glu Val Ile Ala
290                      295                      300

```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 68...1624
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```

AAAAAACCTT AAAACGCTTA AAAAAGTATC GCTTGATCAA GCTCTTTTAC TATTTAATCT      60
TTAAAAAA ATG CTT TTG ATC GTT TTT TTT AAA TTT TAT TTT CAA TAT TCA      109
      Met Leu Leu Ile Val Phe Phe Lys Phe Tyr Phe Gln Tyr Ser
        1              5              10

ATT AAA AAA AAA TCA TTT TAT TTT ATT TTT GTT ATA ATT CAA GCT ATT      157
Ile Lys Lys Lys Ser Phe Tyr Phe Ile Phe Val Ile Ile Gln Ala Ile
15              20              25              30

TTT ATT TTC AAT CTA AGG AGG TGT CGC ATG GAC AAT CAA AAG ATA ACG      205
Phe Ile Phe Asn Leu Arg Arg Cys Arg Met Asp Asn Gln Lys Ile Thr
35              40              45

CAT CAA AAT ATC ACG CAA AAA CAA GGC GAG CTT AAA AGA GAC ATG AAA      253
His Gln Asn Ile Thr Gln Lys Gln Gly Glu Leu Lys Arg Asp Met Lys
50              55              60

```

```

AAA CAA AAA TAC CAA CAA GCC CTA GAA ATC CAA AAT AAG CTT TTT TGT      835
Lys Gln Lys Tyr Gln Gln Ala Leu Glu Ile Gln Asn Lys Leu Phe Cys
230                      235                      240                      245

TTG CAC CAA GCC CTT TTT GTA GAA ACA AAT CCC ATC CCT ATT AAA ATG      883
Leu His Gln Ala Leu Phe Val Glu Thr Asn Pro Ile Pro Ile Lys Met
                      250                      255                      260

GCT ATG CAT TTA GCC GGC TTG ATT GAA AAC CCA AGC TAC AGA CTG CCT      931
Ala Met His Leu Ala Gly Leu Ile Glu Asn Pro Ser Tyr Arg Leu Pro
                      265                      270                      275

TTA GTG GCC CCA AGC AAA GAA ACG ATT CAA CTT TTA GAA AAA ACT TTA      979
Leu Val Ala Pro Ser Lys Glu Thr Ile Gln Leu Leu Glu Lys Thr Leu
                      280                      285                      290

CAA CAA TAT GAG GTA ATT GCA TGAATGGTTC CAATCACATG AAAAATAAAA CCCT 1034
Gln Gln Tyr Glu Val Ile Ala
                      295                      300

AGTGATCAGC GGCGCGACTA GAGGGATTGG CAAGGCGATA TTGTAC      1080

```

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

```

Met Gln Phe His Ser Ser Ser Ala Leu Ile Thr Pro Phe Lys Lys Asp
 1                      5                      10                      15
Leu Ser Val Asp Glu Ala Ala Tyr Glu Thr Leu Ile Lys Arg Gln Ile
                      20                      25                      30
Phe Gln Gly Met Asp Ala Cys Val Pro Val Gly Thr Thr Gly Glu Ser
                      35                      40                      45
Ala Thr Leu Thr His Lys Glu His Met Arg Cys Ile Glu Ile Ala Ile
                      50                      55                      60
Glu Thr Cys Lys Asn Thr Lys Thr Pro Ser Asn Ser Arg Met Lys Val
65                      70                      75                      80
Leu Ala Gly Val Gly Ser Asn Ala Thr Ser Glu Ser Leu Ser Leu Ala
                      85                      90                      95
Lys Phe Ala Gln Lys Ile Gly Ala Asp Ala Ile Leu Cys Val Ser Pro
                      100                      105                      110
Tyr Tyr Asn Arg Pro Thr Gln Gln Gly Leu Phe Glu His Tyr Lys Thr
                      115                      120                      125
Ile Ala Gln Ser Val Glu Ile Pro Val Met Leu Tyr Asp Val Pro Ser
                      130                      135                      140
Arg Thr Gly Val Ser Ile Glu Val Pro Thr Ala Leu Lys Leu Phe Arg
145                      150                      155                      160

```

Ser	Ser	Ala	Leu	Ile	Thr	Pro	Phe	Lys	Lys	Asp	Leu	Ser	Val	Asp	Glu	
			10					15						20		
GCC	GCT	TAT	GAA	ACC	TTG	ATC	AAG	CGC	CAA	ATT	TTT	CAG	GGC	ATG	GAC	211
Ala	Ala	Tyr	Glu	Thr	Leu	Ile	Lys	Arg	Gln	Ile	Phe	Gln	Gly	Met	Asp	
			25					30					35			
GCA	TGC	GTG	CCT	GTT	GGC	ACG	ACA	GGA	GAA	TCC	GCC	ACG	CTC	ACC	CAC	259
Ala	Cys	Val	Pro	Val	Gly	Thr	Thr	Gly	Glu	Ser	Ala	Thr	Leu	Thr	His	
			40				45					50				
AAA	GAG	CAC	ATG	CGT	TGC	ATT	GAA	ATC	GCC	ATA	GAA	ACT	TGC	AAA	AAC	307
Lys	Glu	His	Met	Arg	Cys	Ile	Glu	Ile	Ala	Ile	Glu	Thr	Cys	Lys	Asn	
	55					60					65					
ACT	AAA	ACG	CCC	TCA	AAT	TCG	CGC	ATG	AAA	GTG	TTA	GCC	GGC	GTG	GGC	355
Thr	Lys	Thr	Pro	Ser	Asn	Ser	Arg	Met	Lys	Val	Leu	Ala	Gly	Val	Gly	
	70				75					80				85		
AGT	AAC	GCC	ACG	AGC	GAG	TCC	CTT	TCT	TTA	GCA	AAG	TTC	GCT	CAA	AAA	403
Ser	Asn	Ala	Thr	Ser	Glu	Ser	Leu	Ser	Leu	Ala	Lys	Phe	Ala	Gln	Lys	
				90					95					100		
ATC	GGC	GCG	GAT	GCG	ATT	TTA	TGC	GTA	AGC	CCT	TAT	TAT	AAC	CGC	CCC	451
Ile	Gly	Ala	Asp	Ala	Ile	Leu	Cys	Val	Ser	Pro	Tyr	Tyr	Asn	Arg	Pro	
			105					110					115			
ACC	CAA	CAA	GGC	TTG	TTT	GAA	CAT	TAT	AAA	ACC	ATC	GCT	CAA	TCG	GTG	499
Thr	Gln	Gln	Gly	Leu	Phe	Glu	His	Tyr	Lys	Thr	Ile	Ala	Gln	Ser	Val	
		120					125					130				
GAA	ATC	CCT	GTC	ATG	CTT	TAT	GAT	GTG	CCA	AGT	AGA	ACA	GGC	GTG	TCT	547
Glu	Ile	Pro	Val	Met	Leu	Tyr	Asp	Val	Pro	Ser	Arg	Thr	Gly	Val	Ser	
	135					140					145					
ATT	GAA	GTT	CCA	ACC	GCC	CTC	AAA	CTC	TTT	AGA	GAA	GTC	CCT	AAC	ATT	595
Ile	Glu	Val	Pro	Thr	Ala	Leu	Lys	Leu	Phe	Arg	Glu	Val	Pro	Asn	Ile	
	150					155				160					165	
AAA	GCC	ATT	AAA	GAA	GCG	TCT	GGC	TCT	TTG	AAA	AGG	GTA	ACA	GAA	TTG	643
Lys	Ala	Ile	Lys	Glu	Ala	Ser	Gly	Ser	Leu	Lys	Arg	Val	Thr	Glu	Leu	
				170					175					180		
CAT	TAT	TAT	GAA	AAA	GAT	TTT	AAA	ATT	TTT	AGT	GGG	GAA	GAT	TCG	CTC	691
His	Tyr	Tyr	Glu	Lys	Asp	Phe	Lys	Ile	Phe	Ser	Gly	Glu	Asp	Ser	Leu	
			185					190					195			
AAC	CAC	TCC	ATC	ATG	TTT	TCA	GGG	GGG	TGC	GGC	GTG	ATT	TCA	GTG	ACC	739
Asn	His	Ser	Ile	Met	Phe	Ser	Gly	Gly	Cys	Gly	Val	Ile	Ser	Val	Thr	
		200					205					210				
GGT	AAT	TTA	ATG	CCC	AAT	CTG	ATT	TCA	CAA	ATG	GTC	AAT	TGC	GCG	CTC	787
Gly	Asn	Leu	Met	Pro	Asn	Leu	Ile	Ser	Gln	Met	Val	Asn	Cys	Ala	Leu	
	215					220					225					

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

```

Met Lys Lys Ile Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu
 1             5             10             15
Met His Val His Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe
      20             25             30
Asn Lys Glu Val Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys
      35             40             45
Lys Asp Phe Glu Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His
      50             55             60
Val His Leu Leu Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu
      65             70             75             80
Val Asn Ser Leu Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His
      85             90             95
Phe Lys Ser Val Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro
      100            105            110
Ser Tyr Phe Ala Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys
      115            120            125
Gln Tyr Ile Gln Asp Gln Glu Thr Pro His
      130            135

```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 101...1000
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

```

TGGATTAAAG AGTGAGCGAT TTGGTGC GTG TGGCCAATGA ATATTTTAAAG GACACCCAAT      60
CAACCACCGT GTTTTGTAAAG CCTTAAAGAG GCCTTATAAC  ATG CAA TTT CAT TCA      115
                                     Met Gln Phe His Ser
                                     1             5

TCT AGC GCG TTG ATT ACG CCT TTT AAA AAA GAT TTG AGC GTT GAT GAG      163

```

(B) LOCATION: 105...518
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

```

GTTGCAACTT ATCTTGTTGT TCTTTAGTGG GATACAAGCG GAATTTAAAA CCCTTATTGA      60
CTTTCATAGA AAGTATTTTA ACCTCTTTTT GTTAAATAG GTCT ATG AAA AAA ATT      116
                               Met Lys Lys Ile
                               1

GAT GAT ATG AGA CAC GGA AGA CAT TGT GTT TTT TTA ATG CAT GTG CAT      164
Asp Asp Met Arg His Gly Arg His Cys Val Phe Leu Met His Val His
  5                10                15                20

TTT GTA TTT GTT ACT AAA TAC AGG CGT TCA GCA TTC AAT AAG GAA GTG      212
Phe Val Phe Val Thr Lys Tyr Arg Arg Ser Ala Phe Asn Lys Glu Val
                25                30                35

ATA GAT TTT TTA GGA TCG GTG TTT GCC AAA GTG TGT AAG GAC TTT GAG      260
Ile Asp Phe Leu Gly Ser Val Phe Ala Lys Val Cys Lys Asp Phe Glu
                40                45                50

AGC GAA TTG GTA GAA TTT GAT GGG GAG AGC GAT CAT GTG CAT TTG CTT      308
Ser Glu Leu Val Glu Phe Asp Gly Glu Ser Asp His Val His Leu Leu
                55                60                65

ATC AAC TAC CCT CCA AAA GTG AGC GTG AGT AAG TTA GTT AAT TCT TTA      356
Ile Asn Tyr Pro Pro Lys Val Ser Val Ser Lys Leu Val Asn Ser Leu
                70                75                80

AAA GGC GTT AGC AGT CGT TTG ACT AGA CAA CAC CAT TTC AAA AGC GTT      404
Lys Gly Val Ser Ser Arg Leu Thr Arg Gln His His Phe Lys Ser Val
                85                90                95                100

GAA GCT AGT TTG TGG GGG AAG CAT TTA TGG TCG CCT AGT TAT TTC GCT      452
Glu Ala Ser Leu Trp Gly Lys His Leu Trp Ser Pro Ser Tyr Phe Ala
                105                110                115

GGG AGT TGT GGG GAC GCG CCT TTA GAG ATG ATT AAG CAA TAC ATA CAA      500
Gly Ser Cys Gly Asp Ala Pro Leu Glu Met Ile Lys Gln Tyr Ile Gln
                120                125                130

GAT CAA GAA ACA CCG CAT TAAATTAGCT AACTTTGATT TTAAAGTAGA ACGCGCTA      556
Asp Gln Glu Thr Pro His
                135

AAAAGCGAAT GGATCTAAGT GAAACAATGT TCAAATAGCC TAACGGCTAA ACGCTTACAT      616
CTCCGCCCTA AAGG
                630

```

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

Glu	Lys	Phe	Thr	Pro	Pro	Ile	Asn	Glu	Lys	Glu	Leu	Asn	Arg	Gln	Leu
65					70					75					80
Lys	Glu	Val	Arg	Trp	Phe	Asn	Lys	Glu	Thr	Pro	Thr	Ser	Lys	Asn	Thr
				85					90					95	
Tyr	Lys	Lys	Ile	Gln	Lys	Leu	Ala	Val	Tyr	Lys	Ser	Pro	Leu	Ile	Lys
			100					105					110		
Asp	Tyr	Leu	Tyr	Thr	Ile	Lys	Lys	Leu	Phe	Ala	Thr	Gln	Lys	Lys	Ile
		115					120					125			
Ile	Asp	Leu	Glu	Lys	Asn	Tyr	Lys	Asp	Leu	Arg	Ala	Leu	Lys	Glu	Glu
	130					135					140				
Phe	Ser	Lys	Asp	Leu	Glu	Thr	Asp	Leu	Ser	His	Ser	Lys	Lys	Arg	Phe
145					150					155					160
Glu	Leu	Tyr	Thr	Arg	Leu	Lys	Ser	Met	Ser	Lys	Val	Phe	Ile	Ser	Lys
				165				170						175	
Ser	Ile	Val	Lys	Asn	Leu	Glu	Lys	Ile	Ala	Leu	Asp	Phe	Lys	Ser	Asp
			180					185					190		
Arg	His	Ser	Ile	Ser	Gln	Arg	Ala	Phe	Glu	Phe	Phe	Lys	Tyr	Met	Asn
		195					200					205			
Tyr	Gln	Asn	Leu	Ser	Leu	Thr	Asp	Lys	Gly	Asn	Met	Phe	Leu	Val	Ala
	210					215					220				
Lys	Phe	Phe	Lys	Asp	Ser	Ala	Leu	Leu	Val	Asn	Ile	Ala	Arg	Phe	Glu
225					230					235					240
Met	Lys	Lys	Ile	Asp	Asp	Ser	Val	Lys	Asn	Ser	Asn	Pro	Gln	Asp	Asn
				245				250						255	
Leu	Leu	Asp	Lys	Gln	Val	Trp	Leu	Asn	Leu	Leu	Glu	His	Leu	Lys	Arg
		260					265						270		
Leu	Glu	Glu	Glu	Asn	Tyr	Cys	Phe	Ala	Lys	Lys	Arg	Lys	Glu	Phe	Leu
	275						280					285			
Glu	Thr	Arg	Ala	Met	Glu	Leu	Ser	Lys	Asp	Leu	Lys	Phe	Leu	Thr	Gln
	290					295					300				
Ala	Asn	Glu	Asn	Asp	Leu	Pro	Ile	Tyr	Glu	Arg	Gly	Gln	Arg	Asp	Lys
305					310					315					320
Ile	Ile	Lys	Arg	Cys	Glu	Lys	Ser	Leu	Asn	Phe	Leu	Gln	Lys	Glu	Leu
				325				330						335	
Gln	Cys	Phe	Lys	Thr	Leu	Leu	Lys	Ser	Ala	Ser	Ile	Ala	Leu	Glu	Asn
			340					345					350		
Leu	Gln	Asn	Asn	His	Gln	Ile	Thr	Ala	Val	Thr	Gln	Asp	Thr	Gln	Glu
		355					360					365			
Asn	Thr	Asn	Ala	Leu	Lys	Asn	Thr	Thr	Gln	Asp	Phe	Asn	Lys	Thr	Thr
	370					375					380				
Asn	Glu	Pro	Thr	Asn	Pro	Asn	Asn	Asn	Tyr	Gly	Met	Asp	Phe		
385					390					395					

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

CTT GAA GAG GAA AAT TAT TGT TTT GCT AAG AAA CGA AAA GAA TTC TTA 925
 Leu Glu Glu Glu Asn Tyr Cys Phe Ala Lys Lys Arg Lys Glu Phe Leu
 275 280 285

GAG ACT AGA GCG ATG GAG CTA TCA AAA GAT TTA AAA TTT TTA ACA CAG 973
 Glu Thr Arg Ala Met Glu Leu Ser Lys Asp Leu Lys Phe Leu Thr Gln
 290 295 300

GCT AAT GAA AAT GAT TTG CCC ATT TAT GAA AGA GGG CAA AGG GAT AAA 1021
 Ala Asn Glu Asn Asp Leu Pro Ile Tyr Glu Arg Gly Gln Arg Asp Lys
 305 310 315 320

ATC ATT AAA CGC TGT GAA AAA TCG CTT AAC TTT TTG CAG AAA GAA TTA 1069
 Ile Ile Lys Arg Cys Glu Lys Ser Leu Asn Phe Leu Gln Lys Glu Leu
 325 330 335

CAA TGC TTT AAA ACC TTA TTG AAA AGT GCA AGT ATA GCT TTA GAA AAC 1117
 Gln Cys Phe Lys Thr Leu Leu Lys Ser Ala Ser Ile Ala Leu Glu Asn
 340 345 350

TTG CAA AAT AAC CAT CAA ATC ACA GCC GTT ACA CAA GAC ACG CAA GAA 1165
 Leu Gln Asn Asn His Gln Ile Thr Ala Val Thr Gln Asp Thr Gln Glu
 355 360 365

AAC ACA AAC GCG CTC AAA AAT ACT ACT CAA GAT TTT AAC AAA ACT ACC 1213
 Asn Thr Asn Ala Leu Lys Asn Thr Thr Gln Asp Phe Asn Lys Thr Thr
 370 375 380

AAT GAA CCA ACA AAC CCT AAC AAT AAC TAT GGA ATG GAT TTT TAAAACCAT 1264
 Asn Glu Pro Thr Asn Pro Asn Asn Asn Tyr Gly Met Asp Phe
 385 390 395

CCATAAAATT AAATAACTTT ACTTAGCGTA TTTTTT 1300

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

Arg His Arg Asn Arg Ala Arg Cys Thr Arg Lys Gln Ala Arg Asn Asn
 1 5 10 15
 Lys Ser Phe Arg His Glu Asn Tyr Phe Tyr Lys Val Leu Gly Ser Ala
 20 25 30
 Thr Ser Gln Ile Glu Ser Leu Lys Lys Arg Glu Asn Ala Leu Phe Asp
 35 40 45
 His Leu Asp Ser Leu Lys Ser Leu Leu Glu Lys Thr His Trp Glu Lys
 50 55 60

His	Leu	Asp	Ser	Leu	Lys	Ser	Leu	Leu	Glu	Lys	Thr	His	Trp	Glu	Lys	
50						55					60					
GAA	AAA	TTC	ACG	CCC	CCA	ATA	AAT	GAA	AAA	GAA	CTT	AAT	AGG	CAA	CTT	301
Glu	Lys	Phe	Thr	Pro	Pro	Ile	Asn	Glu	Lys	Glu	Leu	Asn	Arg	Gln	Leu	
65					70				75					80		
AAA	GAA	GTG	AGA	TGG	TTC	AAT	AAA	GAA	ACT	CCA	ACT	TCT	AAA	AAC	ACT	349
Lys	Glu	Val	Arg	Trp	Phe	Asn	Lys	Glu	Thr	Pro	Thr	Ser	Lys	Asn	Thr	
				85					90					95		
TAT	AAG	AAA	ATT	CAA	AAA	TTA	GCT	GTT	TAT	AAA	AGC	CCT	TTA	ATA	AAA	397
Tyr	Lys	Lys	Ile	Gln	Lys	Leu	Ala	Val	Tyr	Lys	Ser	Pro	Leu	Ile	Lys	
			100					105					110			
GAT	TAT	CTT	TAT	ACC	ATT	AAA	AAA	CTT	TTT	GCC	ACA	CAA	AAA	AAG	ATT	445
Asp	Tyr	Leu	Tyr	Thr	Ile	Lys	Lys	Leu	Phe	Ala	Thr	Gln	Lys	Lys	Ile	
		115				120						125				
ATA	GAT	TTA	GAA	AAA	AAT	TAT	AAA	GAT	TTA	AGA	GCC	TTA	AAG	GAA	GAA	493
Ile	Asp	Leu	Glu	Lys	Asn	Tyr	Lys	Asp	Leu	Arg	Ala	Leu	Lys	Glu	Glu	
		130				135					140					
TTT	AGC	AAA	GAT	TTA	GAA	ACT	GAT	TTA	TCC	CAT	TCA	AAA	AAA	CGC	TTT	541
Phe	Ser	Lys	Asp	Leu	Glu	Thr	Asp	Leu	Ser	His	Ser	Lys	Lys	Arg	Phe	
145					150					155				160		
GAA	CTT	TAC	ACT	AGA	CTA	AAG	AGC	ATG	AGC	AAA	GTT	TTT	ATA	AGC	AAA	589
Glu	Leu	Tyr	Thr	Arg	Leu	Lys	Ser	Met	Ser	Lys	Val	Phe	Ile	Ser	Lys	
				165					170					175		
AGC	ATT	GTT	AAA	AAT	TTA	GAA	AAA	ATT	GCT	TTA	GAT	TTT	AAA	AGC	GAT	637
Ser	Ile	Val	Lys	Asn	Leu	Glu	Lys	Ile	Ala	Leu	Asp	Phe	Lys	Ser	Asp	
			180					185					190			
AGA	CAT	AGT	ATT	TCG	CAA	AGA	GCT	TTT	GAA	TTT	TTT	AAG	TAT	ATG	AAT	685
Arg	His	Ser	Ile	Ser	Gln	Arg	Ala	Phe	Glu	Phe	Phe	Lys	Tyr	Met	Asn	
		195				200						205				
TAT	CAA	AAT	TTA	AGC	TTG	ACT	GAT	AAA	GGC	AAT	ATG	TTT	TTA	GTG	GCT	733
Tyr	Gln	Asn	Leu	Ser	Leu	Thr	Asp	Lys	Gly	Asn	Met	Phe	Leu	Val	Ala	
	210					215					220					
AAG	TTT	TTT	AAA	GAT	AGT	GCT	TTA	CTT	GTT	AAT	ATT	GCT	AGG	TTT	GAA	781
Lys	Phe	Phe	Lys	Asp	Ser	Ala	Leu	Leu	Val	Asn	Ile	Ala	Arg	Phe	Glu	
225					230					235				240		
ATG	AAA	AAG	ATA	GAT	GAT	AGT	GTT	AAA	AAT	TCT	AAC	CCA	CAA	GAC	AAT	829
Met	Lys	Lys	Ile	Asp	Asp	Ser	Val	Lys	Asn	Ser	Asn	Pro	Gln	Asp	Asn	
				245					250					255		
TTA	TTA	GAC	AAA	CAA	GTT	TGG	CTC	AAT	CTT	TTA	GAG	CAT	TTA	AAA	AGA	877
Leu	Leu	Asp	Lys	Gln	Val	Trp	Leu	Asn	Leu	Leu	Glu	His	Leu	Lys	Arg	
			260					265					270			

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

```

Met Gly Lys Met Lys Gln Glu Thr Ala Ile Asp Tyr Glu Lys Leu Ala
 1             5             10             15
Asn His Trp Asn Asn Asn Asp Glu Asn Ser Glu Ala Leu Asn Ala Phe
      20             25             30
Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys Lys Ser Gln Lys Ile Arg
      35             40             45
Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala Cys Met Gly Glu Phe Tyr
      50             55             60
His Lys Asn Pro Lys Leu Phe
65             70

```

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 62...1255
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

```

TTGCTAACTC AAAAGGCGAA TTGCAATATT CTAACACGCC TAATATTTAT AAGGCGATTA      60
A AGA CAT AGA AAC AGA GCT AGA TGC ACT AGA AAA CAG GCT AGA AAC AAT      109
  Arg His Arg Asn Arg Ala Arg Cys Thr Arg Lys Gln Ala Arg Asn Asn
    1             5             10             15

AAG AGT TTT AGG CAT GAA AAC TAT TTT TAT AAA GTT TTG GGT AGT GCA      157
Lys Ser Phe Arg His Glu Asn Tyr Phe Tyr Lys Val Leu Gly Ser Ala
      20             25             30

ACT TCT CAA ATA GAA AGT TTG AAA AAA AGA GAA AAT GCC CTA TTT GAT      205
Thr Ser Gln Ile Glu Ser Leu Lys Lys Arg Glu Asn Ala Leu Phe Asp
      35             40             45

CAT TTA GAT AGT CTA AAA AGT TTA TTA GAA AAA ACA CAT TGG GAA AAA      253

```

```

Ser Leu Ala Val Phe Lys Lys Thr Leu Lys Lys Gly Leu Leu Leu Arg
385                      390                      395                      400
Pro Leu Asn Asn Thr Ile Tyr Leu Met Pro Pro Tyr Ile Ile Thr His
                      405                      410                      415
Glu Glu Val Lys Lys Ala Val Ala Gly Leu Val Glu Ile Leu Asp Glu
                      420                      425                      430
Leu Arg Lys Gly
                      435

```

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 82...294
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

```

AAAGCTAAAC AAGAGCAAGA GAAACGCATG GCATAAGAGC CATGCGCTTG GCAGTGAAAC      60
AAAAGAAAAA AAGGAAACAA C ATG GGA AAA ATG AAA CAA GAA ACA GCG ATT      111
                Met Gly Lys Met Lys Gln Glu Thr Ala Ile
                1                      5                      10

GAC TAT GAA AAA TTA GCG AAT CAT TGG AAT AAT AAT GAT GAA AAC AGC      159
Asp Tyr Glu Lys Leu Ala Asn His Trp Asn Asn Asn Asp Glu Asn Ser
                15                      20                      25

GAA GCA CTA AAC GCT TTT GCA GAC GCT TAC CTT TAT AAA CAT GAG AAA      207
Glu Ala Leu Asn Ala Phe Ala Asp Ala Tyr Leu Tyr Lys His Glu Lys
                30                      35                      40

AAG AGT CAA AAG ATT CGG GCA ATA GAG ATA AGT TCT CTA AAC AAA GCC      255
Lys Ser Gln Lys Ile Arg Ala Ile Glu Ile Ser Ser Leu Asn Lys Ala
                45                      50                      55

TGC ATG GGA GAA TTT TAC CAC AAA AAC CCA AAA TTA TTT TAATAACGAT CG      306
Cys Met Gly Glu Phe Tyr His Lys Asn Pro Lys Leu Phe
                60                      65                      70

CTCCAAGGAA CCAACGCCCC ATGACCTCAA GAAAAGAGAA TAGCTTGAAT CGGT      360

```

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

```

Met Asn Phe Gln Glu Asn Leu Ala Ala Leu Asp Leu Glu Tyr Leu Trp
 1           5           10           15
His Pro Cys Ser Gln Met Gln Glu His Gln Asn Phe Pro Ile Ile Pro
      20           25           30
Ile Lys Lys Ala Gln Gly Ile Tyr Leu Tyr Asp Phe Asn Asp Asn Ala
      35           40           45
Tyr Met Asp Leu Ile Ser Ser Trp Trp Val Asn Leu Phe Gly His Asn
      50           55           60
Asn Ala Tyr Ile Ser Gln Gln Leu Lys Asn Gln Ile Asp Asp Leu Glu
      65           70           75           80
His Val Leu Leu Ala Ser Phe Ser His Lys Pro Ile Ile Thr Leu Ser
      85           90           95
Gln Arg Leu Cys Gln Leu Thr His Met Asp Lys Cys Phe Tyr Ala Asp
      100          105          110
Asn Gly Ser Ser Cys Val Glu Ile Ala Leu Lys Met Ser Tyr His Ala
      115          120          125
His Phe Leu Lys Asn Gln Thr Arg Arg Lys Lys Leu Phe Leu Ser Leu
      130          135          140
Ser Asn Ser Tyr His Gly Glu Thr Leu Gly Ala Leu Ser Val Gly Asp
      145          150          155          160
Val Lys Leu Tyr Lys Asp Thr Tyr Thr Pro Leu Leu Leu Lys Asn Leu
      165          170          175
Thr Thr Pro Val Pro Lys Asn Asp His Glu Ile Glu Asn Ser Leu Asn
      180          185          190
Ala Leu Lys Arg Leu Leu Asp Lys His Ser Glu Glu Ile Cys Ala Phe
      195          200          205
Ile Ala Glu Pro Leu Leu Gln Cys Ala Gly Asn Met His Ile Tyr Ser
      210          215          220
Ala Arg Tyr Leu Lys Gln Ala Val Leu Leu Cys Lys Gln Lys Asn Ile
      225          230          235          240
His Ile Ile Phe Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Ser
      245          250          255
Met Phe Ala Tyr Glu Gln Cys Glu Ile Lys Pro Asp Phe Leu Cys Leu
      260          265          270
Ser Lys Gly Ile Ser Gly Gly Tyr Leu Pro Leu Ser Ala Leu Leu Thr
      275          280          285
His Asn Glu Ile Tyr Asn Gln Phe Tyr Ala Pro Tyr Glu Glu Asn Lys
      290          295          300
Ala Phe Leu His Ser His Ser Tyr Thr Gly Asn Ala Leu Ala Cys Ala
      305          310          315          320
Cys Ala Asn Ala Thr Leu Asp Ile Phe Glu Lys Glu Asn Val Ile Glu
      325          330          335
Lys Asn Lys Ala Leu Ser Gly Phe Ile Phe Asn Thr Leu Gln Asn Ala
      340          345          350
Leu Lys Pro Leu Met Glu Gln Gln Val Val Ser Asp Leu Arg His Leu
      355          360          365
Gly Met Val Phe Ala Phe Glu Val Phe Ile Gln Thr Lys Glu Arg Leu
      370          375          380

```


Thr	Gly	Ser	Met	Phe	Ala	Tyr	Glu	Gln	Cys	Glu	Ile	Lys	Pro	Asp	Phe	
255						260					265					
TTA	TGC	TTG	TCT	AAG	GGG	ATT	AGT	GGG	GGG	TAT	TTG	CCT	TTA	AGC	GCA	926
Leu	Cys	Leu	Ser	Lys	Gly	Ile	Ser	Gly	Gly	Tyr	Leu	Pro	Leu	Ser	Ala	
270					275					280					285	
CTA	TTA	ACC	CAT	AAT	GAA	ATC	TAT	AAC	CAA	TTT	TAC	GCC	CCC	TAT	GAA	974
Leu	Leu	Thr	His	Asn	Glu	Ile	Tyr	Asn	Gln	Phe	Tyr	Ala	Pro	Tyr	Glu	
				290					295					300		
GAA	AAT	AAA	GCG	TTT	TTG	CAT	TCG	CAC	AGC	TAC	ACA	GGA	AAC	GCT	TTG	1022
Glu	Asn	Lys	Ala	Phe	Leu	His	Ser	His	Ser	Tyr	Thr	Gly	Asn	Ala	Leu	
			305					310					315			
GCA	TGC	GCA	TGC	GCG	AAC	GCT	ACG	CTG	GAT	ATT	TTT	GAA	AAA	GAA	AAT	1070
Ala	Cys	Ala	Cys	Ala	Asn	Ala	Thr	Leu	Asp	Ile	Phe	Glu	Lys	Glu	Asn	
			320				325					330				
GTT	ATT	GAA	AAG	AAC	AAG	GCT	TTA	AGC	GGG	TTT	ATT	TTT	AAT	ACG	CTC	1118
Val	Ile	Glu	Lys	Asn	Lys	Ala	Leu	Ser	Gly	Phe	Ile	Phe	Asn	Thr	Leu	
	335					340					345					
CAA	AAC	GCA	TTA	AAA	CCC	TTG	ATG	GAG	CAA	CAA	GTG	GTG	TCT	GAT	TTA	1166
Gln	Asn	Ala	Leu	Lys	Pro	Leu	Met	Glu	Gln	Gln	Val	Val	Ser	Asp	Leu	
350					355					360					365	
AGG	CAT	TTG	GGC	ATG	GTC	TTT	GCC	TTT	GAA	GTC	TTT	ATT	CAA	ACC	AAA	1214
Arg	His	Leu	Gly	Met	Val	Phe	Ala	Phe	Glu	Val	Phe	Ile	Gln	Thr	Lys	
				370					375					380		
GAG	CGT	TTG	AGT	TTG	GCG	GTT	TTT	AAA	AAA	ACT	CTA	AAA	AAA	GGC	CTG	1262
Glu	Arg	Leu	Ser	Leu	Ala	Val	Phe	Lys	Lys	Thr	Leu	Lys	Lys	Gly	Leu	
			385					390					395			
TTA	TTA	CGC	CCT	TTA	AAC	AAC	ACC	ATT	TAC	CTC	ATG	CCC	CCT	TAC	ATT	1310
Leu	Leu	Arg	Pro	Leu	Asn	Asn	Thr	Ile	Tyr	Leu	Met	Pro	Pro	Tyr	Ile	
		400					405					410				
ATC	ACG	CAT	GAA	GAA	GTC	AAA	AAG	GCG	GTT	GCG	GGG	CTA	GTG	GAA	ATT	1358
Ile	Thr	His	Glu	Glu	Val	Lys	Lys	Ala	Val	Ala	Gly	Leu	Val	Glu	Ile	
	415					420				425						
CTT	GAT	GAG	TTA	AGA	AAA	GGC	TGAAAGCGTT	TTTAAAAATA	AAATAGTAAA	AAGC						1413
Leu	Asp	Glu	Leu	Arg	Lys	Gly										
430					435											
TTGAATTGGA	TCAAGCGATA	GCTTTTTT														1440

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

30	35	40	45	
GAT AAC GCT TAC ATG GAT TTG ATC AGC TCA TGG TGG GTG AAT CTT TTT				254
Asp Asn Ala Tyr Met Asp Leu Ile Ser Ser Trp Trp Val Asn Leu Phe	50	55	60	
GGG CAT AAT AAC GCC TAC ATC AGC CAG CAA CTC AAA AAT CAA ATT GAT				302
Gly His Asn Asn Ala Tyr Ile Ser Gln Gln Leu Lys Asn Gln Ile Asp	65	70	75	
GAT TTA GAG CAT GTC CTT TTG GCT TCT TTT AGC CAT AAG CCC ATT ATC				350
Asp Leu Glu His Val Leu Leu Ala Ser Phe Ser His Lys Pro Ile Ile	80	85	90	
ACG CTC TCT CAA AGG CTT TGC CAG CTC ACT CAT ATG GAT AAA TGC TTT				398
Thr Leu Ser Gln Arg Leu Cys Gln Leu Thr His Met Asp Lys Cys Phe	95	100	105	
TAT GCG GAT AAC GGC TCA TCT TGT GTT GAA ATC GCT TTG AAA ATG AGC				446
Tyr Ala Asp Asn Gly Ser Ser Cys Val Glu Ile Ala Leu Lys Met Ser	110	115	120	125
TAT CAC GCC CAT TTT TTA AAG AAT CAA ACG CGC CGC AAA AAG CTT TTT				494
Tyr His Ala His Phe Leu Lys Asn Gln Thr Arg Arg Lys Lys Leu Phe	130	135	140	
TTA TCG CTC TCT AAT TCC TAT CAT GGC GAG ACT TTG GGA GCG TTA AGC				542
Leu Ser Leu Ser Asn Ser Tyr His Gly Glu Thr Leu Gly Ala Leu Ser	145	150	155	
GTG GGC GAT GTG AAA CTT TAT AAA GAC ACT TAC ACC CCT TTA TTG CTC				590
Val Gly Asp Val Lys Leu Tyr Lys Asp Thr Tyr Thr Pro Leu Leu Leu	160	165	170	
AAA AAT CTC ACC ACA CCT GTG CCT AAA AAC GAC CAT GAA ATA GAA AAT				638
Lys Asn Leu Thr Thr Pro Val Pro Lys Asn Asp His Glu Ile Glu Asn	175	180	185	
AGT TTG AAC GCT TTA AAG CGT TTG TTA GAC AAG CAT AGT GAA GAA ATT				686
Ser Leu Asn Ala Leu Lys Arg Leu Leu Asp Lys His Ser Glu Glu Ile	190	195	200	205
TGC GCT TTC ATT GCA GAG CCT CTT TTG CAA TGC GCA GGG AAT ATG CAT				734
Cys Ala Phe Ile Ala Glu Pro Leu Leu Gln Cys Ala Gly Asn Met His	210	215	220	
ATT TAT AGC GCA AGA TAT TTA AAA CAA GCC GTT TTA TTG TGC AAG CAA				782
Ile Tyr Ser Ala Arg Tyr Leu Lys Gln Ala Val Leu Leu Cys Lys Gln	225	230	235	
AAA AAC ATC CAC ATT ATT TTT GAT GAA ATC GCT ACC GGG TTT GGG CGC				830
Lys Asn Ile His Ile Ile Phe Asp Glu Ile Ala Thr Gly Phe Gly Arg	240	245	250	
ACA GGG AGC ATG TTT GCT TAT GAA CAA TGC GAA ATT AAG CCG GAT TTT				878

```

305          310          315          320
Tyr Ala His Val Thr Phe Phe Ile Asn Gly Gly Val Glu Thr Pro Phe
          325          330          335
Lys Asn Glu Asn Arg Val Leu Ile Gln Ser Pro Lys Val Thr Tyr
          340          345          350
Asp Leu Lys Pro Glu Met Ser Ala Lys Glu Val Thr Leu Ala Val Leu
          355          360          365
Glu Gln Met Lys Leu Gly Thr Asp Leu Ile Ile Val Asn Phe Ala Asn
          370          375          380
Gly Asp Met Val Gly His Thr Gly Asn Phe Glu Ala Ser Val Lys Ala
385          390          395          400
Val Glu Ala Val Asp Ala Cys Leu Gly Glu Ile Leu Ser Leu Ala Lys
          405          410          415
Lys Leu Asp Tyr Ala Met Leu Leu Thr Ser Asp His Gly Asn Cys Glu
          420          425          430
Arg Met Lys Asp Glu Asn Gln Asn Pro Leu Thr Asn His Thr Ala Gly
          435          440          445
Ser Val Tyr Cys Phe Val Leu Gly Asp Gly Val Lys Ser Ile Lys Asn
          450          455          460
Gly Ala Leu Asn Asn Ile Ala Ser Ser Val Leu Lys Leu Met Gly Leu
465          470          475          480
Lys Ala Pro Ala Thr Met Asp Glu Pro Leu Phe
          485          490

```

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 72...1379
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```

ATAGTAAAT CAAATAACCT TATTTTAACC AAAGGTTATT AAAATTATCC TTATTATAGA      60
GAGTTTTTAA C ATG AAT TTT CAA GAA AAT TTA GCC GCT TTG GAT TTG GAG      110
      Met Asn Phe Gln Glu Asn Leu Ala Ala Leu Asp Leu Glu
          1          5          10

TAT CTT TGG CAC CCT TGT TCG CAA ATG CAA GAG CAT CAA AAT TTC CCC      158
Tyr Leu Trp His Pro Cys Ser Gln Met Gln Glu His Gln Asn Phe Pro
      15          20          25

ATT ATC CCC ATT AAA AAG GCT CAA GGG ATT TAC CTC TAT GAT TTT AAT      206
Ile Ile Pro Ile Lys Lys Ala Gln Gly Ile Tyr Leu Tyr Asp Phe Asn

```

AATGCAAATT GATGACGCAT TATTGCAACG CTTGGAAAAA TTGAGCATGC TAGAGATTAA 1614
AGATGA 1620

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```

Met Ala Gln Lys Thr Leu Leu Ile Ile Thr Asp Gly Ile Gly Tyr Arg
 1           5           10           15
Lys Asp Ser Asp His Asn Ala Phe Phe His Ala Lys Lys Pro Thr Tyr
          20           25           30
Asp Leu Met Phe Lys Thr Leu Pro Tyr Ser Leu Ile Asp Thr His Gly
          35           40           45
Leu Ser Val Gly Leu Pro Lys Gly Gln Met Gly Asn Ser Glu Val Gly
          50           55           60
His Met Cys Ile Gly Ala Gly Arg Val Leu Tyr Gln Asp Leu Val Lys
65           70           75           80
Ile Ser Leu Ser Leu Gln Asn Asp Glu Leu Lys Asn Asn Pro Ala Phe
          85           90           95
Leu Asn Thr Ile Gln Lys Ser Pro Val Val His Leu Met Gly Leu Met
          100          105          110
Ser Asp Gly Gly Val His Ser His Ile Glu His Phe Ile Ala Leu Ala
          115          120          125
Leu Glu Cys Glu Lys Ser His Lys Lys Val Cys Leu His Leu Ile Thr
          130          135          140
Asp Gly Arg Asp Val Ala Pro Lys Ser Ala Leu Thr Tyr Leu Lys Gln
          145          150          155          160
Met Gln Asn Ile Cys Asn Glu Ser Ile Gln Ile Ala Thr Ile Ser Gly
          165          170          175
Arg Phe Tyr Ala Met Asp Arg Asp Lys Arg Phe Glu Arg Ile Glu Leu
          180          185          190
Ala Tyr His Ser Leu Met Gly Leu Asn His Thr Pro Leu Ser Pro Ser
          195          200          205
Glu Tyr Ile Gln Ser Gln Tyr Asp Lys Asn Ile Thr Asp Glu Phe Ile
          210          215          220
Met Pro Ala Cys Phe Lys Asn Tyr Cys Gly Met Gln Asp Asp Glu Ser
          225          230          235          240
Phe Ile Phe Ile Asn Phe Arg Asn Asp Arg Ala Arg Glu Ile Val Ser
          245          250          255
Ala Leu Gly Gln Lys Gln Phe Ser Gly Phe Lys Arg Gln Val Phe Lys
          260          265          270
Lys Leu His Ile Ala Thr Met Thr Pro Tyr Asp Asn Thr Phe Pro Tyr
          275          280          285
Pro Val Leu Phe Pro Lys Glu Ser Val Gln Asn Thr Leu Ala Glu Val
          290          295          300
Val Ser Gln His Asn Leu Thr Gln Ser His Ile Ala Glu Thr Glu Lys

```

Lys	Lys	Leu	His	Ile	Ala	Thr	Met	Thr	Pro	Tyr	Asp	Asn	Thr	Phe	Pro	
			275					280					285			
TAC	CCT	GTT	TTA	TTC	CCC	AAA	GAA	AGC	GTT	CAA	AAC	ACG	CTC	GCT	GAA	974
Tyr	Pro	Val	Leu	Phe	Pro	Lys	Glu	Ser	Val	Gln	Asn	Thr	Leu	Ala	Glu	
		290					295				300					
GTG	GTC	TCT	CAA	CAC	AAC	CTG	ACC	CAA	AGC	CAT	ATC	GCT	GAA	ACT	GAA	1022
Val	Val	Ser	Gln	His	Asn	Leu	Thr	Gln	Ser	His	Ile	Ala	Glu	Thr	Glu	
	305					310				315						
AAA	TAC	GCG	CAT	GTA	ACC	TTT	TTC	ATC	AAT	GGC	GGA	GTG	GAG	ACG	CCT	1070
Lys	Tyr	Ala	His	Val	Thr	Phe	Phe	Ile	Asn	Gly	Gly	Val	Glu	Thr	Pro	
320					325				330						335	
TTT	AAA	AAT	GAA	AAC	CGG	GTG	CTT	ATC	CAA	AGC	CCT	AAA	GTT	ACC	ACT	1118
Phe	Lys	Asn	Glu	Asn	Arg	Val	Leu	Ile	Gln	Ser	Pro	Lys	Val	Thr	Thr	
			340					345					350			
TAT	GAC	TTA	AAG	CCT	GAA	ATG	AGC	GCT	AAA	GAA	GTA	ACC	CTT	GCG	GTG	1166
Tyr	Asp	Leu	Lys	Pro	Glu	Met	Ser	Ala	Lys	Glu	Val	Thr	Leu	Ala	Val	
		355					360					365				
TTA	GAG	CAA	ATG	AAA	CTA	GGC	ACG	GAT	TTG	ATC	ATT	GTG	AAT	TTT	GCT	1214
Leu	Glu	Gln	Met	Lys	Leu	Gly	Thr	Asp	Leu	Ile	Ile	Val	Asn	Phe	Ala	
	370					375						380				
AAT	GGC	GAT	ATG	GTA	GGG	CAT	ACG	GGG	AAT	TTT	GAA	GCG	AGC	GTC	AAA	1262
Asn	Gly	Asp	Met	Val	Gly	His	Thr	Gly	Asn	Phe	Glu	Ala	Ser	Val	Lys	
	385					390				395						
GCG	GTG	GAA	GCA	GTG	GAT	GCA	TGT	TTA	GGG	GAA	ATC	CTT	TCA	CTG	GCT	1310
Ala	Val	Glu	Ala	Val	Asp	Ala	Cys	Leu	Gly	Glu	Ile	Leu	Ser	Leu	Ala	
400				405					410					415		
AAA	AAA	TTG	GAT	TAC	GCC	ATG	CTT	TTA	ACC	AGC	GAT	CAT	GGG	AAT	TGC	1358
Lys	Lys	Leu	Asp	Tyr	Ala	Met	Leu	Leu	Thr	Ser	Asp	His	Gly	Asn	Cys	
			420					425				430				
GAG	CGC	ATG	AAA	GAC	GAA	AAC	CAA	AAC	CCC	TTA	ACC	AAC	CAC	ACC	GCC	1406
Glu	Arg	Met	Lys	Asp	Glu	Asn	Gln	Asn	Pro	Leu	Thr	Asn	His	Thr	Ala	
		435					440					445				
GGG	AGC	GTG	TAT	TGC	TTT	GTT	TTA	GGG	GAT	GGA	GTC	AAA	TCC	ATA	AAA	1454
Gly	Ser	Val	Tyr	Cys	Phe	Val	Leu	Gly	Asp	Gly	Val	Lys	Ser	Ile	Lys	
	450					455					460					
AAC	GGA	GCC	TTA	AAC	AAT	ATC	GCT	AGC	AGC	GTG	TTA	AAA	CTC	ATG	GGC	1502
Asn	Gly	Ala	Leu	Asn	Asn	Ile	Ala	Ser	Ser	Val	Leu	Lys	Leu	Met	Gly	
	465					470				475						
CTT	AAA	GCC	CCA	GCA	ACG	ATG	GAC	GAA	CCC	CTA	TTT	TAACTAAAG	GAAAAG			1554
Leu	Lys	Ala	Pro	Ala	Thr	Met	Asp	Glu	Pro	Leu	Phe					
480				485					490							

50	55	60	
GGG CAT ATG TGT ATT GGG GCT GGT AGG GTG CTC TAT CAG GAT TTA GTC			302
Gly His Met Cys Ile Gly Ala Gly Arg Val Leu Tyr Gln Asp Leu Val			
65	70	75	
AAA ATT TCT TTA AGC CTT CAA AAC GAT GAA TTA AAA AAC AAC CCC GCT			350
Lys Ile Ser Leu Ser Leu Gln Asn Asp Glu Leu Lys Asn Asn Pro Ala			
80	85	90	95
TTT TTA AAC ACG ATC CAA AAA AGC CCT GTG GTG CAT CTT ATG GGT TTA			398
Phe Leu Asn Thr Ile Gln Lys Ser Pro Val Val His Leu Met Gly Leu			
100	105	110	
ATG AGC GAT GGA GGC GTG CAT TCA CAC ATT GAG CAT TTT ATC GCT CTG			446
Met Ser Asp Gly Gly Val His Ser His Ile Glu His Phe Ile Ala Leu			
115	120	125	
GCT TTA GAG TGT GAA AAA TCC CAT AAA AAA GTC TGT CTG CAT TTA ATC			494
Ala Leu Glu Cys Glu Lys Ser His Lys Lys Val Cys Leu His Leu Ile			
130	135	140	
ACC GAT GGG CGC GAT GTC GCT CCT AAA AGC GCT TTA ACT TAT TTA AAA			542
Thr Asp Gly Arg Asp Val Ala Pro Lys Ser Ala Leu Thr Tyr Leu Lys			
145	150	155	
CAA ATG CAA AAT ATC TGC AAT GAA AGC ATT CAA ATC GCT ACC ATA AGC			590
Gln Met Gln Asn Ile Cys Asn Glu Ser Ile Gln Ile Ala Thr Ile Ser			
160	165	170	175
GGT CGT TTT TAT GCC ATG GAT AGG GAT AAG CGC TTT GAA AGG ATT GAG			638
Gly Arg Phe Tyr Ala Met Asp Arg Asp Lys Arg Phe Glu Arg Ile Glu			
180	185	190	
CTT GCG TAT CAT AGC TTA ATG GGG CTT AAT CAC ACG CCT TTA AGC CCT			686
Leu Ala Tyr His Ser Leu Met Gly Leu Asn His Thr Pro Leu Ser Pro			
195	200	205	
AGC GAG TAT ATC CAA AGC CAG TAT GAT AAA AAT ATC ACC GAT GAA TTT			734
Ser Glu Tyr Ile Gln Ser Gln Tyr Asp Lys Asn Ile Thr Asp Glu Phe			
210	215	220	
ATC ATG CCC GCT TGT TTT AAA AAT TAT TGC GGC ATG CAA GAT GAT GAG			782
Ile Met Pro Ala Cys Phe Lys Asn Tyr Cys Gly Met Gln Asp Asp Glu			
225	230	235	
AGT TTT ATT TTT ATC AAT TTC AGG AAT GAT AGG GCT AGA GAA ATC GTG			830
Ser Phe Ile Phe Ile Asn Phe Arg Asn Asp Arg Ala Arg Glu Ile Val			
240	245	250	255
AGC GCT TTA GGC CAA AAA CAA TTC AGT GGC TTT AAG CGC CAA GTT TTT			878
Ser Ala Leu Gly Gln Lys Gln Phe Ser Gly Phe Lys Arg Gln Val Phe			
260	265	270	
AAA AAA CTC CAT ATC GCT ACC ATG ACG CCT TAT GAT AAC ACT TTC CCC			926

```

145          150          155          160
Gly Leu Glu Arg Leu Ala Met Tyr Val Gln Lys Val Glu Asn Ile Leu
          165          170          175
Glu Ile Glu Trp Ala Lys Lys Asn His Asp Ser Val Asn Tyr Ala Gln
          180          185          190
Val His Leu Glu Ser Glu Tyr Glu Phe Ser Lys Tyr His Phe Glu Thr
          195          200          205
Ala Ser Val Lys Arg Leu Leu Glu Met Phe Lys Asn Ala Gln Ala Glu
          210          215          220
Ala Leu His Cys Leu Glu Asn Lys Leu Pro Leu Pro Ala Tyr Asp Phe
225          230          235          240
Val Met Leu Cys Ser His Phe Phe Asn Ile Leu Asp Ala Arg Lys Ala
          245          250          255
Ile Ser Val Ala Glu Arg Gln Asn Tyr Ile Leu Gln Ile Arg Asp Leu
          260          265          270
Ala Lys Gly Cys Ala Leu Leu Tyr Lys Glu Gln Glu Glu Glu Arg Glu
          275          280          285
Glu Arg Leu Lys Asn Ala Leu Thr Lys Ala Glu Asn Gly Val Ser
          290          295          300

```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...1538
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

```

GGCAAAGGAA TGCGATTTTA GCTAACCACA TCACTCTCAT GCAAGAGCTT TAAAAAGTCC      60
TAAAA ATG GCG CAA AAA ACT CTT TTG ATT ATC ACT GAT GGC ATT GGG TAT      110
  Met Ala Gln Lys Thr Leu Leu Ile Ile Thr Asp Gly Ile Gly Tyr
    1             5             10             15

CGT AAA GAT AGC GAT CAT AAC GCT TTC TTC CAT GCC AAA AAA CCC ACT      158
Arg Lys Asp Ser Asp His Asn Ala Phe Phe His Ala Lys Lys Pro Thr
    20             25             30

TAT GAT TTG ATG TTT AAA ACC TTG CCT TAT AGC CTG ATT GAT ACG CAT      206
Tyr Asp Leu Met Phe Lys Thr Leu Pro Tyr Ser Leu Ile Asp Thr His
    35             40             45

GGC TTG AGC GTG GGC TTA CCT AAG GGG CAA ATG GGA AAT TCT GAA GTG      254
Gly Leu Ser Val Gly Leu Pro Lys Gly Gln Met Gly Asn Ser Glu Val

```

CCC TTG CCG GCT TAT GAT TTT GTG ATG TTA TGC TCG CAT TTT TTC AAT	832
Pro Leu Pro Ala Tyr Asp Phe Val Met Leu Cys Ser His Phe Phe Asn	
235 240 245	
ATT TTA GAC GCC AGA AAA GCG ATT TCG GTG GCT GAA AGG CAA AAT TAT	880
Ile Leu Asp Ala Arg Lys Ala Ile Ser Val Ala Glu Arg Gln Asn Tyr	
250 255 260 265	
ATT TTA CAA ATC AGG GAT TTA GCC AAA GGG TGT GCG CTT CTT TAT AAA	928
Ile Leu Gln Ile Arg Asp Leu Ala Lys Gly Cys Ala Leu Leu Tyr Lys	
270 275 280	
GAA CAA GAA GAA GAG AGG GAA GAG CGT TTA AAA AAC GCT TTA ACA AAG	976
Glu Gln Glu Glu Glu Arg Glu Glu Arg Leu Lys Asn Ala Leu Thr Lys	
285 290 295	
GCT GAA AAT GGC GTT AGT TAAGGAAGTG TTGGTAGTTT TGAATCGCCT TTCGCCTT	1032
Ala Glu Asn Gly Val Ser	
300	
TTGAACTCCA AGAATCATGG GATAATAGCG GGTGAATGT GGGGAGTGAA AATAGTGAAT	1092
TTAGCGAGAT TG	1104

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met	Gln	Asp	Phe	Ser	Ser	Leu	Leu	Leu	Lys	Leu	Gln	Glu	Tyr	Trp	Lys
1				5					10					15	
Asn	Gln	Gly	Cys	Leu	Val	Ile	Gln	Pro	Tyr	Asp	Ile	Pro	Ala	Gly	Ala
			20					25					30		
Gly	Thr	Phe	His	Pro	Ala	Thr	Leu	Leu	Arg	Ser	Leu	Asp	Lys	Lys	Pro
		35				40						45			
Trp	Asn	Val	Ala	Tyr	Val	Ala	Pro	Ser	Arg	Arg	Pro	Thr	Asp	Gly	Arg
	50					55					60				
Tyr	Gly	Glu	Asn	Pro	Asn	Arg	Leu	Gly	Ser	Tyr	Tyr	Gln	Phe	Gln	Val
65					70					75				80	
Val	Ile	Lys	Pro	Ser	Pro	Ser	Asn	Ile	Gln	Glu	Leu	Tyr	Leu	Lys	Ser
				85					90					95	
Leu	Glu	Val	Leu	Gly	Ile	Asn	Leu	Asn	Glu	His	Asp	Ile	Arg	Phe	Val
			100					105					110		
Glu	Asp	Asn	Trp	Glu	Ser	Pro	Thr	Leu	Gly	Ala	Trp	Gly	Leu	Gly	Trp
		115					120					125			
Glu	Val	Trp	Leu	Asp	Gly	Met	Glu	Val	Thr	Gln	Phe	Thr	Tyr	Phe	Gln
	130					135					140				
Gln	Val	Gly	Gly	Ile	Ala	Cys	Ser	Pro	Ile	Pro	Val	Glu	Ile	Thr	Tyr

AAA CTA CAA GAG TAT TGG AAG AAT CAA GGC TGT TTG GTG ATC CAG CCT	160
Lys Leu Gln Glu Tyr Trp Lys Asn Gln Gly Cys Leu Val Ile Gln Pro	
10 15 20 25	
TAT GAT ATT CCT GCA GGA GCT GGG ACA TTC CAT CCG GCC ACG CTT TTA	208
Tyr Asp Ile Pro Ala Gly Ala Gly Thr Phe His Pro Ala Thr Leu Leu	
30 35 40	
AGG AGT TTG GAT AAA AAG CCG TGG AAT GTG GCG TAT GTC GCG CCC TCT	256
Arg Ser Leu Asp Lys Lys Pro Trp Asn Val Ala Tyr Val Ala Pro Ser	
45 50 55	
AGA AGG CCT ACT GAT GGG CGC TAT GGG GAA AAC CCT AAC CGC TTG GGG	304
Arg Arg Pro Thr Asp Gly Arg Tyr Gly Glu Asn Pro Asn Arg Leu Gly	
60 65 70	
AGT TAT TAC CAA TTC CAA GTA GTC ATC AAG CCC AGC CCT TCT AAT ATC	352
Ser Tyr Tyr Gln Phe Gln Val Val Ile Lys Pro Ser Pro Ser Asn Ile	
75 80 85	
CAG GAA CTC TAT TTA AAA AGC TTA GAA GTG TTA GGG ATA AAC CTT AAT	400
Gln Glu Leu Tyr Leu Lys Ser Leu Glu Val Leu Gly Ile Asn Leu Asn	
90 95 100 105	
GAG CAT GAT ATA CGA TTT GTA GAA GAC AAT TGG GAG AGT CCG ACT TTA	448
Glu His Asp Ile Arg Phe Val Glu Asp Asn Trp Glu Ser Pro Thr Leu	
110 115 120	
GGG GCA TGG GGG CTT GGC TGG GAA GTG TGG CTT GAT GGC ATG GAA GTT	496
Gly Ala Trp Gly Leu Gly Trp Glu Val Trp Leu Asp Gly Met Glu Val	
125 130 135	
ACG CAA TTC ACT TAT TTC CAG CAA GTG GGG GGC ATT GCT TGT AGC CCT	544
Thr Gln Phe Thr Tyr Phe Gln Gln Val Gly Gly Ile Ala Cys Ser Pro	
140 145 150	
ATT CCT GTA GAG ATC ACT TAC GGC TTA GAA AGA TTA GCG ATG TAT GTG	592
Ile Pro Val Glu Ile Thr Tyr Gly Leu Glu Arg Leu Ala Met Tyr Val	
155 160 165	
CAA AAA GTG GAA AAT ATC CTA GAG ATT GAA TGG GCT AAA AAA AAT CAT	640
Gln Lys Val Glu Asn Ile Leu Glu Ile Glu Trp Ala Lys Lys Asn His	
170 175 180 185	
GAC AGC GTG AAT TAC GCA CAA GTG CAT TTG GAA AGC GAA TAC GAA TTC	688
Asp Ser Val Asn Tyr Ala Gln Val His Leu Glu Ser Glu Tyr Glu Phe	
190 195 200	
AGC AAG TAT CAT TTT GAA ACA GCG AGC GTG AAA CGG CTA TTA GAA ATG	736
Ser Lys Tyr His Phe Glu Thr Ala Ser Val Lys Arg Leu Leu Glu Met	
205 210 215	
TTT AAA AAC GCT CAA GCC GAA GCC TTG CAT TGC TTG GAA AAC AAG CTC	784
Phe Lys Asn Ala Gln Ala Glu Ala Leu His Cys Leu Glu Asn Lys Leu	
220 225 230	

50		55		60	
Trp	Ala	Glu	Leu	Gly	Ile
65		70		75	
Ile	Tyr	Glu	Pro	Asn	Ser
		85		90	
Phe	Asn	Pro	Phe	Asp	Ser
		100		105	
Ser	Tyr	His	Gly	Gly	Leu
		115		120	
Ser	Arg	Lys	Asp	Leu	Lys
		130		135	
Ile	Ser	Leu	Pro	Leu	Gly
145				150	
Asn	Gln	Glu	Leu	Val	Gly
				165	
Gln	Ile	Ile	Gly	Ile	Met
				180	
Leu	Ile	Glu	Ala	Phe	Leu
				195	
Trp	Ala	Lys	Lys	His	Thr
				210	
Gly	Leu	Gly	Tyr	Ser	Leu
225				230	
Pro	Asp	Ser	Gln	Met	Gly
				245	
Ile	Leu	Ser	Leu	Phe	Met
				260	
Ala	Thr	Lys	Asn	Ser	Lys
				275	

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 86...994
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

AGCGAATTAG	CCTTGCTTTT	AAAGGGTAAG	AGTGTGCTAG	AGAGCATGAA	CGATTTGATC	60
AGACGCGCTT	AAAAGGAAAG	AGAGC	ATG	CAA	GAT	112
		Met	Gln	Asp	Phe	
		1		5		

GGG AAT TTT TTA AAC CAG GAG CTT GTG GGA AGA ATT GTC CCC AAA GAC	591
Gly Asn Phe Leu Asn Gln Glu Leu Val Gly Arg Ile Val Pro Lys Asp	
160 165 170	
AGC CAT TTA GGG CAA ATC ATA GGC ATT ATG GTG GAT AAT GAG TTG CGT	639
Ser His Leu Gly Gln Ile Ile Gly Ile Met Val Asp Asn Glu Leu Arg	
175 180 185	
TAT CCC AGC CAA TTG ATT GAA GCG TTT TTA GAG GGG GTT ATC GTG TTT	687
Tyr Pro Ser Gln Leu Ile Glu Ala Phe Leu Glu Gly Val Ile Val Phe	
190 195 200	
TTA ATG GTA ATG TGG GCT AAA AAA CAC ACC AAA ACG CAT GGG TTG CTG	735
Leu Met Val Met Trp Ala Lys Lys His Thr Lys Thr His Gly Leu Leu	
205 210 215 220	
ATT GTG GTT TAT GGT TTG GGG TAT TCC TTG ATG CGC TTT ATT GCG GAA	783
Ile Val Val Tyr Gly Leu Gly Tyr Ser Leu Met Arg Phe Ile Ala Glu	
225 230 235	
TTT TAC AGA GAG CCG GAC AGC CAA ATG GGG GTT TAT TTT TTA AAT TTG	831
Phe Tyr Arg Glu Pro Asp Ser Gln Met Gly Val Tyr Phe Leu Asn Leu	
240 245 250	
AGC ATG GGG CAG ATT TTA AGC TTA TTT ATG GTA ATT GTT TCG TTA GGG	879
Ser Met Gly Gln Ile Leu Ser Leu Phe Met Val Ile Val Ser Leu Gly	
255 260 265	
ATT TTA TTG TAT GCT ACA AAA AAT TCT AAA AAA ATA AAG GAA AAT CAA T	928
Ile Leu Leu Tyr Ala Thr Lys Asn Ser Lys Lys Ile Lys Glu Asn Gln	
270 275 280	
GAAATTTTGTG GATCAAGAAA AAAGAAGACA ATTATTAAAC GAGCGCCATT CTTGCAAGAT	988
GTTTGATAGC C	999

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Met Asn Ala Trp Asn Thr Ile Tyr Asp Gln Phe Asn Pro Ile Ala Phe	
1 5 10 15	
Ser Leu Gly Ser Ile Glu Val His Trp Tyr Gly Leu Ala Tyr Ala Cys	
20 25 30	
Ala Ile Val Thr Ala Phe Tyr Met Ala Leu Arg Met Ile Gln Lys Asp	
35 40 45	
Pro Lys Arg Phe Pro Ile Glu Arg Lys Glu Phe Glu Ser Tyr Phe Leu	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 76...927

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

GCACATAAAA TCGCGCTACT AGGGTATGAA TTTGAAGCGA TCGCTCCTAA AGAATTTGAA      60
ATTTAAGGAT TGATC ATG AAC GCT TGG AAT ACG ATT TAT GAT CAA TTT AAC      111
      Met Asn Ala Trp Asn Thr Ile Tyr Asp Gln Phe Asn
              1              5              10

CCT ATC GCT TTT AGT CTT GGC AGT ATT GAA GTG CAT TGG TAT GGT TTG      159
Pro Ile Ala Phe Ser Leu Gly Ser Ile Glu Val His Trp Tyr Gly Leu
      15              20              25

GCG TAT GCG TGT GCG ATT GTT ACC GCT TTT TAT ATG GCG TTA AGA ATG      207
Ala Tyr Ala Cys Ala Ile Val Thr Ala Phe Tyr Met Ala Leu Arg Met
      30              35              40

ATC CAA AAA GAC CCC AAG CGA TTC CCC ATT GAA AGG AAG GAA TTT GAG      255
Ile Gln Lys Asp Pro Lys Arg Phe Pro Ile Glu Arg Lys Glu Phe Glu
      45              50              55              60

AGT TAT TTT TTA TGG GCG GAG CTT GGC ATT GTG CTA GGG GCA AGG ATA      303
Ser Tyr Phe Leu Trp Ala Glu Leu Gly Ile Val Leu Gly Ala Arg Ile
              65              70              75

GGA TAC ATT CTT ATT TAT GAG CCT AAT TCT GGC TAT TAT TTG ACG CAT      351
Gly Tyr Ile Leu Ile Tyr Glu Pro Asn Ser Gly Tyr Tyr Leu Thr His
              80              85              90

TTT TGG CAA ATC TTT AAC CCT TTT GAT AGC CAT GGG AAT TTT GTA GGC      399
Phe Trp Gln Ile Phe Asn Pro Phe Asp Ser His Gly Asn Phe Val Gly
              95              100              105

ATT CGT GGG ATG AGC TAT CAT GGG GGG TTG GTG GGG TTT TTG ATC GCT      447
Ile Arg Gly Met Ser Tyr His Gly Gly Leu Val Gly Phe Leu Ile Ala
              110              115              120

TCG TAT CTT TAT AGC CGT AAG GAT TTG AAA AAG CTT TTG ATT TAT TTG      495
Ser Tyr Leu Tyr Ser Arg Lys Asp Leu Lys Lys Leu Leu Ile Tyr Leu
              125              130              135              140

GAT TTG ATT GCG ATC AGC CTG CCT TTA GGG TAT GTT TTT GGG AGG ATT      543
Asp Leu Ile Ala Ile Ser Leu Pro Leu Gly Tyr Val Phe Gly Arg Ile
              145              150              155

```

185 190 195

CTG AAT TTA GGG TTT TGAAAGGTTA AAAATGAAAT TTAAATTTTT GAATATGGAT A 747
 Leu Asn Leu Gly Phe
 200

ATGAAAGCGG TTTTATTTTG ATTGAAAAAG AATTGAAACG ATTAAACATT CTCGCTCAAG 807
 TCA 810

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Met	Gln	Gly	Phe	Leu	Leu	Gln	Thr	Gln	Ser	Ile	Arg	Asp	Glu	Asp	Leu	1	5	10	15
Ile	Val	Arg	Val	Leu	Thr	Lys	Asn	Gln	Leu	Lys	Thr	Leu	Tyr	Arg	Phe	20	25	30	
Tyr	Gly	Lys	Arg	His	Ser	Val	Leu	Asn	Val	Gly	Arg	Lys	Ile	Asp	Phe	35	40	45	
Glu	Glu	Glu	Asn	Asp	Asp	Lys	Phe	Leu	Pro	Lys	Leu	Arg	Asn	Ile	Leu	50	55	60	
His	Leu	Gly	Tyr	Ile	Trp	Glu	Arg	Glu	Met	Glu	Arg	Leu	Phe	Phe	Trp	65	70	75	80
Gln	Arg	Phe	Cys	Ala	Leu	Leu	Phe	Arg	His	Leu	Glu	Gly	Val	His	Ser	85	90	95	
Leu	Asp	Ser	Val	Tyr	Phe	Asp	Thr	Leu	Asp	Asp	Gly	Ala	Asn	Lys	Leu	100	105	110	
Ala	Lys	Gln	His	Pro	Leu	Arg	Val	Ile	Leu	Glu	Met	Tyr	Ala	Thr	Leu	115	120	125	
Leu	Asn	Phe	Glu	Gly	Arg	Leu	Gln	Ser	Tyr	Asn	Ser	Cys	Phe	Leu	Cys	130	135	140	
Asp	Ala	Lys	Leu	Glu	Arg	Ser	Val	Ala	Leu	Ala	Gln	Gly	Phe	Ile	Leu	145	150	155	160
Ala	His	Pro	Ser	Cys	Leu	Lys	Ala	Lys	Ser	Leu	Asn	Leu	Glu	Lys	Ile	165	170	175	
Gln	Ala	Phe	Phe	Arg	Thr	Gln	Ser	Thr	Ile	Asp	Leu	Glu	Thr	Glu	Glu	180	185	190	
Val	Glu	Glu	Leu	Trp	Arg	Thr	Leu	Asn	Leu	Gly	Phe					195	200		

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

TCTGCAAATC CCATGTTTTT CCTTAATTTT GCAGTTTTGT TAGGATTGTA TCCAAGTTTT	60
GCTTATAATA AACAAAATTA GCTTAAGAGT AGTG ATG CAA GGG TTT CTT TTA CAA	115
Met Gln Gly Phe Leu Leu Gln	
1 5	
ACA CAA AGC ATA AGA GAT GAA GAT TTG ATC GTG CGC GTT TTA ACC AAA	163
Thr Gln Ser Ile Arg Asp Glu Asp Leu Ile Val Arg Val Leu Thr Lys	
10 15 20	
AAC CAG CTC AAA ACC CTC TAT CGT TTC TAT GGC AAA CGC CAT AGC GTG	211
Asn Gln Leu Lys Thr Leu Tyr Arg Phe Tyr Gly Lys Arg His Ser Val	
25 30 35	
CTG AAT GTG GGG CGT AAA ATT GAT TTT GAA GAA GAA AAC GAT GAT AAG	259
Leu Asn Val Gly Arg Lys Ile Asp Phe Glu Glu Glu Asn Asp Asp Lys	
40 45 50 55	
TTT TTA CCC AAG TTA AGG AAT ATT TTG CAT TTA GGC TAT ATT TGG GAA	307
Phe Leu Pro Lys Leu Arg Asn Ile Leu His Leu Gly Tyr Ile Trp Glu	
60 65 70	
AGA GAA ATG GAG CGC TTG TTT TTT TGG CAA CGC TTT TGC GCT CTC TTG	355
Arg Glu Met Glu Arg Leu Phe Phe Trp Gln Arg Phe Cys Ala Leu Leu	
75 80 85	
TTT AGG CAT TTA GAA GGC GTG CAT TCT TTA GAT AGC GTC TAT TTT GAC	403
Phe Arg His Leu Glu Gly Val His Ser Leu Asp Ser Val Tyr Phe Asp	
90 95 100	
ACT TTA GAT GAT GGG GCT AAC AAA CTC GCC AAA CAG CAC CCC TTA AGA	451
Thr Leu Asp Asp Gly Ala Asn Lys Leu Ala Lys Gln His Pro Leu Arg	
105 110 115	
GTG ATT TTA GAA ATG TAT GCA ACG CTT TTG AAT TTT GAA GGG CGC TTG	499
Val Ile Leu Glu Met Tyr Ala Thr Leu Leu Asn Phe Glu Gly Arg Leu	
120 125 130 135	
CAA AGT TAC AAT TCT TGT TTT TTA TGC GAT GCA AAA TTA GAG CGT TCT	547
Gln Ser Tyr Asn Ser Cys Phe Leu Cys Asp Ala Lys Leu Glu Arg Ser	
140 145 150	
GTC GCT TTA GCG CAA GGG TTT ATT CTA GCG CAC CCC TCT TGT TTG AAA	595
Val Ala Leu Ala Gln Gly Phe Ile Leu Ala His Pro Ser Cys Leu Lys	
155 160 165	
GCT AAA AGC CTA AAT TTA GAA AAA ATC CAA GCT TTT TTT CGC ACT CAA	643
Ala Lys Ser Leu Asn Leu Glu Lys Ile Gln Ala Phe Phe Arg Thr Gln	
170 175 180	
AGC ACG ATT GAT TTA GAA ACA GAA GAA GTA GAA GAA TTA TGG CGC ACG	691
Ser Thr Ile Asp Leu Glu Thr Glu Glu Val Glu Glu Leu Trp Arg Thr	

```

Met Gly Phe Ala Asp Phe Phe Lys Asn Phe Lys Ile Asn Lys Leu Arg
 1           5           10           15
Thr Ala Pro Ser Lys Glu Glu Gln Pro Ser His Trp Val Lys Cys Pro
      20           25           30
Lys Cys Tyr Ala Leu Met Tyr His Lys Glu Val Phe Ser Lys Tyr Ser
      35           40           45
Val Cys Leu Lys Cys His Tyr His Phe Arg Met Lys Ala Ala Glu Arg
      50           55           60
Ile Glu Phe Leu Cys Asp Val Gly Ser Phe Glu Glu Phe Asp Lys His
65           70           75           80
Leu Arg Pro Asn Asp Pro Leu Asn Phe Val Asp Lys Glu Ser Tyr Lys
      85           90           95
Gln Arg Ile Lys Lys Tyr Glu Lys Arg Thr Asn Arg Pro Ser Ser Val
      100          105          110
Ile Ser Gly Glu Ala Lys Ile Asn Arg Met Pro Leu Gln Ile Val Val
      115          120          125
Phe Asp Phe Ser Phe Met Gly Gly Ser Leu Gly Ser Val Glu Gly Glu
      130          135          140
Lys Ile Val Arg Ala Ile Asn Arg Ala Val Ala Lys Arg Glu Ala Leu
145          150          155          160
Leu Ile Val Ser Ala Ser Gly Gly Ala Arg Met Gln Glu Ser Thr Tyr
      165          170          175
Ser Leu Met Gln Met Ala Lys Thr Ser Ala Ala Leu Asn Arg Leu Ser
      180          185          190
Glu Ala Lys Leu Pro Phe Ile Ser Leu Leu Ser Asp Pro Thr Tyr Gly
      195          200          205
Gly Val Ser Ala Ser Phe Ala Phe Leu Gly Asp Leu Ile Ile Ala Glu
      210          215          220
Pro Gly Ala Met Ile Gly Phe Ala Gly Pro Arg Val Ile Lys Gln Thr
225          230          235          240
Ile Gly Ala Asp Leu Pro Glu Gly Phe Gln Thr Ala Glu Phe Leu Leu
      245          250          255
Glu His Gly Leu Ile Asp Met Ile Val His Arg Lys Asp Leu Lys Lys
      260          265          270
Thr Leu Ser Asp Leu Ile Ala Met Met Thr His Lys Thr Ser Lys Ile
      275          280          285
Phe

```

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 95...706
- (D) OTHER INFORMATION:

AGC TTT ATG GGG GGG AGT TTA GGC TCT GTG GAG GGC GAA AAG ATC GTA	550
Ser Phe Met Gly Gly Ser Leu Gly Ser Val Glu Gly Glu Lys Ile Val	
135 140 145	
AGA GCA ATC AAT CGC GCG GTC GCT AAA AGA GAA GCG TTA TTG ATT GTT	598
Arg Ala Ile Asn Arg Ala Val Ala Lys Arg Glu Ala Leu Leu Ile Val	
150 155 160	
TCA GCG AGT GGG GGG GCT AGG ATG CAA GAA TCC ACT TAT TCG CTC ATG	646
Ser Ala Ser Gly Gly Ala Arg Met Gln Glu Ser Thr Tyr Ser Leu Met	
165 170 175	
CAA ATG GCT AAA ACG AGC GCG GCT TTG AAC CGA TTG AGT GAG GCC AAA	694
Gln Met Ala Lys Thr Ser Ala Ala Leu Asn Arg Leu Ser Glu Ala Lys	
180 185 190 195	
CTC CCT TTC ATT TCG CTC TTA AGC GAT CCC ACT TAT GGG GGC GTT AGC	742
Leu Pro Phe Ile Ser Leu Leu Ser Asp Pro Thr Tyr Gly Gly Val Ser	
200 205 210	
GCA TCT TTT GCT TTT TTA GGG GAT CTC ATT ATC GCA GAG CCA GGG GCG	790
Ala Ser Phe Ala Phe Leu Gly Asp Leu Ile Ile Ala Glu Pro Gly Ala	
215 220 225	
ATG ATA GGC TTT GCG GGG CCT AGG GTG ATT AAG CAA ACT ATA GGG GCG	838
Met Ile Gly Phe Ala Gly Pro Arg Val Ile Lys Gln Thr Ile Gly Ala	
230 235 240	
GAT TTG CCT GAG GGC TTT CAA ACA GCG GAA TTT TTA TTA GAG CAT GGC	886
Asp Leu Pro Glu Gly Phe Gln Thr Ala Glu Phe Leu Leu Glu His Gly	
245 250 255	
TTG ATT GAT ATG ATT GTG CAC AGG AAG GAT TTG AAG AAG ACT TTG AGC	934
Leu Ile Asp Met Ile Val His Arg Lys Asp Leu Lys Lys Thr Leu Ser	
260 265 270 275	
GAT CTC ATC GCT ATG ATG ACG CAT AAG ACT TCA AAG ATT TTT TAAAGTTTT	985
Asp Leu Ile Ala Met Met Thr His Lys Thr Ser Lys Ile Phe	
280 285	
AACATTGATG CGTTGCGTGG TGTATTCTAT CGCTAAAAGT TCGCCTTTAG AGTTAGTGAA	1045
AATCTATC	1053

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 110...976
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```

CTTTGTGTTT GTAAAAGAAA CCCTTGCATC ACTACTCTTA AGCTAATTTT GTTTATTATA      60
AGCAAACTT GGATACAATC CTAACAAAC TGCAAAATTA AGGAAAAAC ATG GGA TTT      118
                                   Met Gly Phe
                                   1

GCA GAT TTC TTT AAA AAT TTT AAG ATC AAT AAA TTG CGG ACA GCG CCA      166
Ala Asp Phe Phe Lys Asn Phe Lys Ile Asn Lys Leu Arg Thr Ala Pro
   5                               10                               15

AGT AAG GAA GAA CAG CCA AGC CAT TGG GTG AAA TGC CCT AAA TGT TAT      214
Ser Lys Glu Glu Gln Pro Ser His Trp Val Lys Cys Pro Lys Cys Tyr
  20                               25                               30                               35

GCG TTA ATG TAT CAT AAA GAA GTG TTT AGT AAA TAC AGC GTG TGT TTG      262
Ala Leu Met Tyr His Lys Glu Val Phe Ser Lys Tyr Ser Val Cys Leu
          40                               45                               50

AAA TGC CAT TAC CAT TTC CGC ATG AAA GCG GCT GAA AGG ATT GAA TTT      310
Lys Cys His Tyr His Phe Arg Met Lys Ala Ala Glu Arg Ile Glu Phe
          55                               60                               65

TTA TGC GAT GTG GGG AGT TTT GAA GAG TTT GAC AAG CAT TTA CGG CCT      358
Leu Cys Asp Val Gly Ser Phe Glu Glu Phe Asp Lys His Leu Arg Pro
          70                               75                               80

AAT GAT CCT TTA AAT TTC GTG GAT AAA GAG AGC TAT AAA CAA CGC ATT      406
Asn Asp Pro Leu Asn Phe Val Asp Lys Glu Ser Tyr Lys Lys Gln Arg Ile
          85                               90                               95

AAA AAA TAC GAA AAA AGG ACT AAC CGC CCA AGC TCA GTG ATC AGC GGT      454
Lys Lys Tyr Glu Lys Arg Thr Asn Arg Pro Ser Ser Val Ile Ser Gly
        100                               105                               110                               115

GAG GCT AAA ATC AAC CGC ATG CCT TTG CAG ATC GTG GTG TTT GAT TTT      502
Glu Ala Lys Ile Asn Arg Met Pro Leu Gln Ile Val Val Phe Asp Phe
          120                               125                               130

```

```

AAA ATG TTA GAA AAT CAT CTT AAT ATT AAT TTT TTT ATC GCT GGA GCG      403
Lys Met Leu Glu Asn His Leu Asn Ile Asn Phe Phe Ile Ala Gly Ala
          90                      95                      100

TAT GGG TTT GAA GAA AAT TTT TTA AAG GAT TGT CAA GCT TGG AGT TTG      451
Tyr Gly Phe Glu Glu Asn Phe Leu Lys Asp Cys Gln Ala Trp Ser Leu
          105                      110                      115

AGC GAG ATG ACT TTT AGC CAT GAA GTG GCT AAA ATT GTC TTA TGC GAG      499
Ser Glu Met Thr Phe Ser His Glu Val Ala Lys Ile Val Leu Cys Glu
          120                      125                      130

CAA ATC TAT AGG GCT TTA AGC ATT ATT TTT AAG CAT CCA TAC CAT AAA T      548
Gln Ile Tyr Arg Ala Leu Ser Ile Ile Phe Lys His Pro Tyr His Lys
          135                      140                      145                      150

AGGAGGTGCG CATGCGTTTT TACATTATCT TTACATTTTT GTTTATTGTG GGTTTTGGTG      608
TGTTTGTTTA TAGTATTG                                           626

```

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

```

Met Arg Cys Val Val Tyr Ser Ile Ala Lys Ser Ser Pro Leu Glu Leu
 1          5          10          15
Val Lys Ile Tyr Gln Lys Gln Cys Arg Gln Phe Asp Cys Glu Leu Glu
          20          25          30
Leu Val Asp Leu Phe Pro Lys Asn Thr Ala Asn Ala Gln Lys Val Ser
          35          40          45
Lys Lys Leu Ala Gln Lys Ser Tyr Ser Leu Ala Phe Glu Pro Tyr Leu
          50          55          60
Asn Pro Lys Ala Lys Asn Ile Ala Leu His Pro Lys Ala Gln Arg Gly
65          70          75          80
Asp Ser Phe Ala Phe Ser Lys Met Leu Glu Asn His Leu Asn Ile Asn
          85          90          95
Phe Phe Ile Ala Gly Ala Tyr Gly Phe Glu Glu Asn Phe Leu Lys Asp
          100          105          110
Cys Gln Ala Trp Ser Leu Ser Glu Met Thr Phe Ser His Glu Val Ala
          115          120          125
Lys Ile Val Leu Cys Glu Gln Ile Tyr Arg Ala Leu Ser Ile Ile Phe
          130          135          140
Lys His Pro Tyr His Lys
          145          150

```

(2) INFORMATION FOR SEQ ID NO:467:

				85						90					95				
Lys	Gly	Pro	Leu	Glu	Asn	Arg	His	His	His	Ser	Phe	Thr	Lys	Asn	Tyr				
			100						105					110					
Glu	Lys	Ala	Val	Asn	Gly	Cys	Gln	Lys	Tyr	Phe	His	Ile	Lys	Leu	Pro				
		115					120					125							
Glu	Gly	Ala	Pro	Ser	Asn	Phe	Lys	Ser	Gly	Ser	Tyr	Met	Ala	Thr	Met				
	130						135					140							
Val	Val	Arg	Phe																
145																			

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...547
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

ATGATTGTGC ACAGGAAGGA TTTGAAGAAG ACTTTGAGCG ATCTCATCGC TATGATGACG	60
CATAAGACTT CAAAGATTTT TTAAAGTTTT AACATTG ATG CGT TGC GTG GTG TAT	115
Met Arg Cys Val Val Tyr	
1 5	
TCT ATC GCT AAA AGT TCG CCT TTA GAG TTA GTG AAA ATC TAT CAA AAG	163
Ser Ile Ala Lys Ser Ser Pro Leu Glu Leu Val Lys Ile Tyr Gln Lys	
10 15 20	
CAA TGC AGG CAA TTT GAT TGC GAG CTG GAA TTG GTG GAT TTA TTC CCT	211
Gln Cys Arg Gln Phe Asp Cys Glu Leu Glu Leu Val Asp Leu Phe Pro	
25 30 35	
AAA AAT ACC GCC AAC GCT CAA AAA GTT TCT AAA AAA CTG GCT CAA AAA	259
Lys Asn Thr Ala Asn Ala Gln Lys Val Ser Lys Lys Leu Ala Gln Lys	
40 45 50	
AGC TAC TCT CTA GCT TTT GAG CCG TAT TTA AAC CCT AAG GCA AAA AAT	307
Ser Tyr Ser Leu Ala Phe Glu Pro Tyr Leu Asn Pro Lys Ala Lys Asn	
55 60 65 70	
ATC GCC TTA CAC CCT AAA GCT CAA AGG GGC GAT AGC TTT GCG TTT AGT	355
Ile Ala Leu His Pro Lys Ala Gln Arg Gly Asp Ser Phe Ala Phe Ser	
75 80 85	

```

AAA CTT TCA GTC TAT TCG GCT GGA AGT GGG ATG ATT GGG ATT GAT ATT      255
Lys Leu Ser Val Tyr Ser Ala Gly Ser Gly Met Ile Gly Ile Asp Ile
      45                      50                      55

GAC AAA CGG ACA TTT TAT AAG CGA GCG TTC GCT TTC ACG ATG AAA TCG      303
Asp Lys Arg Thr Phe Tyr Lys Arg Ala Phe Ala Phe Thr Met Lys Ser
      60                      65                      70

TTG TTC GGT GAA AAC TTG CTT TTG TTT GTC AAA TTA AAG CAT TCT GCG      351
Leu Phe Gly Glu Asn Leu Leu Leu Phe Val Lys Leu Lys His Ser Ala
      75                      80                      85                      90

TTG ACG AGC AAA CAC ATG AAA GGG CCT TTA GAA AAC CGC CAT CAC CAT      399
Leu Thr Ser Lys His Met Lys Gly Pro Leu Glu Asn Arg His His His
      95                      100                      105

TCT TTC ACT AAA AAT TAT GAA AAA GCG GTT AAT GGT TGT CAA AAG TAT      447
Ser Phe Thr Lys Asn Tyr Glu Lys Ala Val Asn Gly Cys Gln Lys Tyr
      110                      115                      120

TTC CAT ATT AAA TTG CCT GAA GGC GCT CCT AGC AAC TTC AAA TCA GGT      495
Phe His Ile Lys Leu Pro Glu Gly Ala Pro Ser Asn Phe Lys Ser Gly
      125                      130                      135

TCA TAC ATG GCC ACT ATG GTG GTG CGT TTT TAAAGCGTTA TTTGGGGTAT TCT      548
Ser Tyr Met Ala Thr Met Val Val Arg Phe
      140                      145

TTAATACCCCT TATCGTCTTT TAAAATACCA TCTTTTAAAA GCACAAATTT ATTTTTTATAGC      608
CCTTTTTTTAA ATCTTCTTAA A                                           629

```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```

Ile Ser Leu Ser Val Lys His Thr Asp Asn Val Ile Ser Leu Arg Lys
 1              5              10              15
Glu Asn Gly Val Arg Thr Leu Ile Ser Leu Gly Ile Leu Leu Ser Val
      20              25              30
Leu Ser Gly Asp Asp Leu Lys Leu Tyr Ser Lys Leu Ser Val Tyr Ser
      35              40              45
Ala Gly Ser Gly Met Ile Gly Ile Asp Ile Asp Lys Arg Thr Phe Tyr
      50              55              60
Lys Arg Ala Phe Ala Phe Thr Met Lys Ser Leu Phe Gly Glu Asn Leu
      65              70              75              80
Leu Leu Phe Val Lys Leu Lys His Ser Ala Leu Thr Ser Lys His Met

```

(2) INFORMATION FOR SEQ ID NO:463:

(A) LENGTH: 629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 82...525
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

- 734 -

```

AATATTGATT GAAGAAGCTT AAAAATCCCA TTTTTTAAAA TTAAAATAAG GTTTTATCGA 1621
TCCCTATTTG ACTCAAAAAG AGTCTTATTC CATTATCAAT CAATTAAAAA AGGTTATTCA 1681
AAAATAACCA TACAATTATA AAAATCTTC 1710

```

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

```

Met Val Val Phe Thr Lys Arg Val Ala Leu Ser Leu Phe Val Gly Ile
 1             5             10             15
Leu Val Ser Ala Val Leu Met His Ser Leu His Leu Ser Gln Leu Val
             20             25             30
Glu Tyr Ile Tyr His Lys Ile Thr Ser Val Phe Tyr Thr Tyr Glu Pro
             35             40             45
Glu Lys Gly Leu Asn Phe Asn Leu Ser Asn Leu Tyr Val Phe Gly Phe
             50             55             60
Leu Ile Phe Leu Gly Val Leu Ser Gln Val Ile Leu Lys Ser Gly Ser
65             70             75             80
Val Gln Asn Phe Val Lys Lys Ala Lys Lys Tyr Ser Lys Asn Ala Lys
             85             90             95
Thr Pro Glu Phe Ile Ala Phe Phe Ser Gly Ile Ile Ile Phe Val Asp
             100            105            110
Asp Tyr Phe Asn Ala Leu Thr Val Gly Gln Ile Ser Lys Ser Leu Asn
             115            120            125
Asp Ala His Asn Ser Thr Arg Glu Arg Leu Ala Tyr Ile Ile Asp Ser
             130            135            140
Thr Ser Ala Pro Val Cys Leu Leu Val Pro Ile Ser Ser Trp Gly Ala
145            150            155            160
Tyr Ile Met Gly Ile Met Asn Asn Asp Ser Ser Pro Leu Leu Lys Asp
             165            170            175
Ser Phe Ser Val Leu Val Gln Ser Leu Ser Ser Asn Tyr Tyr Ala Ile
             180            185            190
Phe Ala Leu Ile Ala Val Phe Leu Thr Ile Leu Trp Gln Ile Asn Leu
             195            200            205
Pro Ser Met Arg Lys Tyr Gln Asn Ile Gly Val Lys Asp Phe Tyr Ser
             210            215            220
Glu Gln Glu Glu Ser Ser Ser Lys Leu Ala Pro Leu Ser Leu Leu Pro
225            230            235            240
Leu Ser Ile Leu Leu Leu Ile Val Ser Ile Ser Ser Leu Leu Phe Tyr
             245            250            255
Thr Gly Val Ile Leu Lys Asn Thr Asp Ala Ser Phe Ser Leu Phe Tyr
             260            265            270
Gly Gly Leu Phe Ser Leu Ile Val Thr Tyr Leu Leu Ala Tyr Lys Phe
             275            280            285
Leu Glu Lys Gly Ser Phe Phe Lys Leu Met Leu Asp Gly Phe Lys Ser
290            295            300

```

ACA GGA GTG ATT TTA AAA AAC ACT GAT GCG AGT TTT TCG CTC TTT TAT	935
Thr Gly Val Ile Leu Lys Asn Thr Asp Ala Ser Phe Ser Leu Phe Tyr	
260 265 270	
GGA GGG TTG TTT TCG CTC ATC GTT ACT TAT CTT TTA GCT TAT AAG TTT	983
Gly Gly Leu Phe Ser Leu Ile Val Thr Tyr Leu Leu Ala Tyr Lys Phe	
275 280 285	
TTA GAA AAA GGG AGC TTT TTT AAA CTC ATG TTG GAT GGC TTT AAG AGT	1031
Leu Glu Lys Gly Ser Phe Phe Lys Leu Met Leu Asp Gly Phe Lys Ser	
290 295 300	
GTG GGG CCG GCG ATA CTA GTC TTA ACG CTC GCT TGG GCT ATC GGG CCT	1079
Val Gly Pro Ala Ile Leu Val Leu Thr Leu Ala Trp Ala Ile Gly Pro	
305 310 315 320	
GTG ATT AGA GAT GAC GCT CAA ACA GGG CTT TAC TTG GCT AAC ATC AGC	1127
Val Ile Arg Asp Asp Ala Gln Thr Gly Leu Tyr Leu Ala Asn Ile Ser	
325 330 335	
AAG GGG TTT TTA AAT AAT GGA GGA GGC GTG TAT ATG CCT TTA ATC TTT	1175
Lys Gly Phe Leu Asn Asn Gly Gly Gly Val Tyr Met Pro Leu Ile Phe	
340 345 350	
TTT TTA ATC TCT GGG TTT ATC GCT TTT TCT ACC GGC ACA AGC TGG GGA	1223
Phe Leu Ile Ser Gly Phe Ile Ala Phe Ser Thr Gly Thr Ser Trp Gly	
355 360 365	
GCG TTT GCG ATC ATG CTT CCC ATT GGA GCG GGC ATG GCT AGT GAA AGC	1271
Ala Phe Ala Ile Met Leu Pro Ile Gly Ala Gly Met Ala Ser Glu Ser	
370 375 380	
GAT ATT ATT TTG ATT GTT TCA GCG ATT CTC TCA GGC GCG GTT TAT GGC	1319
Asp Ile Ile Leu Ile Val Ser Ala Ile Leu Ser Gly Ala Val Tyr Gly	
385 390 395 400	
GAT CAC ACA AGC CCT ATT TCT GAC ACG ACT ATA CTA TCG GCT ACG GGG	1367
Asp His Thr Ser Pro Ile Ser Asp Thr Thr Ile Leu Ser Ala Thr Gly	
405 410 415	
GCA GGG TGT TCG GTG CAA AGC CAT TTT ATC ACG CAA CTC CCT TAT GCG	1415
Ala Gly Cys Ser Val Gln Ser His Phe Ile Thr Gln Leu Pro Tyr Ala	
420 425 430	
ACC ATT GCG ATG CTT TGC AGC GCG GTG AGT TTG GGG GTG GCA AGC TTT	1463
Thr Ile Ala Met Leu Cys Ser Ala Val Ser Leu Gly Val Ala Ser Phe	
435 440 445	
ATG TAT TCG CGT TCG CTC GCT CTT TTA ATC GGT GTG GCT TTG CTT GTG	1511
Met Tyr Ser Arg Ser Leu Ala Leu Leu Ile Gly Val Ala Leu Leu Val	
450 455 460	
GGG GTG TTT TAT CTT TTA AAA AAA TTT TAT GGT GAA AAT CTA AAA ACT TG	1561
Gly Val Phe Tyr Leu Leu Lys Lys Phe Tyr Gly Glu Asn Leu Lys Thr	
465 470 475 480	

GAA TAT ATT TAT CAT AAA ATC ACT TCC GTT TTT TAC ACT TAC GAG CCA	263
Glu Tyr Ile Tyr His Lys Ile Thr Ser Val Phe Tyr Thr Tyr Glu Pro	
35 40 45	
GAA AAG GGG CTT AAT TTC AAT CTT TCC AAC CTC TAT GTT TTT GGG TTT	311
Glu Lys Gly Leu Asn Phe Asn Leu Ser Asn Leu Tyr Val Phe Gly Phe	
50 55 60	
TTA ATC TTT TTA GGC GTC TTA AGC CAA GTG ATT TTA AAA TCC GGT AGC	359
Leu Ile Phe Leu Gly Val Leu Ser Gln Val Ile Leu Lys Ser Gly Ser	
65 70 75 80	
GTG CAA AAC TTT GTC AAA AAA GCT AAA AAA TAC TCA AAA AAC GCT AAA	407
Val Gln Asn Phe Val Lys Lys Ala Lys Lys Tyr Ser Lys Asn Ala Lys	
85 90 95	
ACT CCC GAA TTT ATC GCC TTT TTT TCA GGT ATC ATT ATT TTT GTA GAT	455
Thr Pro Glu Phe Ile Ala Phe Phe Ser Gly Ile Ile Ile Phe Val Asp	
100 105 110	
GAT TAT TTT AAC GCC CTA ACC GTG GGG CAA ATC TCA AAG TCT TTA AAC	503
Asp Tyr Phe Asn Ala Leu Thr Val Gly Gln Ile Ser Lys Ser Leu Asn	
115 120 125	
GAC GCT CAT AAC TCC ACA CGA GAG CGC TTG GCT TAT ATT ATA GAC TCC	551
Asp Ala His Asn Ser Thr Arg Glu Arg Leu Ala Tyr Ile Ile Asp Ser	
130 135 140	
ACT TCA GCG CCG GTG TGC TTG CTA GTC CCC ATT TCT AGT TGG GGG GCG	599
Thr Ser Ala Pro Val Cys Leu Leu Val Pro Ile Ser Ser Trp Gly Ala	
145 150 155 160	
TAT ATT ATG GGG ATC ATG AAT AAC GAC AGC TCG CCC TTA TTA AAA GAT	647
Tyr Ile Met Gly Ile Met Asn Asn Asp Ser Ser Pro Leu Leu Lys Asp	
165 170 175	
AGT TTT TCG GTG CTT GTG CAA AGC TTA AGC AGT AAT TAT TAT GCC ATT	695
Ser Phe Ser Val Leu Val Gln Ser Leu Ser Ser Asn Tyr Tyr Ala Ile	
180 185 190	
TTT GCA CTC ATT GCA GTC TTT CTC ACC ATT TTA TGG CAA ATC AAC CTC	743
Phe Ala Leu Ile Ala Val Phe Leu Thr Ile Leu Trp Gln Ile Asn Leu	
195 200 205	
CCT AGC ATG AGA AAG TAT CAA AAC ATA GGC GTG AAG GAT TTT TAT AGC	791
Pro Ser Met Arg Lys Tyr Gln Asn Ile Gly Val Lys Asp Phe Tyr Ser	
210 215 220	
GAA CAA GAA GAA AGC TCT TCA AAA CTA GCC CCC TTG AGT TTG TTA CCC	839
Glu Gln Glu Glu Ser Ser Ser Lys Leu Ala Pro Leu Ser Leu Leu Pro	
225 230 235 240	
CTT TCT ATT TTA TTG TTG ATT GTG TCC ATT TCA TCA TTG CTT TTT TAT	887
Leu Ser Ile Leu Leu Leu Ile Val Ser Ile Ser Ser Leu Leu Phe Tyr	
245 250 255	

Asp	Leu	Ala	Pro	Asn	Tyr	Lys	Asp	Phe	Asp	Phe	Ile	Leu	Thr	Gly	Gly	
				85					90					95		
Glu	Pro	Ser	Leu	Tyr	Phe	Asn	Asn	Pro	Ile	Leu	Ile	Ser	Val	Leu	Glu	
			100					105					110			
His	Phe	Tyr	Arg	Gln	Lys	Ile	Pro	Leu	Cys	Val	Glu	Ser	Asn	Gly	Ser	
		115					120					125				
Ile	Phe	Phe	Glu	Phe	Ser	Pro	Ile	Leu	Lys	Glu	Leu	His	Phe	Thr	Leu	
		130					135					140				
Ser	Val	Lys	Leu	Ser	Phe	Ser	Leu	Glu	Glu	Glu	Ser	Lys	Arg	Ile	His	
		145				150				155					160	
Leu	Lys	Ala	Leu	Gln	Asn	Ile	Leu	Asn	Asn	Ala	Lys	Ser	Ala	His	Phe	
			165					170						175		
Lys	Phe	Val	Leu	Glu	Ser	Gln	Asn	Ala	Ala	Gln	Ser	Ile	Ile	Glu	Ile	
		180						185					190			
Gln	Ser	Leu	Leu	Lys	Gln	Leu	Ser	Leu	Lys	Asn	Asn	Glu	Ile	Phe	Leu	
		195					200					205				
Met	Pro	Leu	Gly	Thr	Asn	Asn	Asn	Glu	Leu	Asp	Lys	Asn	Leu	Lys	Thr	
		210				215					220					
Leu	Ala	Pro	Leu	Ala	Ile	Lys	His	Gly	Phe	Arg	Leu	Ser	Asp	Arg	Leu	
		225				230				235					240	
His	Ile	Arg	Leu	Trp	Asp	Asn	Gln	Lys	Gly	Phe						
			245						250							

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 120...1559
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

TAAAGAATTT	TGTGAATATT	GATTGTCTCT	TTTAATTGAA	ATTTAAAGAT	TAGTTTAAAG	60
GATTTTATTC	GGTGGGATTG	TCAGCATCAA	GCCTCATTGT	TCCTATTAGC	GTTATTTTA	119

ATG	GTG	GTT	TTT	ACT	AAA	AGA	GTC	GCA	CTC	TCG	TTA	TTT	GTG	GGC	ATT	167
Met	Val	Val	Phe	Thr	Lys	Arg	Val	Ala	Leu	Ser	Leu	Phe	Val	Gly	Ile	
1				5				10					15			

TTA	GTG	AGC	GCT	GTT	TTA	ATG	CAT	TCG	TTA	CAC	CTT	TCC	CAA	CTC	GTA	215
Leu	Val	Ser	Ala	Val	Leu	Met	His	Ser	Leu	His	Leu	Ser	Gln	Leu	Val	
		20					25					30				

	145	150	155	
AAG CGG ATC CAT CTT AAA GCC TTA CAA AAT ATC TTA AAT AAC GCT AAA				591
Lys Arg Ile His Leu Lys Ala Leu Gln Asn Ile Leu Asn Asn Ala Lys				
	160	165	170	
AGC GCG CAT TTT AAA TTT GTT TTA GAG AGC CAA AAC GCC GCT CAA TCT				639
Ser Ala His Phe Lys Phe Val Leu Glu Ser Gln Asn Ala Ala Gln Ser				
	175	180	185	
ATT ATA GAA ATT CAA AGC CTC TTG AAA CAA CTC TCC TTA AAA AAT AAT				687
Ile Ile Glu Ile Gln Ser Leu Leu Lys Gln Leu Ser Leu Lys Asn Asn				
	190	195	200	
GAA ATC TTT TTA ATG CCT TTA GGC ACA AAT AAC AAC GAG CTA GAC AAA				735
Glu Ile Phe Leu Met Pro Leu Gly Thr Asn Asn Asn Glu Leu Asp Lys				
	205	210	215	220
AAT CTA AAA ACC CTA GCC CCC CTA GCC ATA AAG CAT GGT TTC AGG CTA				783
Asn Leu Lys Thr Leu Ala Pro Leu Ala Ile Lys His Gly Phe Arg Leu				
	225	230	235	
AGC GAT AGG CTT CAT ATC CGC TTG TGG GAT AAT CAA AAA GGG TTT TAAAA				833
Ser Asp Arg Leu His Ile Arg Leu Trp Asp Asn Gln Lys Gly Phe				
	240	245	250	
AGTTAATCAT GACCATCAAA GTTTTTTCGC CCAAATACCC CACTGAATTA GAAGAATTTT				893
ATGCTGAGCG TATCGCTGAC AACCCCTTTAG GGTTTATCCA ACGCTTGGAT CTTTTGCCTA				953
GTATTAGCGG GTTCGTTCAA AAATTGCGCG AGCATGGCGG GGAATTTTTT GAAATGAGAG				1013
AGGGTAACAA GCTCATTGGG ATTTGTGGGC TTAATCCTAT CAATCAAACA GAAGCCGAGC				1073
TGTGCAA				1080

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met	Lys	Leu	Pro	Val	Val	Glu	Ser	Phe	Phe	Ser	Leu	Gln	Gly	Glu	Gly
1				5				10					15		
Lys	Arg	Ile	Gly	Lys	Pro	Ser	Leu	Phe	Leu	Arg	Leu	Gly	Gly	Cys	Asn
			20					25					30		
Leu	Ser	Cys	Lys	Gly	Phe	Asn	Cys	Lys	Thr	Leu	Leu	Asn	Asp	Glu	Ile
		35					40					45			
Leu	Thr	Gly	Cys	Asp	Ser	Leu	Tyr	Ala	Val	His	Pro	Lys	Phe	Lys	Thr
	50					55					60				
Ser	Trp	Asp	Tyr	Tyr	Asn	Glu	Pro	Lys	Pro	Leu	Ile	Glu	Arg	Leu	Glu
65					70					75				80	

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 76...828
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

CTTTTTCAAT AAAATCATCA GCGATGAAAA ACAATGCTTT TTCCACGCTA AACCCCTTACA	60
CCAGATCCCT TAAAA ATG AAA CTC CCG GTC GTT GAG AGC TTT TTT TCC TTA	111
Met Lys Leu Pro Val Val Glu Ser Phe Phe Ser Leu	
1 5 10	
CAA GGT GAA GGA AAA AGG ATA GGC AAG CCC AGT CTT TTT TTG CGC TTA	159
Gln Gly Glu Gly Lys Arg Ile Gly Lys Pro Ser Leu Phe Leu Arg Leu	
15 20 25	
GGG GGG TGT AAC CTT TCA TGC AAG GGC TTT AAT TGT AAA ACC TTA TTG	207
Gly Gly Cys Asn Leu Ser Cys Lys Gly Phe Asn Cys Lys Thr Leu Leu	
30 35 40	
AAT GAT GAA ATC CTA ACA GGT TGC GAC AGC TTG TAT GCG GTG CAT CCC	255
Asn Asp Glu Ile Leu Thr Gly Cys Asp Ser Leu Tyr Ala Val His Pro	
45 50 55 60	
AAA TTC AAA ACA TCT TGG GAT TAT TAT AAT GAG CCT AAG CCC TTG ATT	303
Lys Phe Lys Thr Ser Trp Asp Tyr Tyr Asn Glu Pro Lys Pro Leu Ile	
65 70 75	
GAA CGA TTA GAG GAT TTA GCC CCT AAT TAT AAG GAT TTT GAT TTC ATT	351
Glu Arg Leu Glu Asp Leu Ala Pro Asn Tyr Lys Asp Phe Asp Phe Ile	
80 85 90	
CTT ACA GGC GGG GAG CCA AGC TTG TAT TTC AAT AAC CCT ATT TTA ATC	399
Leu Thr Gly Gly Glu Pro Ser Leu Tyr Phe Asn Asn Pro Ile Leu Ile	
95 100 105	
AGC GTT TTA GAG CAT TTT TAT CGC CAA AAA ATC CCT TTA TGT GTA GAG	447
Ser Val Leu Glu His Phe Tyr Arg Gln Lys Ile Pro Leu Cys Val Glu	
110 115 120	
AGT AAT GGT TCT ATT TTT TTT GAA TTT AGC CCT ATT TTA AAA GAA TTG	495
Ser Asn Gly Ser Ile Phe Phe Glu Phe Ser Pro Ile Leu Lys Glu Leu	
125 130 135 140	
CAT TTC ACT CTA AGC GTC AAA CTC TCT TTT TCT TTA GAG GAA GAA AGC	543
His Phe Thr Leu Ser Val Lys Leu Ser Phe Ser Leu Glu Glu Glu Ser	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```

Met Asn Leu Asn Phe Met Pro Leu Leu His Ala Tyr Asn His Ala Ser
 1           5           10           15
Ile Asp Phe His Phe Asn Ser Ser Ala Arg Asp Phe Cys Val His Glu
          20           25           30
Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln
          35           40           45
Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser
          50           55           60
Gln Ile Leu Gly Val Arg Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys
65           70           75           80
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr
          85           90           95
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Lys Asn Leu
          100          105          110
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His
          115          120          125
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu
          130          135          140
Asn Ala Gln Lys Thr Lys Gln Val Leu Glu Gln Ile Ala Gln Phe Gly
145          150          155          160
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn
          165          170          175
His Gln Glu Gly Leu Lys Ile Leu Gln Asn Gln Thr Lys Phe Ala His
          180          185          190
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe
          195          200          205
Asn Ala Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala
          210          215          220
Phe Ser Val Lys Glu Asn Leu Glu Phe Phe Lys Gln Lys Asn Leu Ser
225          230          235          240
Val Asp Ser Asp Thr Leu Lys Thr Leu Lys Asn Gln Ala His Pro Phe
          245          250          255
Lys Ile Leu Glu Gly Asp Val Met Cys His Tyr Pro Tyr Gly Lys Phe
          260          265          270
Phe Asp Ala Leu Glu Leu Glu Lys Glu Gly Glu Arg Phe Leu Lys Lys
          275          280          285
Glu Val Ala Pro Thr Gly Leu Leu Asp Gly Lys Lys Ala Leu Tyr Ala
          290          295          300
Lys Asn Leu Ser Leu Glu Ile Glu Lys Glu Phe Gln His Asn Leu Leu
305          310          315          320
Ser Ser His Ala Lys Thr Leu Gly Ser Arg Arg Phe Phe Trp Val Phe
          325          330          335
Val Glu Asn Val Thr Ser Gln Tyr Val Lys Glu Lys Ala Gln Phe Glu
          340          345          350
Leu Gly Phe Tyr Leu Pro Lys Gly Ser Tyr Ala Ser Ala Leu Leu Lys
          355          360          365
Glu Ile Lys His Glu Lys Gly Glu Asn Asn Asp Glu Phe
          370          375          380

```

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 base pairs

Phe	Ser	Val	Lys	Glu	Asn	Leu	Glu	Phe	Phe	Lys	Gln	Lys	Asn	Leu	Ser	
225					230					235					240	
GTT	GAT	TCA	GAC	ACT	CTA	AAA	ACC	CTT	AAA	AAC	CAA	GCC	CAC	CCC	TTT	827
Val	Asp	Ser	Asp	Thr	Leu	Lys	Thr	Leu	Lys	Asn	Gln	Ala	His	Pro	Phe	
				245					250					255		
AAA	ATC	TTA	GAA	GGC	GAT	GTG	ATG	TGC	CAT	TAC	CCT	TAT	GGG	AAG	TTT	875
Lys	Ile	Leu	Glu	Gly	Asp	Val	Met	Cys	His	Tyr	Pro	Tyr	Gly	Lys	Phe	
			260					265					270			
TTT	GAC	GCT	TTA	GAA	TTA	GAA	AAA	GAG	GGC	GAA	AGG	TTT	TTG	AAA	AAA	923
Phe	Asp	Ala	Leu	Glu	Leu	Glu	Lys	Glu	Gly	Glu	Arg	Phe	Leu	Lys	Lys	
		275					280					285				
GAA	GTT	GCG	CCT	ACG	GGG	TTA	CTA	GAC	GGC	AAA	AAA	GCT	CTT	TAT	GCA	971
Glu	Val	Ala	Pro	Thr	Gly	Leu	Leu	Asp	Gly	Lys	Lys	Ala	Leu	Tyr	Ala	
		290				295					300					
AAA	AAT	TTG	AGT	TTA	GAA	ATT	GAA	AAA	GAA	TTC	CAG	CAT	AAC	CTT	TTA	1019
Lys	Asn	Leu	Ser	Leu	Glu	Ile	Glu	Lys	Glu	Phe	Gln	His	Asn	Leu	Leu	
305					310					315					320	
AGT	AGC	CAT	GCT	AAA	ACG	CTA	GGC	TCT	AGG	CGG	TTT	TTT	TGG	GTG	TTT	1067
Ser	Ser	His	Ala	Lys	Thr	Leu	Gly	Ser	Arg	Arg	Phe	Phe	Trp	Val	Phe	
				325					330					335		
GTA	GAA	AAT	GTA	ACT	TCT	CAA	TAC	GTG	AAA	GAA	AAA	GCG	CAA	TTT	GAA	1115
Val	Glu	Asn	Val	Thr	Ser	Gln	Tyr	Val	Lys	Glu	Lys	Ala	Gln	Phe	Glu	
			340					345					350			
TTG	GGA	TTT	TAC	TTG	CCT	AAA	GGG	AGT	TAT	GCG	AGC	GCG	TTG	CTC	AAA	1163
Leu	Gly	Phe	Tyr	Leu	Pro	Lys	Gly	Ser	Tyr	Ala	Ser	Ala	Leu	Leu	Lys	
		355					360					365				
GAA	ATC	AAG	CAT	GAG	AAA	GGA	GAA	AAT	AAT	GAC	GAA	TTT	TGAAAAGATT	ATC		1215
Glu	Ile	Lys	His	Glu	Lys	Gly	Glu	Asn	Asn	Asp	Glu	Phe				
		370				375				380						
GCGCAAAACA	GGATCAAAAC	GAACGCGGTT	TTAGCGACTT	ATTGCGTGAT	TTTTGCTTTT											1275
ATCGGGTTGT	TGGTGGATGT	CATTAGAATT	AATGCTAATG	ATTTAGGAAT	AGCTCTTTT											1335
AAACTCATGA	CTTTT															1350

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

1	5	10	15	
ATT GAT TTT CAT TTC AAT TCT AGT GCT AGG GAT TTT TGC GTG CAT GAA				155
Ile Asp Phe His Phe Asn Ser Ser Ala Arg Asp Phe Cys Val His Glu	20	25	30	
GTG CCT TTG TAT GAA TTT AGT AAC ACG GGC GAA CAT GCC GTT ATT CAA				203
Val Pro Leu Tyr Glu Phe Ser Asn Thr Gly Glu His Ala Val Ile Gln	35	40	45	
GTG AGG AAA AGC GGT TTA AGC ACT TTA GAA ATG CTT CAG ATT TTT TCT				251
Val Arg Lys Ser Gly Leu Ser Thr Leu Glu Met Leu Gln Ile Phe Ser	50	55	60	
CAA ATT TTA GGG GTA AGA ATC GCT GAA TTG GGT TAT GCG GGC TTG AAA				299
Gln Ile Leu Gly Val Arg Ile Ala Glu Leu Gly Tyr Ala Gly Leu Lys	65	70	75	80
GAT AAA AAC GCG CTG ACG ACT CAA TTC ATC TCA CTC CCT AAA AAA TAC				347
Asp Lys Asn Ala Leu Thr Thr Gln Phe Ile Ser Leu Pro Lys Lys Tyr	85	90	95	
GCC CCT TTA TTA GAA AAA AAT ACG AGC AAC TTT CAA GAA AAA AAC CTT				395
Ala Pro Leu Leu Glu Lys Asn Thr Ser Asn Phe Gln Glu Lys Asn Leu	100	105	110	
AAA ATC CTG TCT TTG AAT TAC CAC CAC AAT AAA ATC AAA TTG GGG CAT				443
Lys Ile Leu Ser Leu Asn Tyr His His Asn Lys Ile Lys Leu Gly His	115	120	125	
TTG AAA GGG AAT CGC TTT TTT ATG CGT TTT AAA AAA ATG ACC CCT CTA				491
Leu Lys Gly Asn Arg Phe Phe Met Arg Phe Lys Lys Met Thr Pro Leu	130	135	140	
AAC GCT CAA AAA ACA AAG CAG GTT TTA GAA CAA ATC GCG CAG TTT GGA				539
Asn Ala Gln Lys Thr Lys Gln Val Leu Glu Gln Ile Ala Gln Phe Gly	145	150	155	160
ATG CCT AAT TAT TTT GGC TCG CAA CGC TTT GGG AAG TTC AAT GAC AAC				587
Met Pro Asn Tyr Phe Gly Ser Gln Arg Phe Gly Lys Phe Asn Asp Asn	165	170	175	
CAC CAA GAG GGT TTA AAA ATC TTA CAA AAT CAA ACG AAA TTC GCC CAT				635
His Gln Glu Gly Leu Lys Ile Leu Gln Asn Gln Thr Lys Phe Ala His	180	185	190	
CAA AAA TTA AAC GCT TTT TTA ATT TCA AGC TAT CAA AGT TAT TTG TTT				683
Gln Lys Leu Asn Ala Phe Leu Ile Ser Ser Tyr Gln Ser Tyr Leu Phe	195	200	205	
AAC GCG CTT TTA AGC AAA CGA TTA GAA ATC AGT AAA ATC ATT AGC GCT				731
Asn Ala Leu Leu Ser Lys Arg Leu Glu Ile Ser Lys Ile Ile Ser Ala	210	215	220	
TTT AGT GTC AAA GAA AAT TTA GAA TTT TTT AAA CAA AAA AAT TTA AGC				779

```

1           5           10           15
Ala Ala Gly Phe Val Gln Leu Ile Ser Asn Tyr Ile Asn Gln Phe Ser
20           25           30
Ser Thr Leu Phe Val Thr Asn Leu Pro Ala Gln Asp Ile Ile Tyr Val
35           40           45
Pro Gly Tyr Glu Val Ser Gly Thr Ala Lys Tyr Lys Gly Phe Ser Leu
50           55           60
Gly Leu Ser Val Ala Arg Ser Trp Pro Ser Leu Lys Gly Arg Leu Ile
65           70           75           80
Ala Asp Val Tyr Glu Leu Ala Ala Thr Thr Gly Asn Val Phe Ile Leu
85           90           95
Thr Ala Ser Tyr Lys Ile Pro Arg Thr Gly Leu Ser Ile Thr Trp Leu
100          105          110
Ser Arg Phe Val Thr Asp Leu Ser Tyr Cys Ser Tyr Ser Pro Tyr Arg
115          120          125
Asn Gly Pro Thr Asp Ile Asp Arg Arg Pro Ser Asn Cys Pro Lys Thr
130          135          140
Pro Gly Ile Phe His Val His Lys Pro Gly Tyr Gly Val Ser Ser Phe
145          150          155          160
Phe Val Thr Tyr Lys Pro Thr Tyr Lys Lys Leu Lys Gly Leu Ser Leu
165          170          175
Asn Ala Val Phe Asn Asn Val Phe Asn Gln Gln Tyr Ile Asp Gln Ala
180          185          190
Ser Pro Val Met Ser Pro Asp Glu Pro Asn Gln Asp Lys Tyr Ala Arg
195          200          205
Gly Met Ala Glu Pro Gly Phe Asn Ala Arg Phe Glu Ile Ser Tyr Lys
210          215          220
Phe
225

```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...1202
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```

AATTTTGAAA ACATTGACTC AGTTTCGCTC TCAAGGGCGT TTAATTCAAG GATCAAAGC      59

ATG AAT TTA AAT TTT ATG CCC CTA TTG CAT GCT TAT AAC CAT GCG AGC      107
Met Asn Leu Asn Phe Met Pro Leu Leu His Ala Tyr Asn His Ala Ser

```

Lys	Gly	Arg	Leu	Ile	Ala	Asp	Val	Tyr	Glu	Leu	Ala	Ala	Thr	Thr	Gly		
				80					85					90			
AAT	GTG	TTT	ATT	TTG	ACG	GCA	AGT	TAT	AAA	ATC	CCA	CGC	ACT	GGT	CTT	399	
Asn	Val	Phe	Ile	Leu	Thr	Ala	Ser	Tyr	Lys	Ile	Pro	Arg	Thr	Gly	Leu		
			95					100					105				
AGC	ATC	ACT	TGG	CTT	TCA	CGC	TTC	GTT	ACG	GAT	TTG	AGT	TAT	TGC	TCT	447	
Ser	Ile	Thr	Trp	Leu	Ser	Arg	Phe	Val	Thr	Asp	Leu	Ser	Tyr	Cys	Ser		
		110					115					120					
TAT	AGC	CCT	TAT	CGT	AAC	GGC	CCT	ACG	GAT	ATT	GAC	AGA	CGG	CCT	AGT	495	
Tyr	Ser	Pro	Tyr	Arg	Asn	Gly	Pro	Thr	Asp	Ile	Asp	Arg	Arg	Pro	Ser		
	125					130					135						
AAT	TGC	CCT	AAA	ACG	CCC	GGG	ATT	TTT	CAT	GTT	CAT	AAA	CCC	GGT	TAT	543	
Asn	Cys	Pro	Lys	Thr	Pro	Gly	Ile	Phe	His	Val	His	Lys	Pro	Gly	Tyr		
140						145				150					155		
GGG	GTG	AGC	AGT	TTT	TTT	GTA	ACC	TAC	AAA	CCC	ACC	TAT	AAG	AAG	CTT	591	
Gly	Val	Ser	Ser	Phe	Phe	Val	Thr	Tyr	Lys	Pro	Thr	Tyr	Lys	Lys	Leu		
				160					165					170			
AAA	GGG	TTG	AGC	TTG	AAT	GCG	GTG	TTT	AAC	AAT	GTT	TTT	AAC	CAA	CAA	639	
Lys	Gly	Leu	Ser	Leu	Asn	Ala	Val	Phe	Asn	Asn	Val	Phe	Asn	Gln	Gln		
			175				180					185					
TAT	ATT	GAT	CAA	GCA	AGC	CCG	GTG	ATG	AGC	CCT	GAT	GAA	CCC	AAT	CAA	687	
Tyr	Ile	Asp	Gln	Ala	Ser	Pro	Val	Met	Ser	Pro	Asp	Glu	Pro	Asn	Gln		
		190					195					200					
GAC	AAA	TAC	GCA	AGA	GGC	ATG	GCA	GAG	CCT	GGC	TTT	AAC	GCT	AGA	TTT	735	
Asp	Lys	Tyr	Ala	Arg	Gly	Met	Ala	Glu	Pro	Gly	Phe	Asn	Ala	Arg	Phe		
	205					210					215						
GAA	ATT	TCC	TAT	AAG	TTT	TAATAATGGA	TCTAAAAATA	AGGATTTCAT	GGGTAGCG	791							
Glu	Ile	Ser	Tyr	Lys	Phe												
220					225												
GATCTAATCA	AAAATAAAAC	ATTCTTTAGA														821	

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Met Trp Asn Phe Asn Thr Glu Tyr Ser Ser Gln Tyr Phe Asp Phe Arg

Gln	Thr	Ser	Leu	Glu	Tyr	Leu	Lys	Ala	Met	His	Ser	His	Ile	Leu	Lys
130						135					140				
Lys	Glu	Ala	Pro	Phe	Ala	Val	Gly	Leu	Phe	Ala	Gly	Glu	Thr	Leu	Glu
145					150					155					160
Lys	Pro	His	Phe	Leu	Ser	Met	Ser	Leu	Cys	Lys	Gln	Gln	Cys	Glu	Leu
			165						170					175	
Glu	Ala	Asp	Leu	Ile	Glu	Ser	Val	Leu	Gln	Ile	Lys	Ser	Glu	Ile	Ile
		180						185					190		
Thr	Pro	Leu	Ala	Phe	Gln	Arg	Gly	Leu	Glu	Lys	Lys	Ala	Lys	Lys	Gln
	195					200						205			
Ile	Lys	Lys	Val	Val	Leu	Pro	Glu	Ser	Glu	Lys	Met	Lys	Gly	Phe	
210						215					220				

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...753
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

TATGCCTGGA	GGTTTGGTGT	GGATGCGTCA	AGATAATTTG	CGNCTACAAC	CGCAATTTAA	60
AGCCAGAAAT	TGGGCAAA	ATG TGG AAT	TTT AAC ACC	GAA TAC AGC	AGT CAG	111
	Met Trp Asn	Phe Asn Thr	Glu Tyr Ser	Ser Gln		
	1		5		10	
TAT TTT GAT	TTT AGA GCC	GCC GGT	TTT GTC CAA	TTG ATT TCT	AAT TAC	159
Tyr Phe Asp	Phe Arg Ala	Ala Gly	Phe Val Gln	Leu Ile Ser	Asn Tyr	
	15		20		25	
ATC AAT CAA	TTT TCT TCA	ACG CTT	TTT GTA ACC	AAC TTG CCC	GCA CAA	207
Ile Asn Gln	Phe Ser Ser	Thr Leu Phe	Val Thr Asn	Leu Pro Ala	Gln	
	30		35		40	
GAT ATT ATT	TAT GTG CCT	GGT TAT GAA	GTT TCA GGG	ACG GCT AAA	TAC	255
Asp Ile Ile	Tyr Val Pro	Gly Tyr Glu	Val Ser Gly	Thr Ala Lys	Tyr	
	45		50		55	
AAG GGC TTT	TCT TTA GGC	TTG AGC GTG	GCG CGA TCA	TGG CCT TCT	TTA	303
Lys Gly Phe	Ser Leu Gly	Leu Ser Val	Ala Arg Ser	Trp Pro Ser	Leu	
	60		65		70	75
AAG GGG CGT	TTG ATC GCT	GAT GTG TAT	GAA TTG GCG	GCC ACG ACA	GGC	351

```

AGT TTG GAA TAT TTG AAA GCC ATG CAC TCT CAT ATT CTC AAA AAA GAA      548
Ser Leu Glu Tyr Leu Lys Ala Met His Ser His Ile Leu Lys Lys Glu
              135                      140                      145

GCC CCT TTC GCT GTA GGG TTA TTT GCG GGC GAA ACG CTT GAA AAA CCA      596
Ala Pro Phe Ala Val Gly Leu Phe Ala Gly Glu Thr Leu Glu Lys Pro
              150                      155                      160

CAT TTT TTA AGC ATG TCT CTT TGC AAG CAA CAA TGC GAA TTA GAA GCG      644
His Phe Leu Ser Met Ser Leu Cys Lys Gln Gln Cys Glu Leu Glu Ala
              165                      170                      175

GAT CTG ATT GAA AGC GTG TTG CAA ATA AAA AGC GAG ATT ATT ACC CCT      692
Asp Leu Ile Glu Ser Val Leu Gln Ile Lys Ser Glu Ile Ile Thr Pro
              180                      185                      190

TTA GCC TTT CAA AGG GGT TTG GAA AAA AAG GCT AAA AAA CAG ATT AAA      740
Leu Ala Phe Gln Arg Gly Leu Glu Lys Lys Ala Lys Lys Gln Ile Lys
              195                      200                      205                      210

AAA GTG GTT TTA CCA GAG AGC GAA AAG ATG AAA GGA TTT TGAAAGCTGC AC      791
Lys Val Val Leu Pro Glu Ser Glu Lys Met Lys Gly Phe
              215                      220

ATCGTTTGAA TTTAATGGGC GCGGTAGGAT TGATCTTATT AGGCGATAAA GAA      844

```

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

```

Met Gln Gly Leu Trp Ile Tyr Pro Glu Asp Thr Glu Val Leu Gly Val
 1              5              10              15
Ala Cys Lys Ser Leu Leu Lys Ala Leu Thr Pro Arg Tyr Gln Lys Val
              20              25              30
Ala Leu Phe Ser Pro Ile Ser Gly Gly Cys Glu Ser Leu Glu Glu Cys
              35              40              45
Glu Ser Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys
              50              55              60
Ala Leu Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr
              65              70              75              80
Ile Leu Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile
              85              90              95
Asn Leu Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu
              100             105             110
Asn Thr Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala
              115             120             125

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 111...779
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

```

GTCGTTATTC GCGCTTAATG AGAACAGAGG TTTTAAAC TATGGTTTCG TTTAGGTTTA      60
ATTAAATTC GCTACAATTA AATAAAACG ATAATTTAG AGAGATTGGC  ATG CAA      116
                                     Met Gln
                                     1

GGT TTA TGG ATT TAT CCA GAG GAT ACA GAA GTT TTA GGG GTT GCT TGT      164
Gly Leu Trp Ile Tyr Pro Glu Asp Thr Glu Val Leu Gly Val Ala Cys
      5                      10                      15

AAG AGC CTT TTA AAA GCA CTA ACG CCA CGC TAT CAA AAA GTC GCC TTG      212
Lys Ser Leu Leu Lys Ala Leu Thr Pro Arg Tyr Gln Lys Val Ala Leu
      20                      25                      30

TTT TCG CCC ATT AGT GGA GGG TGT GAG AGC TTG GAG GAG TGC GAG AGC      260
Phe Ser Pro Ile Ser Gly Gly Cys Glu Ser Leu Glu Glu Cys Glu Ser
      35                      40                      45                      50

TTG AAC CCT TTA GAA TTT CAT AGT GCG ATA AGC AAA CAA AAG GCT TTA      308
Leu Asn Pro Leu Glu Phe His Ser Ala Ile Ser Lys Gln Lys Ala Leu
      55                      60                      65

GAG CTT GCG AGC ACC GCT CAA GAA GAG TTA CTA TTT GAA ACG ATT CTC      356
Glu Leu Ala Ser Thr Ala Gln Glu Glu Leu Leu Phe Glu Thr Ile Leu
      70                      75                      80

AAA CGC TAT GAT GAA TTA CAA TCC ACG CAT GAT TTT GTC ATT AAT TTG      404
Lys Arg Tyr Asp Glu Leu Gln Ser Thr His Asp Phe Val Ile Asn Leu
      85                      90                      95

GGG TGT GCG CCG AAG TTT TTC TTA AAC GCT CCT TTA GAT TTA AAC ACC      452
Gly Cys Ala Pro Lys Phe Phe Leu Asn Ala Pro Leu Asp Leu Asn Thr
      100                      105                      110

ATT TTA GCC AAG CAT TTA AAC GCT TCT GTT GTG GCT GTC GCG CAA ACG      500
Ile Leu Ala Lys His Leu Asn Ala Ser Val Val Ala Val Ala Gln Thr
      115                      120                      125                      130

```

```

AGATGTAGGT AACAAAGAGA CAGATTTGAT TGTTGAGGAT TTTTCTAGTT ACAGCAATGA      60
AAGAAAAAGG GCTTTAG GTG TTG AAG CTC AAT CTT AAA AAA TCT TTT CAA      110
          Val Leu Lys Leu Asn Leu Lys Lys Ser Phe Gln
              1              5              10

AAA GAT TTT GAT AAA TTG CTT TTG AAT GGG TTT GAT GAT AGC GTT TTG      158
Lys Asp Phe Asp Lys Leu Leu Leu Asn Gly Phe Asp Asp Ser Val Leu
              15              20              25

AAT GAA GTC ATT CTA ACC TTA AGA AAA AAA GAA CCG CTA GAT CCA CAA      206
Asn Glu Val Ile Leu Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln
              30              35              40

TTT CAA GAT CAT GCC TTA AAG GGA AAG TGG AAA CCT TTT AGG GAA TGC      254
Phe Gln Asp His Ala Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys
              45              50              55

CAC ATT AAG CCT GAT GTT TTG CTT GTG TAT TTA GTG AAA GAT GAT GAA      302
His Ile Lys Pro Asp Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu
        60              65              70              75

CTG ATT TTG TTA AGG TTA GGC AGT CAT AGC GAG CTG TTT TAATCCACCC AC      353
Leu Ile Leu Leu Arg Leu Gly Ser His Ser Glu Leu Phe
              80              85

ACCCCTTATA ACGCTTAAAC CAAATCGCTT GCGCTATAAT GAACTGATAT TATATTTTAA      413
AAGGAATAAA CA      425

```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

Val Leu Lys Leu Asn Leu Lys Lys Ser Phe Gln Lys Asp Phe Asp Lys
  1              5              10              15
Leu Leu Leu Asn Gly Phe Asp Asp Ser Val Leu Asn Glu Val Ile Leu
              20              25              30
Thr Leu Arg Lys Lys Glu Pro Leu Asp Pro Gln Phe Gln Asp His Ala
              35              40              45
Leu Lys Gly Lys Trp Lys Pro Phe Arg Glu Cys His Ile Lys Pro Asp
              50              55              60
Val Leu Leu Val Tyr Leu Val Lys Asp Asp Glu Leu Ile Leu Leu Arg
        65              70              75              80
Leu Gly Ser His Ser Glu Leu Phe
              85

```

(2) INFORMATION FOR SEQ ID NO:453:

65					70					75					80					
GTA	AGG	TTA	GGC	AGT	CAT	AGC	GAG	CTG	TTT	TGA	ACG	CCC	AC	CCC	CTT	A	TAAC	353		
Val	Arg	Leu	Gly	Ser	His	Ser	Glu	Leu	Phe											
				85					90											

GCTTAAACCA ACTACCCCCC TTTTTTAGGG ATAAATTTAG GGTGGAACA CCGCTTA 410

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met	Leu	Thr	Ile	Glu	Thr	Ser	Lys	Lys	Phe	Asp	Lys	Asp	Leu	Lys	Ile
1				5					10					15	
Leu	Val	Lys	Asn	Gly	Phe	Asp	Leu	Lys	Leu	Leu	Tyr	Lys	Val	Val	Gly
			20					25					30		
Asn	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Ala	Pro	Lys	Tyr	Lys	Asp	His	Pro
		35					40					45			
Leu	Lys	Gly	Gly	Leu	Lys	Asp	Phe	Arg	Glu	Cys	His	Leu	Lys	Pro	Asp
	50					55					60				
Leu	Leu	Leu	Val	Tyr	Gln	Ile	Lys	Lys	Gln	Glu	Asn	Thr	Leu	Phe	Leu
65					70					75					80
Val	Arg	Leu	Gly	Ser	His	Ser	Glu	Leu	Phe						
				85					90						

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 78...341
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

	100		105		110
Glu Lys Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile					
	115		120		125
Leu Ala Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys					
	130		135		140
Asp Pro Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln					
145		150		155	160
Glu Ile Glu Asn Lys Ile Glu Glu Arg Lys Arg Ala Lys Glu Arg Lys					
	165		170		175
Asp Phe Leu Lys Ala Asp Ser Ile Arg Glu Glu Leu Leu Lys Gln Lys					
	180		185		190
Ile Ala Leu Met Asp Thr Pro Gln Gly Thr Ile Trp Glu Lys Phe Phe					
195		200		205	

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...329
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

TTTTAAAAGC ATAGAGGATT TTAAGAAGCA TTGTGAAAAC TTATAAATAA GATTTAAAA	59
ATG CTG ACG ATT GAA ACC AGT AAA AAA TTT GAT AAG GAT CTT AAA ATT	107
Met Leu Thr Ile Glu Thr Ser Lys Lys Phe Asp Lys Asp Leu Lys Ile	
1 5 10 15	
CTT GTT AAA AAC GGG TTT GAT TTA AAG CTT TTG TAT AAA GTG GTT GGA	155
Leu Val Lys Asn Gly Phe Asp Leu Lys Leu Leu Tyr Lys Val Val Gly	
20 25 30	
AAT TTA GCC ACA GAG CAA CCC CTA GCT CCC AAA TAC AAA GAC CAC CCA	203
Asn Leu Ala Thr Glu Gln Pro Leu Ala Pro Lys Tyr Lys Asp His Pro	
35 40 45	
CTC AAA GGC GGT TTA AAA GAT TTT AGG GAA TGC CAC TTA AAA CCG GAT	251
Leu Lys Gly Gly Leu Lys Asp Phe Arg Glu Cys His Leu Lys Pro Asp	
50 55 60	
TTA TTG CTT GTC TAT CAA ATT AAA AAA CAA GAA AAC ACC CTC TTT TTA	299
Leu Leu Leu Val Tyr Gln Ile Lys Lys Gln Glu Asn Thr Leu Phe Leu	

Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn Glu Lys
 100 105 110
 TTG GAT CAA AAC CCT AAA AAC AAG GCT TTA AAG GGC GAA ATT TTA GCG 440
 Leu Asp Gln Asn Pro Lys Asn Lys Ala Leu Lys Gly Glu Ile Leu Ala
 115 120 125 130
 AAT TTG AAA TTC ATA GAA GAA CTG CTT GGC ATC GGG TTT AAA GAC CCT 488
 Asn Leu Lys Phe Ile Glu Glu Leu Leu Gly Ile Gly Phe Lys Asp Pro
 135 140 145
 AGC GCC TAT TTC CAA TTA GGC GTG AGT GAA AGC GAA AAA CAA GAA ATT 536
 Ser Ala Tyr Phe Gln Leu Gly Val Ser Glu Ser Glu Lys Gln Glu Ile
 150 155 160
 GAA AAC AAG ATA GAA GAA AGA AAA CGC GCC AAA GAG CGA AAA GAT TTT 584
 Glu Asn Lys Ile Glu Glu Arg Lys Arg Ala Lys Glu Arg Lys Asp Phe
 165 170 175
 TTA AAA GCC GAT AGC ATC AGA GAA GAG CTT TTG AAA CAA AAA ATC GCT 632
 Leu Lys Ala Asp Ser Ile Arg Glu Glu Leu Leu Lys Gln Lys Ile Ala
 180 185 190
 TTG ATG GAC ACC CCA CAA GGC ACG ATC TGG GAG AAG TTT TTT TAAACACCT 683
 Leu Met Asp Thr Pro Gln Gly Thr Ile Trp Glu Lys Phe Phe
 195 200 205
 CCAATTTTAC CTTTTTACAC ATTCTAGCAA CAACTTTCAG CATT 727

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met His Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser
 1 5 10 15
 Leu Gly Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly
 20 25 30
 Glu Ile Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu
 35 40 45
 Asn Phe Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys
 50 55 60
 Ile Tyr Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn
 65 70 75 80
 Pro Asn Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn
 85 90 95
 Val Ser Lys Ala Leu Ser Val Leu Glu Ser Met Leu Ser Ser Thr Asn

```

465          470          475          480
Lys Ala Leu Glu Lys His Gln Lys Met Met Lys Asp Met His Gly Lys
          485          490          495
Asp Met His His Thr Lys Lys Lys Lys
          500          505

```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...674
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```

GAAGCGTGCC AAACCCGTTG CCCTTTGGCG TGGAGCTTGC CAAATATTGG  ATG CAT      56
                                     Met His
                                     1

AAC GGC TTT GTG AAT ATC AAT AAC GAA AAA ATG TCT AAA AGT TTG GGG      104
Asn Gly Phe Val Asn Ile Asn Asn Glu Lys Met Ser Lys Ser Leu Gly
      5              10              15

AAT AGC TTT TTT GTT AAA GAC GCT CTC AAA AAC TAT GAT GGC GAA ATT      152
Asn Ser Phe Phe Val Lys Asp Ala Leu Lys Asn Tyr Asp Gly Glu Ile
      20              25              30

TTG CGC AAT TAC TTA CTA GGG GTG CAT TAT CGC TCT GTT TTG AAT TTC      200
Leu Arg Asn Tyr Leu Leu Gly Val His Tyr Arg Ser Val Leu Asn Phe
      35              40              45              50

AAT GAA GAA GAC TTG TTA GTG AGT AAA AAA CGC TTG GAT AAA ATC TAT      248
Asn Glu Glu Asp Leu Leu Val Ser Lys Lys Arg Leu Asp Lys Ile Tyr
          55              60              65

CGT TTA AAA CAG CGC GTT TTA GGG ACT CTT GGA GGA ATA AAT CCA AAC      296
Arg Leu Lys Gln Arg Val Leu Gly Thr Leu Gly Gly Ile Asn Pro Asn
          70              75              80

TTT AAA AAA GAA ATT TTA GAG TGC ATG CAA GAT GAT TTA AAC GTT TCT      344
Phe Lys Lys Glu Ile Leu Glu Cys Met Gln Asp Asp Leu Asn Val Ser
          85              90              95

AAA GCG TTG AGC GTT TTA GAA AGC ATG CTT TCT TCC ACT AAT GAA AAA      392

```


Leu Gln Ser Thr Trp Phe Leu Glu Lys Leu Ala Ala Phe Asp Arg Glu
 35 40 45
 Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser Gly Ala Tyr Gly
 50 55 60
 Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr Lys Ala Lys Ile
 65 70 75 80
 Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe Arg Phe Ser Thr
 85 90 95
 Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg Asp Pro Arg Gly
 100 105 110
 Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp Asp Leu Val Gly
 115 120 125
 Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile Lys Phe Pro Asp
 130 135 140
 Phe Ile His Thr Gln Lys Arg Asp Pro Gln Thr Asn Leu Pro Asn His
 145 150 155 160
 Asp Met Val Trp Asp Phe Trp Ser Asn Val Pro Glu Ser Leu Tyr Gln
 165 170 175
 Val Thr Trp Val Met Ser Asp Arg Gly Ile Pro Lys Ser Phe Arg His
 180 185 190
 Met Asp Gly Phe Gly Ser His Thr Phe Ser Leu Ile Asn Ala Lys Gly
 195 200 205
 Glu Arg Phe Trp Val Lys Phe His Phe His Thr Met Gln Gly Val Lys
 210 215 220
 His Leu Thr Asn Glu Glu Ala Ala Glu Val Arg Lys Tyr Asp Pro Asp
 225 230 235 240
 Ser Asn Gln Arg Asp Leu Phe Asn Ala Ile Ala Arg Gly Asp Phe Pro
 245 250 255
 Lys Trp Lys Leu Ser Ile Gln Val Met Pro Glu Glu Asp Ala Lys Lys
 260 265 270
 Tyr Arg Phe His Pro Phe Asp Val Thr Lys Ile Trp Tyr Leu Gln Asp
 275 280 285
 Tyr Pro Leu Met Glu Val Gly Ile Val Glu Leu Asn Lys Asn Pro Glu
 290 295 300
 Asn Tyr Phe Ala Glu Val Glu Gln Ala Ala Phe Ser Pro Ala Asn Val
 305 310 315 320
 Val Pro Gly Ile Gly Tyr Ser Pro Asp Arg Met Leu Gln Gly Arg Leu
 325 330 335
 Phe Ser Tyr Gly Asp Thr His Arg Tyr Arg Leu Gly Val Asn Tyr Pro
 340 345 350
 Gln Ile Pro Val Asn Lys Pro Arg Cys Pro Phe His Ser Ser Ser Arg
 355 360 365
 Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu Gln Asn Tyr Thr
 370 375 380
 Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser Ala Arg Asp Pro
 385 390 395 400
 Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu Val Trp Asn Trp
 405 410 415
 Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Thr Gln Pro Gly Asp Tyr
 420 425 430
 Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu His Asp Thr Ile
 435 440 445
 Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile Val Asp Lys Gln
 450 455 460
 Leu Glu His Phe Lys Lys Ala Asp Pro Lys Tyr Ala Glu Gly Val Lys

```

TCT TCT AGC AGA GAT GGT TAC ATG CAA AAC GGA TAC TAC GGC TCT TTA      1334
Ser Ser Ser Arg Asp Gly Tyr Met Gln Asn Gly Tyr Tyr Gly Ser Leu
365                               370                               375                               380

CAA AAC TAT ACG CCT AGC TCA TTG CCT GGC TAT AAA GAA GAT AAG AGC      1382
Gln Asn Tyr Thr Pro Ser Ser Leu Pro Gly Tyr Lys Glu Asp Lys Ser
                               385                               390                               395

GCG AGA GAT CCT AAG TTC AAC TTA GCT CAT ATT GAG AAA GAG TTT GAA      1430
Ala Arg Asp Pro Lys Phe Asn Leu Ala His Ile Glu Lys Glu Phe Glu
                               400                               405                               410

GTG TGG AAT TGG GAT TAC AGA GCT GAT GAT AGC GAT TAC TAC ACC CAA      1478
Val Trp Asn Trp Asp Tyr Arg Ala Asp Asp Ser Asp Tyr Tyr Thr Gln
                               415                               420                               425

CCA GGT GAT TAC TAC CGC TCA TTG CCA GCT GAT GAA AAA GAA AGG TTG      1526
Pro Gly Asp Tyr Tyr Arg Ser Leu Pro Ala Asp Glu Lys Glu Arg Leu
                               430                               435                               440

CAT GAC ACT ATT GGA GAG TCT TTA GCT CAT GTT ACC CAT AAG GAA ATT      1574
His Asp Thr Ile Gly Glu Ser Leu Ala His Val Thr His Lys Glu Ile
445                               450                               455                               460

GTG GAT AAA CAA TTG GAG CAT TTC AAG AAA GCT GAC CCC AAA TAC GCT      1622
Val Asp Lys Gln Leu Glu His Phe Lys Lys Ala Asp Pro Lys Tyr Ala
                               465                               470                               475

GAG GGA GTT AAA AAA GCT CTT GAA AAA CAC CAA AAA ATG ATG AAA GAC      1670
Glu Gly Val Lys Lys Ala Leu Glu Lys His Gln Lys Met Met Lys Asp
                               480                               485                               490

ATG CAT GGA AAA GAC ATG CAC CAC ACA AAA AAG AAA AAG TAACCCTTTT CT      1721
Met His Gly Lys Asp Met His His Thr Lys Lys Lys Lys
                               495                               500                               505

TTAAGCGTTC TTATTTTSTA GGAACGCTTT GTCTTTCAAA ATTTAGGTTT TTGGATACT      1780

```

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

Met Val Asn Lys Asp Val Lys Gln Thr Thr Ala Phe Gly Ala Pro Val
 1             5             10             15
Trp Asp Asp Asn Asn Val Ile Thr Ala Gly Pro Arg Gly Pro Val Leu
                20                25                30

```

Lys	Phe	Pro	Asp	Phe	Ile	His	Thr	Gln	Lys	Arg	Asp	Pro	Gln	Thr	Asn	
				145					150					155		
TTG	CCT	AAC	CAT	GAC	ATG	GTA	TGG	GAT	TTT	TGG	AGT	AAT	GTT	CCT	GAA	710
Leu	Pro	Asn	His	Asp	Met	Val	Trp	Asp	Phe	Trp	Ser	Asn	Val	Pro	Glu	
			160					165					170			
AGC	TTA	TAC	CAA	GTA	ACA	TGG	GTT	ATG	AGC	GAT	AGG	GGT	ATT	CCT	AAA	758
Ser	Leu	Tyr	Gln	Val	Thr	Trp	Val	Met	Ser	Asp	Arg	Gly	Ile	Pro	Lys	
		175					180					185				
TCT	TTC	CGC	CAC	ATG	GAT	GGT	TTT	GGC	AGC	CAC	ACT	TTC	AGT	CTT	ATC	806
Ser	Phe	Arg	His	Met	Asp	Gly	Phe	Gly	Ser	His	Thr	Phe	Ser	Leu	Ile	
	190					195					200					
AAC	GCG	AAA	GGC	GAA	CGC	TTT	TGG	GTG	AAA	TTC	CAC	TTT	CAC	ACC	ATG	854
Asn	Ala	Lys	Gly	Glu	Arg	Phe	Trp	Val	Lys	Phe	His	Phe	His	Thr	Met	
205					210					215					220	
CAA	GGC	GTT	AAG	CAT	TTG	ACT	AAC	GAA	GAA	GCC	GCA	GAA	GTT	AGG	AAG	902
Gln	Gly	Val	Lys	His	Leu	Thr	Asn	Glu	Glu	Ala	Ala	Glu	Val	Arg	Lys	
				225					230					235		
TAT	GAT	CCG	GAT	TCC	AAT	CAA	AGG	GAT	TTA	TTC	AAT	GCG	ATC	GCT	AGA	950
Tyr	Asp	Pro	Asp	Ser	Asn	Gln	Arg	Asp	Leu	Phe	Asn	Ala	Ile	Ala	Arg	
			240					245					250			
GGG	GAT	TTC	CCA	AAA	TGG	AAA	TTA	AGC	ATT	CAA	GTG	ATG	CCA	GAA	GAA	998
Gly	Asp	Phe	Pro	Lys	Trp	Lys	Leu	Ser	Ile	Gln	Val	Met	Pro	Glu	Glu	
	255						260					265				
GAT	GCT	AAG	AAG	TAT	CGA	TTC	CAT	CCG	TTT	GAT	GTA	ACT	AAA	ATT	TGG	1046
Asp	Ala	Lys	Lys	Tyr	Arg	Phe	His	Pro	Phe	Asp	Val	Thr	Lys	Ile	Trp	
	270					275					280					
TAT	CTC	CAA	GAT	TAT	CCA	TTG	ATG	GAA	GTG	GGC	ATT	GTG	GAG	TTG	AAT	1094
Tyr	Leu	Gln	Asp	Tyr	Pro	Leu	Met	Glu	Val	Gly	Ile	Val	Glu	Leu	Asn	
285					290					295					300	
AAA	AAT	CCT	GAA	AAC	TAT	TTC	GCA	GAA	GTG	GAA	CAA	GCG	GCA	TTC	AGT	1142
Lys	Asn	Pro	Glu	Asn	Tyr	Phe	Ala	Glu	Val	Glu	Gln	Ala	Ala	Phe	Ser	
				305					310					315		
CCG	GCT	AAT	GTC	GTT	CCT	GGA	ATT	GGC	TAT	AGC	CCT	GAT	AGG	ATG	TTA	1190
Pro	Ala	Asn	Val	Val	Pro	Gly	Ile	Gly	Tyr	Ser	Pro	Asp	Arg	Met	Leu	
			320					325					330			
CAA	GGG	CGC	TTG	TTC	TCT	TAT	GGA	GAC	ACA	CAC	CGC	TAC	CGC	TTA	GGC	1238
Gln	Gly	Arg	Leu	Phe	Ser	Tyr	Gly	Asp	Thr	His	Arg	Tyr	Arg	Leu	Gly	
		335					340					345				
GTT	AAT	TAT	CCT	CAA	ATA	CCG	GTT	AAT	AAA	CCA	AGA	TGC	CCA	TTC	CAC	1286
Val	Asn	Tyr	Pro	Gln	Ile	Pro	Val	Asn	Lys	Pro	Arg	Cys	Pro	Phe	His	
	350					355					360					

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 195...1709
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

```

TTGTTTTTAA TCTTTCTTAT TTTCATTAAT TGTTACGAAT AGAAATACTT AAGGGGGTTT      60
TTCATTCTTA AAAAAAGGAT TTTTAAAGGA AATTGAATCT TGTTAGTCTT TGTATAACAA      120
ATTATGTGAT AATCACCACA AGTAATCGGC TTAGTGTCAT ATTACGAAGA TTTAAGATCA      180
TAAAAGGAAA AAAG ATG GTT AAT AAA GAT GTG AAA CAA ACC ACT GCT TTT      230
          Met Val Asn Lys Asp Val Lys Gln Thr Thr Ala Phe
                1                5                10

GGC GCT CCC GTT TGG GAT GAC AAC AAT GTG ATT ACG GCC GGC CCT AGA      278
Gly Ala Pro Val Trp Asp Asp Asn Asn Val Ile Thr Ala Gly Pro Arg
                15                20                25

GGT CCT GTT TTA TTA CAA AGC ACT TGG TTT TTG GAA AAG TTA GCG GCG      326
Gly Pro Val Leu Leu Gln Ser Thr Trp Phe Leu Glu Lys Leu Ala Ala
                30                35                40

TTT GAC AGA GAA AGA ATC CCT GAA AGG GTG GTG CAT GCT AAA GGA AGC      374
Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Lys Gly Ser
                45                50                55                60

GGA GCT TAT GGC ACT TTC ACT GTG ACT AAA GAC ATC ACT AAA TAC ACT      422
Gly Ala Tyr Gly Thr Phe Thr Val Thr Lys Asp Ile Thr Lys Tyr Thr
                65                70                75

AAA GCG AAA ATT TTC TCT AAA GTG GGC AAA AAA ACC GAA TGC TTC TTC      470
Lys Ala Lys Ile Phe Ser Lys Val Gly Lys Lys Thr Glu Cys Phe Phe
                80                85                90

AGA TTT TCT ACT GTG GCT GGT GAA AGA GGC AGT GCG GAT GCG GTG AGA      518
Arg Phe Ser Thr Val Ala Gly Glu Arg Gly Ser Ala Asp Ala Val Arg
                95                100                105

GAC CCT AGA GGT TTT GCG ATG AAG TAT TAC ACT GAA GAA GGT AAC TGG      566
Asp Pro Arg Gly Phe Ala Met Lys Tyr Tyr Thr Glu Glu Gly Asn Trp
                110                115                120

GAT TTA GTG GGG AAC AAC ACG CCT GTT TTC TTT ATC CGT GAT GCG ATC      614
Asp Leu Val Gly Asn Asn Thr Pro Val Phe Phe Ile Arg Asp Ala Ile
                125                130                135                140

AAA TTC CCT GAT TTC ATC CAC ACT CAA AAA CGA GAT CCT CAA ACC AAT      662

```

205

210

215

GGG ATA CTA GAA TGC AAA TGATGCACAA TTTGAGTTTT TTGGGCATGT TTTTAGCC 794
 Gly Ile Leu Glu Cys Lys
 220

GCTTTGAGCA TGTCTTTAGG GCATTGTGTG GGCATGT 831

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Met	Pro	Ala	Arg	Gln	Ser	Phe	Thr	Asp	Leu	Lys	Asn	Leu	Val	Leu	Cys
1				5					10					15	
Asp	Ile	Gly	Asn	Thr	Arg	Ile	His	Phe	Ala	Gln	Asn	Tyr	Gln	Leu	Phe
			20					25					30		
Ser	Ser	Ala	Lys	Glu	Asp	Leu	Lys	Arg	Leu	Gly	Ile	Gln	Lys	Glu	Ile
		35					40					45			
Phe	Tyr	Ile	Ser	Val	Asn	Glu	Asn	Glu	Lys	Ala	Leu	Leu	Asn	Cys	
	50					55				60					
Tyr	Pro	Asn	Ala	Lys	Asn	Ile	Ala	Gly	Phe	Phe	His	Leu	Glu	Thr	Asp
65					70					75				80	
Tyr	Val	Gly	Leu	Gly	Ile	Asp	Arg	Gln	Met	Ala	Cys	Leu	Ala	Val	Asn
				85					90					95	
Asn	Gly	Val	Val	Val	Asp	Ala	Gly	Ser	Ala	Ile	Thr	Ile	Asp	Leu	Ile
			100					105					110		
Lys	Glu	Gly	Lys	His	Leu	Gly	Gly	Cys	Ile	Leu	Pro	Gly	Leu	Ala	Gln
		115					120					125			
Tyr	Ile	His	Ala	Tyr	Lys	Lys	Ser	Ala	Lys	Ile	Leu	Glu	Gln	Pro	Phe
	130					135					140				
Lys	Ala	Leu	Asp	Ser	Leu	Glu	Val	Leu	Pro	Lys	Ser	Thr	Arg	Asp	Ala
145					150					155				160	
Val	Asn	Tyr	Gly	Met	Val	Leu	Ser	Val	Ile	Ala	Cys	Ile	Gln	His	Leu
				165					170					175	
Ala	Lys	Asn	Gln	Lys	Ile	Tyr	Leu	Cys	Gly	Gly	Asp	Ala	Lys	Tyr	Leu
		180						185					190		
Ser	Ala	Phe	Leu	Pro	His	Ser	Val	Cys	Lys	Glu	Arg	Leu	Val	Phe	Asp
	195						200					205			
Gly	Met	Glu	Ile	Ala	Leu	Lys	Lys	Ala	Gly	Ile	Leu	Glu	Cys	Lys	
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1780 base pairs
- (B) TYPE: nucleic acid

AACAAAGAGC GAGAGAGCAT CAAGAAAGAG ATGAAAAAGA GCTTGAAGAA AGAAGAAAAG	60
CTTTAGAAAT GAATAAGAAG TAGGCCT ATG CCA GCT AGG CAA TCT TTT ACA GAT	114
Met Pro Ala Arg Gln Ser Phe Thr Asp	
1 5	
TTG AAA AAC CTG GTT TTG TGC GAT ATA GGC AAC ACG CGT ATC CAT TTT	162
Leu Lys Asn Leu Val Leu Cys Asp Ile Gly Asn Thr Arg Ile His Phe	
10 15 20 25	
GCA CAA AAC TAT CAG CTC TTT TCA AGC GCT AAA GAA GAT TTA AAG CGT	210
Ala Gln Asn Tyr Gln Leu Phe Ser Ser Ala Lys Glu Asp Leu Lys Arg	
30 35 40	
TTG GGT ATT CAA AAG GAA ATT TTT TAC ATT AGC GTG AAT GAA GAA AAT	258
Leu Gly Ile Gln Lys Glu Ile Phe Tyr Ile Ser Val Asn Glu Glu Asn	
45 50 55	
GAA AAA GCC CTT TTG AAT TGT TAC CCT AAC GCT AAA AAT ATT GCA GGG	306
Glu Lys Ala Leu Leu Asn Cys Tyr Pro Asn Ala Lys Asn Ile Ala Gly	
60 65 70	
TTT TTT CAT TTA GAA ACC GAC TAT GTA GGG CTT GGG ATA GAC CGG CAA	354
Phe Phe His Leu Glu Thr Asp Tyr Val Gly Leu Gly Ile Asp Arg Gln	
75 80 85	
ATG GCG TGT CTG GCG GTA AAT AAT GGC GTG GTG GTG GAT GCC GGG AGT	402
Met Ala Cys Leu Ala Val Asn Asn Gly Val Val Val Asp Ala Gly Ser	
90 95 100 105	
GCG ATT ACG ATA GAT TTA ATC AAA GAG GGC AAG CAT TTA GGA GGG TGT	450
Ala Ile Thr Ile Asp Leu Ile Lys Glu Gly Lys His Leu Gly Gly Cys	
110 115 120	
ATT TTA CCC GGT TTA GCC CAA TAT ATT CAT GCG TAT AAA AAA AGC GCT	498
Ile Leu Pro Gly Leu Ala Gln Tyr Ile His Ala Tyr Lys Lys Ser Ala	
125 130 135	
AAA ATT TTA GAG CAA CCT TTC AAG GCC TTA GAT TCT TTA GAA GTT TTA	546
Lys Ile Leu Glu Gln Pro Phe Lys Ala Leu Asp Ser Leu Glu Val Leu	
140 145 150	
CCT AAA AGC ACT AGA GAC GCT GTG AAT TAC GGC ATG GTT TTG AGC GTC	594
Pro Lys Ser Thr Arg Asp Ala Val Asn Tyr Gly Met Val Leu Ser Val	
155 160 165	
ATT GCT TGT ATC CAG CAT TTA GCC AAA AAT CAA AAA ATC TAT CTT TGT	642
Ile Ala Cys Ile Gln His Leu Ala Lys Asn Gln Lys Ile Tyr Leu Cys	
170 175 180 185	
GGG GGC GAT GCG AAG TAT TTG AGC GCG TTT TTA CCC CAT TCT GTT TGC	690
Gly Gly Asp Ala Lys Tyr Leu Ser Ala Phe Leu Pro His Ser Val Cys	
190 195 200	
AAG GAG CGT TTG GTT TTT GAC GGG ATG GAA ATC GCT CTT AAA AAA GCA	738
Lys Glu Arg Leu Val Phe Asp Gly Met Glu Ile Ala Leu Lys Lys Ala	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

```

Met Pro Cys Ile Ile Lys Thr Thr Pro Leu Ser Met Ile Ile Lys Glu
 1           5           10           15
Cys Ile Arg Met Asn Thr Asn Lys Ala Leu Phe Leu Asp Arg Asp Gly
          20           25           30
Ile Ile Asn Ile Asp Lys Gly Tyr Val Ser Gln Lys Glu Asp Phe Glu
          35           40           45
Phe Gln Lys Gly Ile Phe Glu Leu Leu Lys His Ala Lys Ser Leu Gly
          50           55           60
Tyr Lys Leu Leu Leu Ile Thr Asn Gln Ser Gly Ile Asn Arg Gly Tyr
65           70           75           80
Tyr Thr Leu Lys Asp Phe Glu Gln Leu Thr Gln Tyr Leu Gln Glu Ser
          85           90           95
Leu Phe Lys Glu Leu Gly Phe Asn Leu Asp Gly Ile Tyr Phe Cys Arg
          100          105          110
His Ala Pro Glu Glu Asn Cys Ala Cys Arg Lys Pro Lys Pro Ser Leu
          115          120          125
Ile Leu Gln Ala Ala Lys Glu His Gln Ile Cys Leu Glu Gln Ser Phe
          130          135          140
Met Ile Gly Asp Lys Glu Ser Asp Met Leu Ala Gly Leu Asn Ala Lys
145          150          155          160
Val Lys Asn Asn Leu Leu Leu Ile Gln Asn Pro Leu Lys Thr Pro His
          165          170          175
Ser Trp Ile Gln Cys Lys Asp Phe Lys Glu Met Ile Asp Leu Ile Lys
          180          185          190

```

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 88...756
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

																1																	5																																																															
ACA	CCA	CTC	AGC	ATG	ATC	ATA	AAG	GAG	TGC	ATT	CGC	ATG	AAC	ACT	AAC	221																																																																																
Thr	Pro	Leu	Ser	Met	Ile	Ile	Lys	Glu	Cys	Ile	Arg	Met	Asn	Thr	Asn																																																																																	
10							15							20																																																																																		
AAA	GCC	CTT	TTT	TTG	GAC	AGA	GAC	GGC	ATT	ATC	AAT	ATT	GAT	AAA	GGC	269																																																																																
Lys	Ala	Leu	Phe	Leu	Asp	Arg	Asp	Gly	Ile	Ile	Asn	Ile	Asp	Lys	Gly																																																																																	
25							30							35																																																																																		
TAT	GTG	AGT	CAA	AAA	GAA	GAT	TTT	GAG	TTT	CAA	AAA	GGG	ATT	TTT	GAA	317																																																																																
Tyr	Val	Ser	Gln	Lys	Glu	Asp	Phe	Glu	Phe	Gln	Lys	Gly	Ile	Phe	Glu																																																																																	
40							45							50							55																																																																											
TTG	CTA	AAG	CAT	GCG	AAA	TCT	TTA	GGC	TAC	AAA	CTG	CTT	TTA	ATC	ACC	365																																																																																
Leu	Leu	Lys	His	Ala	Lys	Ser	Leu	Gly	Tyr	Lys	Leu	Leu	Leu	Ile	Thr																																																																																	
60							65							70																																																																																		
AAC	CAA	TCT	GGG	ATC	AAC	CGA	GGC	TAT	TAC	ACC	CTT	AAA	GAT	TTT	GAA	413																																																																																
Asn	Gln	Ser	Gly	Ile	Asn	Arg	Gly	Tyr	Tyr	Thr	Leu	Lys	Asp	Phe	Glu																																																																																	
75							80							85																																																																																		
CAA	CTC	ACC	CAA	TAC	CTC	CAA	GAA	AGC	TTG	TTC	AAA	GAA	TTA	GGT	TTT	461																																																																																
Gln	Leu	Thr	Gln	Tyr	Leu	Gln	Glu	Ser	Leu	Phe	Lys	Glu	Leu	Gly	Phe																																																																																	
90							95							100																																																																																		
AAT	CTG	GAT	GGC	ATC	TAT	TTT	TGC	AGG	CAC	GCC	CCA	GAA	GAA	AAT	TGC	509																																																																																
Asn	Leu	Asp	Gly	Ile	Tyr	Phe	Cys	Arg	His	Ala	Pro	Glu	Glu	Asn	Cys																																																																																	
105							110							115																																																																																		
GCT	TGC	AGG	AAG	CCA	AAG	CCT	TCT	TTG	ATT	TTG	CAA	GCT	GCT	AAA	GAG	557																																																																																
Ala	Cys	Arg	Lys	Pro	Lys	Pro	Ser	Leu	Ile	Leu	Gln	Ala	Ala	Lys	Glu																																																																																	
120							125							130							135																																																																											
CAT	CAA	ATT	TGC	TTG	GAG	CAA	TCT	TTT	ATG	ATA	GGC	GAT	AAA	GAG	AGC	605																																																																																
His	Gln	Ile	Cys	Leu	Glu	Gln	Ser	Phe	Met	Ile	Gly	Asp	Lys	Glu	Ser																																																																																	
140							145							150																																																																																		
GAC	ATG	TTA	GCC	GGC	TTG	AAC	GCT	AAA	GTT	AAA	AAT	AAC	CTT	TTG	CTC	653																																																																																
Asp	Met	Leu	Ala	Gly	Leu	Asn	Ala	Lys	Val	Lys	Asn	Asn	Leu	Leu	Leu																																																																																	
155							160							165																																																																																		
ATT	CAA	AAC	CCT	TTA	AAA	ACT	CCT	CAT	TCT	TGG	ATA	CAA	TGT	AAA	GAT	701																																																																																
Ile	Gln	Asn	Pro	Leu	Lys	Thr	Pro	His	Ser	Trp	Ile	Gln	Cys	Lys	Asp																																																																																	
170							175							180																																																																																		
TTT	AAA	GAG	ATG	ATA	GAT	CTA	ATC	AAA	TAAGGACAAG							AATGCGTTAT							ATTGATG							755																																																																		
Phe	Lys	Glu	Met	Ile	Asp	Leu	Ile	Lys																																																																																								
185							190																																																																																									
ATGAATTAGA																AAATCAAACG																ATTTTAATCA																CCGGTGGGGC																TGGCTTTGTA																GGCAGTAATC																815
TAGCCTT																																																																																																822

(2) INFORMATION FOR SEQ ID NO:442:

Phe Lys Gly Gln Cys Ala
85

TATTATTTGT GGGGGAAGAG CGAACGGCTT T

444

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Met	Lys	Ala	Gln	Lys	Ser	Gly	Val	Tyr	Asn	Val	Gly	Tyr	Ser	Gln	Ala
1				5					10					15	
Arg	Ser	Tyr	Asn	Glu	Ile	Val	Ser	Ile	Leu	Lys	Glu	His	Leu	Gly	Asp
			20					25					30		
Phe	Lys	Val	Ser	Tyr	Ile	Lys	Asn	Pro	Tyr	Ala	Phe	Phe	Gln	Lys	His
		35				40						45			
Thr	Gln	Ala	His	Ile	Glu	Pro	Ala	Ile	Leu	Asp	Leu	Asp	Tyr	Thr	Pro
	50				55					60					
Leu	Tyr	Asp	Leu	Glu	Ser	Gly	Ile	Lys	Asp	Tyr	Leu	Pro	His	Ile	His
65				70					75					80	
Ala	Ile	Phe	Lys	Gly	Gln	Cys	Ala								
				85											

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 153...728
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

CAGCATGCCG	TTGTTTTTAA	TGGGGATTTT	TTTAAGCAAA	ATTCCGTTT	CTTACAGGAA	60
ATTTTTCAAT	CTTTTGTCTA	AAATTTTAAAT	GGGGGTTTTT	GGGCTTTATA	TCCTTTATAT	120
GGGGATCATG	CTCATTAACC	ACAAAATGCC	TC ATG CCA	TGC ATC ATC	AAA ACA	173
			Met	Pro	Cys Ile Ile Lys Thr	

```

Glu Lys Ile Asp Tyr Thr Val Ala Ser Glu Leu Ser Ala Lys Asn Glu
      260                      265                      270
Lys Phe Ser Gly Phe Leu Lys Ser Val Val Asp Tyr Asp Pro Asn His
      275                      280                      285
Pro Gln Arg Tyr Lys Asp Glu Phe Asp Glu Val Lys Lys Lys Glu Glu
      290                      295                      300
Leu Tyr Pro Asn Pro Ser Leu Ser Phe
305                      310

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 112...375
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

AACTCGCCTT AGGCGCGATG GCGTTTAAGG AAGTCAAGCT TTTTGAATTT GGCGAGCAAT      60
TAAGGGATTT TGTACTATAT TGAAGATGTG ATCCAAGCGA GCGTGAAAGC G ATG AAG      117
                                     Met Lys
                                     1

GCT CAA AAA AGC GGG GTT TAT AAT GTG GGT TAT TCC CAA GCC AGA AGT      165
Ala Gln Lys Ser Gly Val Tyr Asn Val Gly Tyr Ser Gln Ala Arg Ser
      5                      10                      15

TAT AAT GAA ATC GTT AGC ATT TTA AAA GAG CAT TTA GGG GAT TTT AAA      213
Tyr Asn Glu Ile Val Ser Ile Leu Lys Glu His Leu Gly Asp Phe Lys
      20                      25                      30

GTG AGT TAT ATC AAA AAC CCT TAT GCT TTC TTC CAA AAG CAC ACC CAA      261
Val Ser Tyr Ile Lys Asn Pro Tyr Ala Phe Phe Gln Lys His Thr Gln
      35                      40                      45                      50

GCA CAC ATT GAG CCT GCT ATT TTG GAT TTG GAT TAC ACC CCT TTA TAC      309
Ala His Ile Glu Pro Ala Ile Leu Asp Leu Asp Tyr Thr Pro Leu Tyr
      55                      60                      65

GAT TTG GAA AGC GGC ATT AAA GAT TAT TTG CCC CAT ATC CAT GCG ATT      357
Asp Leu Glu Ser Gly Ile Lys Asp Tyr Leu Pro His Ile His Ala Ile
      70                      75                      80

TTT AAA GGA CAG TGC GCA TGAAAAAAT CTTAGTCATA GGCGATCTGA TCGCTGAT      413

```

CCA AAC CAC CCA CAA CGC TAT AAA GAT GAA TTT GAT GAG GTT AAA AAG 973
 Pro Asn His Pro Gln Arg Tyr Lys Asp Glu Phe Asp Glu Val Lys Lys
 290 295 300

AAA GAG GAG TTA TAC CCT AAC CCA TCG CTT TCT TTT TAAAAATGAG ATTTTA 1025
 Lys Glu Glu Leu Tyr Pro Asn Pro Ser Leu Ser Phe
 305 310

AAAAACGCTT TAAGTGTTTT TGTAAAAAAT AGCAAAGAGC TTGATTTTAA TCA 1078

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met	Lys	Pro	Gln	Asp	Ile	Glu	Ile	Val	Gln	Ser	Val	Leu	Glu	Ile	Thr	1	5	10	15
Gly	Pro	Ile	Lys	Pro	Thr	Glu	Val	Tyr	Asp	Lys	Ala	Lys	Glu	Leu	Phe	20	25	30	
Glu	Lys	Gly	Glu	Ile	Thr	Asn	Met	Phe	Asp	Cys	Gly	Gly	Lys	Thr	Pro	35	40	45	
His	Gln	Ser	Val	Ser	Ser	Tyr	Ile	Tyr	Thr	Ala	Leu	Asn	Lys	Gly	Glu	50	55	60	
Glu	Leu	Pro	Phe	Lys	Lys	Val	Gln	Glu	Asn	Pro	Thr	Leu	Ile	Ala	Leu	65	70	75	80
Lys	Asp	Ala	Ala	Lys	Glu	Leu	Gly	Leu	Asp	Ala	Gln	Lys	Ile	Ser	Ala	85	90	95	
Pro	Ser	Ser	Lys	Ile	Ala	His	Glu	Arg	Asp	Leu	His	Pro	Phe	Leu	Thr	100	105	110	
Tyr	Met	Ala	Ile	Asn	Asn	Glu	Asn	Leu	Lys	Cys	Tyr	Thr	Lys	Thr	Ile	115	120	125	
Phe	His	Glu	Glu	Ser	Ser	Lys	Ser	Ile	Lys	Gly	Met	Asp	Arg	Trp	Leu	130	135	140	
Tyr	Pro	Asp	Met	Val	Gly	Val	Arg	Phe	Leu	His	Ala	Glu	Leu	Ser	Asn	145	150	155	160
Glu	Asn	Leu	Ile	Ala	Phe	Ser	Lys	Lys	Phe	Asp	Thr	Leu	Pro	Ile	Lys	165	170	175	
Leu	Val	Ser	Phe	Glu	Leu	Lys	Lys	Glu	Ile	Ser	Val	His	Asn	Cys	Arg	180	185	190	
Glu	Cys	Tyr	Phe	Gln	Ala	Ile	Ser	Asn	Ser	Ser	Trp	Ala	Asn	Glu	Gly	195	200	205	
Tyr	Leu	Val	Gly	Arg	His	Ile	Asp	Thr	His	Asn	Pro	Gln	Leu	Met	Asp	210	215	220	
Leu	Leu	Lys	Arg	Leu	His	Ala	Ser	Phe	Gly	Ile	Gly	Val	Ile	Asp	Leu	225	230	235	240
Arg	Thr	Asn	Glu	Asp	Lys	Ser	Ala	Ile	Leu	Leu	Asn	Ala	Lys	Tyr	Lys	245	250	255	

Lys	Gly	Glu	Glu	Leu	Pro	Phe	Lys	Lys	Val	Gln	Glu	Asn	Pro	Thr	Leu	
			65					70					75			
ATC	GCT	TTA	AAA	GAC	GCG	GCT	AAA	GAG	CTA	GGT	TTA	GAC	GCT	CAA	AAA	349
Ile	Ala	Leu	Lys	Asp	Ala	Ala	Lys	Glu	Leu	Gly	Leu	Asp	Ala	Gln	Lys	
		80					85					90				
ATA	AGC	GCT	CCA	AGC	TCT	AAA	ATC	GCG	CAT	GAA	AGG	GAT	TTG	CAC	CCC	397
Ile	Ser	Ala	Pro	Ser	Ser	Lys	Ile	Ala	His	Glu	Arg	Asp	Leu	His	Pro	
	95					100					105					
TTT	TTA	ACC	TAC	ATG	GCT	ATT	AAT	AAC	GAA	AAT	TTG	AAA	TGC	TAC	ACG	445
Phe	Leu	Thr	Tyr	Met	Ala	Ile	Asn	Asn	Glu	Asn	Leu	Lys	Cys	Tyr	Thr	
110					115				120						125	
AAA	ACC	ATT	TTT	CAT	GAA	GAG	AGT	TCA	AAA	TCA	ATA	AAA	GGC	ATG	GAC	493
Lys	Thr	Ile	Phe	His	Glu	Glu	Ser	Ser	Lys	Ser	Ile	Lys	Gly	Met	Asp	
				130					135					140		
AGG	TGG	CTT	TAT	CCG	GAC	ATG	GTG	GGG	GTT	AGG	TTT	TTG	CAC	GCT	GAA	541
Arg	Trp	Leu	Tyr	Pro	Asp	Met	Val	Gly	Val	Arg	Phe	Leu	His	Ala	Glu	
			145					150					155			
TTA	TCT	AAT	GAA	AAT	TTA	ATC	GCT	TTT	TCT	AAG	AAA	TTT	GAC	ACT	TTA	589
Leu	Ser	Asn	Glu	Asn	Leu	Ile	Ala	Phe	Ser	Lys	Lys	Phe	Asp	Thr	Leu	
		160					165					170				
CCC	ATT	AAA	CTG	GTG	AGC	TTT	GAA	TTG	AAA	AAA	GAA	ATC	AGC	GTG	CAT	637
Pro	Ile	Lys	Leu	Val	Ser	Phe	Glu	Leu	Lys	Lys	Glu	Ile	Ser	Val	His	
	175					180					185					
AAT	TGC	AGG	GAG	TGT	TAC	TTT	CAA	GCG	ATT	TCC	AAC	AGC	TCG	TGG	GCT	685
Asn	Cys	Arg	Glu	Cys	Tyr	Phe	Gln	Ala	Ile	Ser	Asn	Ser	Ser	Trp	Ala	
190					195					200					205	
AAT	GAA	GGG	TAT	TTA	GTG	GGC	CGT	CAT	ATT	GAT	ACG	CAC	AAT	CCT	CAA	733
Asn	Glu	Gly	Tyr	Leu	Val	Gly	Arg	His	Ile	Asp	Thr	His	Asn	Pro	Gln	
				210					215					220		
CTC	ATG	GAT	TTG	TTG	AAG	CGT	TTG	CAT	GCG	AGT	TTT	GGG	ATT	GGC	GTG	781
Leu	Met	Asp	Leu	Leu	Lys	Arg	Leu	His	Ala	Ser	Phe	Gly	Ile	Gly	Val	
			225					230					235			
ATT	GAT	TTA	AGA	ACT	AAT	GAG	GAT	AAA	AGC	GCT	ATT	TTA	TTG	AAC	GCT	829
Ile	Asp	Leu	Arg	Thr	Asn	Glu	Asp	Lys	Ser	Ala	Ile	Leu	Leu	Asn	Ala	
		240					245					250				
AAA	TAC	AAA	GAA	AAG	ATT	GAT	TAC	ACC	GTG	GCT	TCA	GAG	CTT	AGC	GCG	877
Lys	Tyr	Lys	Glu	Lys	Ile	Asp	Tyr	Thr	Val	Ala	Ser	Glu	Leu	Ser	Ala	
	255					260					265					
AAA	AAT	GAA	AAA	TTC	AGC	GGT	TTT	TTA	AAG	AGC	GTT	GTG	GAT	TAT	GAC	925
Lys	Asn	Glu	Lys	Phe	Ser	Gly	Phe	Leu	Lys	Ser	Val	Val	Asp	Tyr	Asp	
270					275					280					285	

```

Lys Ile Ala His Ala Leu Ala Asp Asn Ile Val Ser Ala Thr Phe Leu
      115              120              125
Ala Cys Ala Ser Pro Lys Ile Leu Ala Pro Ser Met Asn Thr Asn Met
      130              135              140
Leu Asn Ser Pro Ile Thr Gln Ser Asn Leu Lys Arg Leu Lys Asp Ser
145              150              155              160
Asn His Ile Ile Leu Asp Thr Lys Asn Ala Leu Leu Ala Cys Asp Thr
      165              170              175
Lys Gly Asp Gly Ala Met Ala Glu Pro Leu Glu Ile Leu Phe Lys Ala
      180              185              190
Ala Gln Thr Leu Leu Lys Asp Ala Tyr Phe Glu Asn Arg Glu Val Ile
      195              200              205
Val Met Gly Gly Ala Ser Ile Glu Lys Ile Asp Ser Val Arg Thr Ile
      210              215              220
Ser Asn Thr Phe
225

```

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 71...1009
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

TCCCAAGCCC TAAAGGCGCT TCAATCATTG ATTTTAAAGG CAGTTATGAA GAGTATTTGG      60
CGAGCAAAAA ATG AAA CCG CAA GAC ATT GAA ATC GTT CAA AGC GTT TTA      109
      Met Lys Pro Gln Asp Ile Glu Ile Val Gln Ser Val Leu
        1              5              10

GAG ATT ACA GGA CCG ATT AAG CCT ACT GAA GTG TAT GAT AAA GCC AAA      157
Glu Ile Thr Gly Pro Ile Lys Pro Thr Glu Val Tyr Asp Lys Ala Lys
      15              20              25

GAG CTT TTT GAA AAA GGT GAG ATT ACA AAC ATG TTT GAT TGT GGG GGC      205
Glu Leu Phe Glu Lys Gly Glu Ile Thr Asn Met Phe Asp Cys Gly Gly
      30              35              40              45

AAA ACC CCG CAC CAG AGC GTT AGT TCT TAT ATT TAT ACA GCC TTA AAC      253
Lys Thr Pro His Gln Ser Val Ser Ser Tyr Ile Tyr Thr Ala Leu Asn
      50              55              60

AAG GGC GAA GAA CTG CCT TTT AAA AAA GTG CAA GAA AAC CCA ACC TTA      301

```

[illegible]

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met	Asn	Phe	Leu	Glu	Asp	Leu	Phe	Tyr	Pro	Leu	Arg	Leu	Leu	Glu	Asn
1				5					10					15	
Lys	Arg	Val	Leu	Leu	Leu	Val	Ser	Gly	Ser	Ile	Ala	Ala	Tyr	Lys	Ser
			20					25					30		
Leu	Glu	Leu	Val	Arg	Leu	Leu	Phe	Lys	Ser	Gly	Ala	Ser	Ile	Gln	Val
			35				40					45			
Val	Met	Ser	Lys	Gly	Ala	Lys	Lys	Phe	Ile	Lys	Pro	Leu	Ser	Phe	Glu
	50					55					60				
Ala	Leu	Ser	His	His	Lys	Val	Leu	His	Asp	Arg	Asn	Glu	Lys	Trp	Tyr
65					70				75					80	
Tyr	Asn	His	Gln	Asn	Ala	Leu	His	His	Asn	His	Ile	Ala	Cys	Ala	Ala
			85						90				95		
Asn	Ala	Asp	Leu	Leu	Ile	Phe	Ala	Pro	Leu	Ser	Thr	Asn	Ser	Leu	Ser
			100					105					110		

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

AGCCATAATA ACAACCAATG GCTAGAGCCT GATGATTTGT TGAAATTATT	ATG AAT	56
	Met Asn	
	1	
TTT TTA GAA GAT TTG TTT TAC CCC TTA AGA TTG TTA GAA AAC AAG CGT		104
Phe Leu Glu Asp Leu Phe Tyr Pro Leu Arg Leu Leu Glu Asn Lys Arg		
5 10 15		
GTT TTA TTG CTC GTG AGC GGT TCT ATT GCA GCG TAT AAA TCC CTA GAA		152
Val Leu Leu Leu Val Ser Gly Ser Ile Ala Ala Tyr Lys Ser Leu Glu		
20 25 30		
TTA GTG CGC TTG TTG TTT AAA AGC GGG GCT AGT ATC CAA GTG GTG ATG		200
Leu Val Arg Leu Leu Phe Lys Ser Gly Ala Ser Ile Gln Val Val Met		
35 40 45 50		
AGT AAG GGT GCG AAA AAA TTC ATC AAA CCC TTA AGT TTT GAA GCT TTG		248
Ser Lys Gly Ala Lys Lys Phe Ile Lys Pro Leu Ser Phe Glu Ala Leu		
55 60 65		
AGC CAC CAT AAA GTC TTG CAT GAT CGT AAT GAA AAA TGG TAT TAC AAC		296
Ser His His Lys Val Leu His Asp Arg Asn Glu Lys Trp Tyr Tyr Asn		
70 75 80		
CAC CAA AAC GCC TTA CAC CAT AAC CAC ATC GCA TGC GCT GCT AAT GCT		344
His Gln Asn Ala Leu His His Asn His Ile Ala Cys Ala Ala Asn Ala		
85 90 95		
GAT TTG CTC ATC TTT GCC CCT TTA AGC ACT AAC AGC TTG TCT AAA ATC		392
Asp Leu Leu Ile Phe Ala Pro Leu Ser Thr Asn Ser Leu Ser Lys Ile		
100 105 110		
GCT CAC GCT TTA GCG GAT AAT ATC GTA AGC GCG ACT TTT TTA GCT TGC		440
Ala His Ala Leu Ala Asp Asn Ile Val Ser Ala Thr Phe Leu Ala Cys		
115 120 125 130		
GCT TCC CCT AAA ATC CTA GCC CCT AGC ATG AAC ACT AAC ATG CTC AAT		488
Ala Ser Pro Lys Ile Leu Ala Pro Ser Met Asn Thr Asn Met Leu Asn		

205 210 215

GGG GCT GTT TTA ACC GAT GAA GGG CAT TAAGCAATAA CATTCTTGTT TGGCTTT 790
 Gly Ala Val Leu Thr Asp Glu Gly His
 220 225

AATATTGTTT TTTAAACTT TGTTTTATGG TAAAGCTTTT A 831

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Glu His Arg Val Phe Thr Ile Ala Asn Phe Phe Ser Ser Asn His
 1 5 10 15
 Asp Phe Ile Thr Gly Phe Phe Val Val Leu Thr Ala Val Leu Met Phe
 20 25 30
 Leu Ile Ser Leu Gly Ala Ser Arg Lys Met Gln Met Val Pro Met Gly
 35 40 45
 Leu Gln Asn Val Tyr Glu Ser Ile Ile Ser Ala Ile Leu Ser Val Ala
 50 55 60
 Lys Asp Ile Ile Gly Glu Leu Ala Arg Lys Tyr Phe Pro Leu Ala
 65 70 75 80
 Gly Thr Ile Ala Leu Tyr Val Phe Phe Ser Asn Met Ile Gly Ile Ile
 85 90 95
 Pro Gly Phe Glu Ser Pro Thr Ala Ser Trp Ser Phe Thr Leu Val Leu
 100 105 110
 Ala Leu Ile Val Phe Phe Tyr Tyr His Phe Glu Gly Ile Arg Val Gln
 115 120 125
 Gly Phe Phe Lys Tyr Phe Ala His Phe Ala Gly Pro Val Lys Trp Leu
 130 135 140
 Ala Pro Phe Met Phe Pro Ile Glu Ile Ile Ser His Phe Ser Arg Ile
 145 150 155 160
 Val Ser Leu Ser Phe Arg Leu Phe Gly Asn Ile Lys Gly Asp Asp Met
 165 170 175
 Phe Leu Leu Ile Met Leu Leu Leu Val Pro Trp Ala Val Pro Val Ala
 180 185 190
 Pro Phe Met Val Leu Phe Phe Met Gly Ile Leu Gln Ala Phe Val Phe
 195 200 205
 Met Ile Leu Thr Tyr Val Tyr Leu Ala Gly Ala Val Leu Thr Asp Glu
 210 215 220
 Gly His
 225

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

CGTTAAAAAG CTTGGTTTAA TGAGTTTTTA AAACCTAATT GCTACAATTA AGGAAATTTT	60
CAATAAGGCT TAGAGAAACT TTTTC ATG GAA CAC AGA GTA TTT ACT ATT GCT	112
Met Glu His Arg Val Phe Thr Ile Ala	
1 5	
AAT TTT TTT AGC TCC AAT CAT GAT TTT ATC ACC GGG TTT TTT GTC GTT	160
Asn Phe Phe Ser Ser Asn His Asp Phe Ile Thr Gly Phe Phe Val Val	
10 15 20 25	
TTG ACA GCG GTT TTG ATG TTT TTA ATC TCG CTT GGC GCG TCG CGC AAA	208
Leu Thr Ala Val Leu Met Phe Leu Ile Ser Leu Gly Ala Ser Arg Lys	
30 35 40	
ATG CAG ATG GTA CCT ATG GGT TTG CAG AAT GTG TAT GAG AGC ATC ATT	256
Met Gln Met Val Pro Met Gly Leu Gln Asn Val Tyr Glu Ser Ile Ile	
45 50 55	
AGC GCG ATT TTG AGC GTG GCT AAG GAT ATT ATA GGC GAA GAA TTA GCC	304
Ser Ala Ile Leu Ser Val Ala Lys Asp Ile Ile Gly Glu Glu Leu Ala	
60 65 70	
CGC AAA TAC TTC CCC CTA GCT GGC ACG ATC GCT TTG TAT GTC TTT TTT	352
Arg Lys Tyr Phe Pro Leu Ala Gly Thr Ile Ala Leu Tyr Val Phe Phe	
75 80 85	
TCT AAC ATG ATA GGC ATC ATT CCT GGC TTT GAA TCC CCT ACG GCT AGC	400
Ser Asn Met Ile Gly Ile Ile Pro Gly Phe Glu Ser Pro Thr Ala Ser	
90 95 100 105	
TGG AGC TTT ACG CTG GTT TTA GCG CTG ATT GTG TTT TTT TAT TAC CAT	448
Trp Ser Phe Thr Leu Val Leu Ala Leu Ile Val Phe Phe Tyr Tyr His	
110 115 120	
TTT GAA GGC ATT AGA GTG CAG GGC TTT TTT AAG TAT TTC GCT CAT TTT	496
Phe Glu Gly Ile Arg Val Gln Gly Phe Phe Lys Tyr Phe Ala His Phe	
125 130 135	
GCA GGT CCT GTG AAA TGG CTC GCC CCT TTC ATG TTC CCT ATT GAG ATC	544
Ala Gly Pro Val Lys Trp Leu Ala Pro Phe Met Phe Pro Ile Glu Ile	
140 145 150	
ATC TCG CAT TTT TCT AGG ATC GTG TCT TTA TCG TTT CGT TTG TTT GGG	592
Ile Ser His Phe Ser Arg Ile Val Ser Leu Ser Phe Arg Leu Phe Gly	
155 160 165	
AAT ATC AAG GGC GAT GAC ATG TTC TTG CTC ATC ATG CTT TTA TTA GTG	640
Asn Ile Lys Gly Asp Asp Met Phe Leu Leu Ile Met Leu Leu Leu Val	
170 175 180 185	
CCT TGG GCG GTT CCT GTA GCG CCT TTT ATG GTG TTG TTT TTC ATG GGG	688
Pro Trp Ala Val Pro Val Ala Pro Phe Met Val Leu Phe Phe Met Gly	
190 195 200	
ATT TTA CAA GCT TTT GTT TTT ATG ATC CTC ACT TAT GTG TAT TTG GCA	736
Ile Leu Gln Ala Phe Val Phe Met Ile Leu Thr Tyr Val Tyr Leu Ala	

CTT ATT GTG AAA AAT GGT AAA TTT GAG CTT TTA GAA AAT ATC ACT TTT T 393
 Leu Ile Val Lys Asn Gly Lys Phe Glu Leu Leu Glu Asn Ile Thr Phe
 100 105 110

AGATTTTAC AGAAAGTAAA TCGGATTTC TTAACATTCT TAAGCTAATA TA 445

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Met	Arg	Phe	Leu	Asn	Asn	Lys	His	Arg	Glu	Lys	Gly	Leu	Lys	Ala	Glu
1				5					10					15	
Glu	Glu	Ala	Cys	Gly	Phe	Leu	Lys	Ser	Leu	Gly	Phe	Glu	Met	Val	Glu
			20					25					30		
Arg	Asn	Phe	Phe	Ser	Gln	Phe	Gly	Glu	Ile	Asp	Ile	Ile	Ala	Leu	Lys
		35					40					45			
Lys	Gly	Val	Leu	His	Phe	Ile	Glu	Val	Lys	Ser	Gly	Glu	Asn	Phe	Asp
	50					55					60				
Pro	Ile	Tyr	Ala	Ile	Thr	Pro	Ser	Lys	Leu	Lys	Lys	Met	Ile	Lys	Thr
65					70					75				80	
Ile	Arg	Cys	Tyr	Leu	Ser	Gln	Lys	Asp	Pro	Asn	Ser	Asp	Phe	Cys	Ile
			85						90					95	
Asp	Ala	Leu	Ile	Val	Lys	Asn	Gly	Lys	Phe	Glu	Leu	Leu	Glu	Asn	Ile
			100					105						110	
Thr	Phe														

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 86...763
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

Leu Val Ala Ile Thr Ile Gln Ala Cys Gly Tyr Lys Ala Pro Pro Phe
      20              25              30
Asn Glu Lys Pro Ala Lys Lys Thr Ser Asn Ser Ser Asn Ser Ser Met
      35              40              45
Gln Thr Pro Thr Asn Ser Thr Thr Pro Glu Phe Leu Asn Gln Pro
      50              55              60

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...392
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```

ATTTACAAAG CGTGTGGAT ACCCCCAAGA TGATTCGTTT GGAAAATTGA  ATG CGC      56
                                     Met Arg
                                     1

TTT TTG AAC AAC AAA CAT AGA GAA AAG GGC TTA AAG GCT GAA GAA GAA      104
Phe Leu Asn Asn Lys His Arg Glu Lys Gly Leu Lys Ala Glu Glu Glu
      5              10              15

GCT TGC GGA TTT TTA AAA TCG TTA GGT TTT GAA ATG GTG GAG AGG AAC      152
Ala Cys Gly Phe Leu Lys Ser Leu Gly Phe Glu Met Val Glu Arg Asn
      20              25              30

TTT TTT TCA CAA TTT GGC GAA ATT GAT ATT ATC GCT TTG AAA AAA GGG      200
Phe Phe Ser Gln Phe Gly Glu Ile Asp Ile Ile Ala Leu Lys Lys Gly
      35              40              45              50

GTT TTG CAT TTC ATT GAA GTC AAA AGC GGG GAA AAT TTT GAT CCC ATT      248
Val Leu His Phe Ile Glu Val Lys Ser Gly Glu Asn Phe Asp Pro Ile
              55              60              65

TAT GCG ATC ACG CCG AGC AAA TTA AAA AAG ATG ATT AAA ACG ATC CGC      296
Tyr Ala Ile Thr Pro Ser Lys Leu Lys Lys Met Ile Lys Thr Ile Arg
              70              75              80

TGT TAT TTG TCC CAA AAA GAT CCC AAT AGC GAT TTT TGC ATA GAC GCT      344
Cys Tyr Leu Ser Gln Lys Asp Pro Asn Ser Asp Phe Cys Ile Asp Ala
      85              90              95

```

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 82...270
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

ACTTAAAGGC ATAAAAACCT TAAGCTTTTT GAGTTTCAAA AGGGTTTCAA GCTTTTTTATA      60
AGACTTTTTT TGAATGAGTA A GGA GAA AAT ATT TTG TTC CAT AAA CTG ATC      111
              Gly Glu Asn Ile Leu Phe His Lys Leu Ile
                1                5                10

TTA ACA TGC TTT TTA GCG CTT GTA GCA ATA ACC ATT CAA GCT TGC GGT      159
Leu Thr Cys Phe Leu Ala Leu Val Ala Ile Thr Ile Gln Ala Cys Gly
              15                20                25

TAT AAA GCC CCT CCA TTC AAT GAA AAA CCC GCT AAA AAA ACT TCA AAC      207
Tyr Lys Ala Pro Pro Phe Asn Glu Lys Pro Ala Lys Lys Thr Ser Asn
              30                35                40

AGC TCT AAT TCT TCT ATG CAA ACG CCC ACC AAC AGC ACC ACG CCA GAA      255
Ser Ser Asn Ser Ser Met Gln Thr Pro Thr Asn Ser Thr Thr Pro Glu
              45                50                55

TTT TTA AAT CAG CCT TAAAATCACT GCTCTTGTTT AAGGGCTTTG ATTTCTAGGG T      311
Phe Leu Asn Gln Pro
              60

TTTTGTGGCT AACTTTTGAN STTCGCTTTC ATCATGCGTT ACCATAATG      360

```

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

Gly Glu Asn Ile Leu Phe His Lys Leu Ile Leu Thr Cys Phe Leu Ala
  1                5                10                15

```

	5	10	15	
ATC TAT GCC AAT CAT TTA AAA TTA TTG GAT AAT GAA ATC AGT GAA AAA				152
Ile Tyr Ala Asn His Leu Lys Leu Leu Asp Asn Glu Ile Ser Glu Lys				
	20	25	30	
GAC ATT TTT AAT AAA GCC ATC AAT CAA AAA CGA ATT CAA ATG GCT CTT				200
Asp Ile Phe Asn Lys Ala Ile Asn Gln Lys Arg Ile Gln Met Ala Leu				
	35	40	45	50
AAT CTC ATC TTT AAG CTT GTT TTT GCC TTT GTT AGT AAC CAC TTC TTC				248
Asn Leu Ile Phe Lys Leu Val Phe Ala Phe Val Ser Asn His Phe Phe				
	55	60	65	
CAC GCT TTT AGA CGA CAG AAT CTC TAT AAT CGT GTC TTT AAT CGC TGT				296
His Ala Phe Arg Arg Gln Asn Leu Tyr Asn Arg Val Phe Asn Arg Cys				
	70	75	80	
GTC TTT AAC CTT GAC TTC ATT CAA AAG CTT TTC ATT ACT CAA TTC TAACG				346
Val Phe Asn Leu Asp Phe Ile Gln Lys Leu Phe Ile Thr Gln Phe				
	85	90	95	
AAATAGAAGC CTTAAGGTAG CGTCTGCCAT TTTGAGAGAC CAGATTCA				394

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Lys	Leu	His	Phe	Lys	Ala	Phe	His	Ala	Leu	Phe	Tyr	Pro	Ser	Asn	Arg
1				5					10					15	
Asp	Asn	Ile	Tyr	Ala	Asn	His	Leu	Lys	Leu	Leu	Asp	Asn	Glu	Ile	Ser
			20					25					30		
Glu	Lys	Asp	Ile	Phe	Asn	Lys	Ala	Ile	Asn	Gln	Lys	Arg	Ile	Gln	Met
		35					40					45			
Ala	Leu	Asn	Leu	Ile	Phe	Lys	Leu	Val	Phe	Ala	Phe	Val	Ser	Asn	His
	50					55				60					
Phe	Phe	His	Ala	Phe	Arg	Arg	Gln	Asn	Leu	Tyr	Asn	Arg	Val	Phe	Asn
	65				70				75					80	
Arg	Cys	Val	Phe	Asn	Leu	Asp	Phe	Ile	Gln	Lys	Leu	Phe	Ile	Thr	Gln
				85				90						95	
Phe															

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

```

Leu Ile Ala Lys Asp Gly Gly Val Leu Ala Arg Thr Gly His Thr Glu
 130              135              140
Ala Ser Val Asp Leu Cys Lys Leu Ala Gly Leu Lys Pro Val Ser Val
145              150              155              160
Ile Cys Glu Ile Met Lys Glu Asp Gly Ser Met Ala Arg Arg Gly Asp
              165              170              175
Lys Phe Leu Ser Asp Phe Ala Leu Lys His Asn Leu Lys Thr Leu Tyr
              180              185              190
Val Ser Asp Leu Ile Ser Tyr Arg Leu Glu Asn Glu Ser Leu Leu Lys
              195              200              205
Met Phe Cys Gln Glu Glu Arg Glu Phe Leu Lys His Gln Thr Gln Cys
              210              215              220
Tyr Thr Phe Leu Asp His Gln Gln Lys Asn His Tyr Ala Phe Lys Phe
225              230              235              240
Lys Gly Ala Lys Thr His Asp Leu Ala Pro Leu Val Arg Phe His Pro
              245              250              255
Ile Lys Glu Asp Phe Asp Phe Leu Thr Thr Asp Ala Phe Glu Val Phe
              260              265              270
Phe Lys Ala Leu Glu Tyr Leu Lys His Glu Gly Gly Tyr Leu Ile Phe
              275              280              285
Met Asn Thr His Ser Lys Glu Asn Asn Val Val Lys Asp Phe Gly Ile
              290              295              300
Gly Ala Leu Val Leu Lys Asn Leu Gly Ile Lys Asp Phe Arg Leu Leu
305              310              315              320
Ser Ser Cys Glu Asp Arg Gln Tyr Lys Ala Leu Ser Gly Phe Gly Leu
              325              330              335
Lys Leu Val Glu Thr Ile Ser Leu
              340

```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...341
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

GATTTATCCT TGCATAAAAC AATCTCGCTT GGCGATAAAA AACGCTCTAA  AAA CTT      56
                                     Lys Leu
                                     1

CAT TTT AAA GCG TTT CAC GCA CTT TTC TAT CCT AGC AAT AGA GAC AAT      104
His Phe Lys Ala Phe His Ala Leu Phe Tyr Pro Ser Asn Arg Asp Asn

```

```

CGT TTC CAC CCT ATC AAA GAG GAT TTT GAT TTT TTA ACG ACT GAT GCG      878
Arg Phe His Pro Ile Lys Glu Asp Phe Asp Phe Leu Thr Thr Asp Ala
      255                      260                      265

TTT GAA GTG TTT TTT AAA GCG TTA GAA TAT TTA AAG CAC GAA GGG GGC      926
Phe Glu Val Phe Phe Lys Ala Leu Glu Tyr Leu Lys His Glu Gly Gly
      270                      275                      280

TAT TTG ATC TTT ATG AAC ACC CAT TCT AAA GAA AAC AAT GTC GTT AAA      974
Tyr Leu Ile Phe Met Asn Thr His Ser Lys Glu Asn Asn Val Val Lys
      285                      290                      295                      300

GAT TTT GGG ATC GGG GCG TTG GTG TTA AAA AAT TTG GGG ATA AAG GAT      1022
Asp Phe Gly Ile Gly Ala Leu Val Leu Lys Asn Leu Gly Ile Lys Asp
      305                      310                      315

TTC AGG CTC TTA AGC TCT TGT GAA GAC AGG CAG TAT AAG GCT TTG AGC      1070
Phe Arg Leu Leu Ser Ser Cys Glu Asp Arg Gln Tyr Lys Ala Leu Ser
      320                      325                      330

GGG TTT GGG CTT AAG CTT GTA GAA ACG ATT AGC CTT TAAGAGGCTC GTTAAG      1122
Gly Phe Gly Leu Lys Leu Val Glu Thr Ile Ser Leu
      335                      340

TTTTATTGAA TGTGTTGTAA TGTTTTTAAG GTATAATAAA CTCTTTTAA      1172

```

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

Met Ile Leu Lys Arg Val Thr Glu Ala Leu Glu Ala Tyr Lys Asn Gly
 1           5           10           15
Glu Met Leu Ile Val Met Asp Asp Glu Asp Arg Glu Asn Glu Gly Asp
      20           25           30
Leu Val Leu Ala Gly Ile Phe Ser Thr Pro Glu Lys Ile Asn Phe Met
      35           40           45
Ala Thr His Ala Arg Gly Leu Ile Cys Val Ser Leu Thr Lys Asp Leu
      50           55           60
Ala Lys Lys Phe Glu Leu Pro Pro Met Val Ser Val Asn Asp Ser Asn
      65           70           75           80
His Glu Thr Ala Phe Thr Val Ser Ile Asp Ala Lys Glu Ala Arg Thr
      85           90           95
Gly Ile Ser Ala Phe Glu Arg His Leu Thr Ile Glu Leu Leu Cys Lys
      100          105          110
Asp Thr Thr Lys Pro Ser Asp Phe Val Arg Pro Gly His Ile Phe Pro
      115          120          125

```

Asn	Glu	Gly	Asp	Leu	Val	Leu	Ala	Gly	Ile	Phe	Ser	Thr	Pro	Glu	Lys	
30						35				40						
ATC	AAT	TTC	ATG	GCC	ACG	CAT	GCT	AGG	GGG	TTG	ATT	TGC	GTG	TCT	TTG	254
Ile	Asn	Phe	Met	Ala	Thr	His	Ala	Arg	Gly	Leu	Ile	Cys	Val	Ser	Leu	
45					50				55					60		
ACC	AAA	GAT	TTA	GCG	AAA	AAA	TTT	GAA	TTA	CCC	CCT	ATG	GTT	AGC	GTG	302
Thr	Lys	Asp	Leu	Ala	Lys	Lys	Phe	Glu	Leu	Pro	Pro	Met	Val	Ser	Val	
				65				70						75		
AAT	GAT	TCT	AAC	CAT	GAG	ACC	GCT	TTC	ACG	GTT	TCC	ATT	GAC	GCT	AAA	350
Asn	Asp	Ser	Asn	His	Glu	Thr	Ala	Phe	Thr	Val	Ser	Ile	Asp	Ala	Lys	
			80					85					90			
GAA	GCC	AGA	ACC	GGG	ATT	TCT	GCT	TTT	GAA	AGG	CAT	TTA	ACG	ATT	GAA	398
Glu	Ala	Arg	Thr	Gly	Ile	Ser	Ala	Phe	Glu	Arg	His	Leu	Thr	Ile	Glu	
		95					100					105				
TTA	TTG	TGT	AAA	GAC	ACC	ACC	AAA	CCG	AGC	GAT	TTT	GTG	CGC	CCG	GGG	446
Leu	Leu	Cys	Lys	Asp	Thr	Thr	Lys	Pro	Ser	Asp	Phe	Val	Arg	Pro	Gly	
	110					115					120					
CAT	ATT	TTC	CCT	TTG	ATC	GCC	AAA	GAC	GGG	GGC	GTG	TTA	GCG	CGC	ACG	494
His	Ile	Phe	Pro	Leu	Ile	Ala	Lys	Asp	Gly	Gly	Val	Leu	Ala	Arg	Thr	
125					130				135						140	
GGC	CAT	ACT	GAA	GCG	AGC	GTG	GAT	TTG	TGC	AAA	TTA	GCT	GGA	TTA	AAG	542
Gly	His	Thr	Glu	Ala	Ser	Val	Asp	Leu	Cys	Lys	Leu	Ala	Gly	Leu	Lys	
				145				150						155		
CCC	GTG	AGC	GTG	ATT	TGT	GAA	ATC	ATG	AAA	GAA	GAT	GGC	TCT	ATG	GCG	590
Pro	Val	Ser	Val	Ile	Cys	Glu	Ile	Met	Lys	Glu	Asp	Gly	Ser	Met	Ala	
			160					165					170			
AGA	AGG	GGG	GAT	AAA	TTT	TTG	AGC	GAT	TTC	GCC	CTC	AAA	CAT	AAC	CTT	638
Arg	Arg	Gly	Asp	Lys	Phe	Leu	Ser	Asp	Phe	Ala	Leu	Lys	His	Asn	Leu	
		175					180					185				
AAA	ACT	CTC	TAT	GTC	TCT	GAT	TTG	ATT	AGC	TAT	CGT	TTG	GAA	AAT	GAA	686
Lys	Thr	Leu	Tyr	Val	Ser	Asp	Leu	Ile	Ser	Tyr	Arg	Leu	Glu	Asn	Glu	
	190					195					200					
AGT	TTG	CTG	AAA	ATG	TTT	TGT	CAA	GAA	GAA	AGG	GAA	TTT	TTA	AAA	CAC	734
Ser	Leu	Leu	Lys	Met	Phe	Cys	Gln	Glu	Glu	Arg	Glu	Phe	Leu	Lys	His	
205					210					215				220		
CAA	ACG	CAA	TGC	TAC	ACT	TTT	TTA	GAT	CAC	CAG	CAA	AAA	AAC	CAT	TAC	782
Gln	Thr	Gln	Cys	Tyr	Thr	Phe	Leu	Asp	His	Gln	Gln	Lys	Asn	His	Tyr	
				225					230					235		
GCT	TTT	AAG	TTT	AAA	GGC	GCA	AAA	ACC	CAT	GAT	TTA	GCC	CCT	TTA	GTG	830
Ala	Phe	Lys	Phe	Lys	Gly	Ala	Lys	Thr	His	Asp	Leu	Ala	Pro	Leu	Val	
			240					245					250			

Glu	Asn	His	Ser	Lys	Tyr	Arg	Asp	Ile	Pro	Phe	Ala	Glu	Val	Ser	Leu
			100					105					110		
Ile	Tyr	Gly	Tyr	Lys	Gln	Phe	Phe	Pro	Lys	Lys	Glu	Arg	Tyr	Gly	Phe
		115					120					125			
Arg	Phe	Tyr	Val	Ser	Leu	Asp	Tyr	Ala	Tyr	Gly	Phe	Phe	Leu	Lys	Asn
		130				135					140				
Lys	Gly	Val	Leu	Gly	Asp	Ser	Leu	Arg	Glu	Ser	Ser	Gln	Ile	Pro	Lys
145					150					155					160
Ser	Tyr	Arg	Glu	Lys	Leu	Gln	Arg	Lys	Glu	Thr	Phe	Ile	Asn	Ala	Ile
				165					170					175	
Phe	Tyr	Gly	Ala	Gly	Ala	Asp	Phe	Leu	Tyr	Lys	Arg	Ala	Phe	Gly	Thr
			180					185					190		
Leu	Ile	Leu	Gly	Met	Asn	Phe	Val	Gly	Glu	Thr	Trp	Phe	Tyr	Glu	Thr
		195					200					205			
Lys	Ile	Phe	Lys	Lys	Trp	Ala	Lys	Asp	Pro	Leu	Ser	Val	Tyr	His	Pro
	210					215					220				
Tyr	Met	Phe	Gln	Val	Met	Leu	Asn	Val	Gly	Tyr	Arg	Tyr	Arg	Phe	Ser
225					230					235					240
Arg	Tyr	Lys	Asn	Trp	Ala	Ile	Glu	Leu	Gly	Ala	Arg	Ile	Pro	Phe	Leu
				245					250					255	
Thr	Asn	Asp	Tyr	Phe	Lys	Thr	Pro	Leu	Tyr	Thr	Leu	His	Phe	Lys	Arg
			260					265					270		
Asn	Ile	Ser	Val	Tyr	Leu	Thr	Ser	Thr	Tyr	Asp	Phe				
		275						280							

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 75...1106
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

TAATCGTTAT TAAACATGCT ATATTTCTTT TTTCTATAAA ACTCAATATT ATTGAATAAA	60
ACTAGGGAGT TAGA ATG ATC TTA AAA CGA GTT ACT GAA GCT TTA GAA GCG	110
Met Ile Leu Lys Arg Val Thr Glu Ala Leu Glu Ala	
1 5 10	
TAT AAA AAT GGC GAA ATG CTC ATT GTT ATG GAC GAT GAA GAC AGA GAA	158
Tyr Lys Asn Gly Glu Met Leu Ile Val Met Asp Asp Glu Asp Arg Glu	
15 20 25	
AAT GAG GGG GAT TTG GTT TTA GCT GGG ATT TTT TCT ACC CCT GAG AAA	206

TTT TAT GGC GCG GGA GCT GAC TTT TTA TAC AAA CGC GCT TTT GGA ACG	576
Phe Tyr Gly Ala Gly Ala Asp Phe Leu Tyr Lys Arg Ala Phe Gly Thr	
180 185 190	
CTG ATT TTA GGG ATG AAT TTC GTG GGA GAA ACC TGG TTT TAT GAA ACA	624
Leu Ile Leu Gly Met Asn Phe Val Gly Glu Thr Trp Phe Tyr Glu Thr	
195 200 205	
AAG ATT TTT AAA AAG TGG GCT AAA GAT CCT TTG AGC GTT TAT CAC CCT	672
Lys Ile Phe Lys Lys Trp Ala Lys Asp Pro Leu Ser Val Tyr His Pro	
210 215 220	
TAC ATG TTT CAA GTG ATG TTG AAT GTG GGG TAT CGT TAC CGC TTT TCA	720
Tyr Met Phe Gln Val Met Leu Asn Val Gly Tyr Arg Tyr Arg Phe Ser	
225 230 235 240	
AGG TAT AAG AAT TGG GCG ATA GAA TTG GGT GCG CGC ATC CCT TTT TTA	768
Arg Tyr Lys Asn Trp Ala Ile Glu Leu Gly Ala Arg Ile Pro Phe Leu	
245 250 255	
ACC AAT GAT TAT TTT AAA ACC CCT TTA TAC ACC CTT CAT TTC AAG CGC	816
Thr Asn Asp Tyr Phe Lys Thr Pro Leu Tyr Thr Leu His Phe Lys Arg	
260 265 270	
AAT ATT TCT GTC TAT CTC ACT TCA ACT TAT GAC TTT TAGTTTTTTTA AATTTT	868
Asn Ile Ser Val Tyr Leu Thr Ser Thr Tyr Asp Phe	
275 280	
TGAAAACCTAG AATTAAAACC GCTTTTTATA AACTGG	904

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Arg Ile Lys Lys Glu Arg Leu Asn Lys Leu Leu Lys Arg Gly Phe Leu	
1 5 10 15	
Ala Phe Phe Leu Ser Val Tyr Leu Arg Ala Asp Asp Leu Val Thr Tyr	
20 25 30	
Thr Ile Ile Lys Glu Lys Asp Leu Gly Tyr Gln Arg Phe Leu Ala Lys	
35 40 45	
Lys Cys Leu Arg Gly Lys Thr His Pro Pro Cys Phe Thr Lys Pro Lys	
50 55 60	
Lys Pro Lys Arg Lys Leu Phe Asn Ile Asp Lys Ser Ser His Tyr Tyr	
65 70 75 80	
Gly Thr Ser Val Val Gln Met Ser Trp Leu Gln Ser Arg Glu Lys Phe	
85 90 95	

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...852
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

CGC ATA AAA AAA GAA CGC TTG AAC AAA CTG CTT AAA AGG GGG TTT TTA	48
Arg Ile Lys Lys Glu Arg Leu Asn Lys Leu Leu Lys Arg Gly Phe Leu	
1 5 10 15	
CGC TTC TTT TTG AGC GTG TAT TTA AGG GCT GAT GAT TTG GTT ACT TAC	96
Ala Phe Phe Leu Ser Val Tyr Leu Arg Ala Asp Asp Leu Val Thr Tyr	
20 25 30	
ACC ATC ATC AAA GAA AAA GAT CTA GGA TAC CAG CGG TTT TTA GCC AAG	144
Thr Ile Ile Lys Glu Lys Asp Leu Gly Tyr Gln Arg Phe Leu Ala Lys	
35 40 45	
AAG TGT TTA AGG GGT AAA ACC CAC CCT CCG TGT TTT ACT AAG CCT AAA	192
Lys Cys Leu Arg Gly Lys Thr His Pro Pro Cys Phe Thr Lys Pro Lys	
50 55 60	
AAG CCT AAA AGA AAA CTT TTT AAT ATA GAC AAA AGC TCC CAC TAT TAT	240
Lys Pro Lys Arg Lys Leu Phe Asn Ile Asp Lys Ser Ser His Tyr Tyr	
65 70 75 80	
GGC ACA AGC GTG GTG CAA ATG TCA TGG CTA CAG AGT AGG GAA AAA TTT	288
Gly Thr Ser Val Val Gln Met Ser Trp Leu Gln Ser Arg Glu Lys Phe	
85 90 95	
GAA AAC CAT TCA AAA TAC CGA GAC ATT CCT TTT GCT GAA GTC AGT TTG	336
Glu Asn His Ser Lys Tyr Arg Asp Ile Pro Phe Ala Glu Val Ser Leu	
100 105 110	
ATT TAT GGC TAT AAA CAA TTT TTT CCT AAA AAA GAG CGC TAC GGC TTC	384
Ile Tyr Gly Tyr Lys Gln Phe Phe Pro Lys Lys Glu Arg Tyr Gly Phe	
115 120 125	
CGT TTT TAT GTC TCT TTG GAT TAC GCT TAT GGG TTT TTT CTT AAA AAT	432
Arg Phe Tyr Val Ser Leu Asp Tyr Ala Tyr Gly Phe Phe Leu Lys Asn	
130 135 140	
AAG GGC GTG TTG GGC GAT AGT TTG AGG GAG AGT TCG CAA ATC CCT AAA	480
Lys Gly Val Leu Gly Asp Ser Leu Arg Glu Ser Ser Gln Ile Pro Lys	
145 150 155 160	
AGC TAT AGA GAA AAA TTG CAA AGA AAA GAG ACT TTT ATT AAC GCT ATT	528
Ser Tyr Arg Glu Lys Leu Gln Arg Lys Glu Thr Phe Ile Asn Ala Ile	
165 170 175	

AAA GTG TTA CAG AAA AAC GTG AAG TGATTGCATG GCGTTATTAG AGATTATCCA 693
 Lys Val Leu Gln Lys Asn Val Lys
 190 195

TTACCCTTCT AAAATCTTAA GAACGATTTC TAAAGAGGTC GTT 736

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Met	Met	Gly	Tyr	Ile	Pro	Tyr	Val	Ile	Glu	Asn	Thr	Asp	Arg	Gly	Glu	1	5	10	15
Arg	Ser	Tyr	Asp	Ile	Tyr	Ser	Arg	Leu	Leu	Lys	Asp	Arg	Ile	Val	Leu	20	25	30	
Leu	Ser	Gly	Glu	Ile	Asn	Asp	Ser	Val	Ala	Ser	Ser	Ile	Val	Ala	Gln	35	40	45	
Leu	Leu	Phe	Leu	Glu	Ala	Glu	Asp	Pro	Glu	Lys	Asp	Ile	Gly	Leu	Tyr	50	55	60	
Ile	Asn	Ser	Pro	Gly	Gly	Val	Ile	Thr	Ser	Gly	Leu	Ser	Ile	Tyr	Asp	65	70	75	80
Thr	Met	Asn	Phe	Ile	Arg	Pro	Asp	Val	Ser	Thr	Ile	Cys	Ile	Gly	Gln	85	90	95	
Ala	Ala	Ser	Met	Gly	Ala	Phe	Leu	Leu	Ser	Cys	Gly	Ala	Lys	Gly	Lys	100	105	110	
Arg	Phe	Ser	Leu	Pro	His	Ser	Arg	Ile	Met	Ile	His	Gln	Pro	Leu	Gly	115	120	125	
Gly	Ala	Gln	Gly	Gln	Ala	Ser	Asp	Ile	Glu	Ile	Ile	Ser	Asn	Glu	Ile	130	135	140	
Leu	Arg	Leu	Lys	Gly	Leu	Met	Asn	Ser	Ile	Leu	Ala	Gln	Asn	Ser	Gly	145	150	155	160
Gln	Ser	Leu	Glu	Gln	Ile	Ala	Lys	Asp	Thr	Asp	Arg	Asp	Phe	Tyr	Met	165	170	175	
Ser	Ala	Lys	Glu	Ala	Lys	Glu	Tyr	Gly	Leu	Ile	Asp	Lys	Val	Leu	Gln	180	185	190	
Lys	Asn	Val	Lys													195			

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

```

GCAACAAGAA ATTTTAGAGA AAATGAGACC CAACGCTCAA AAAATTCAAG CGGGTTAAAC      60
GGCTAAAAAG GAGAG ATG ATG GGA TAC ATT CCT TAT GTA ATA GAG AAT ACC      111
      Met Met Gly Tyr Ile Pro Tyr Val Ile Glu Asn Thr
            1                5                10

GAT CGT GGG GAG CGT AGC TAT GAT ATT TAC TCG CGC CTT TTA AAG GAT      159
Asp Arg Gly Glu Arg Ser Tyr Asp Ile Tyr Ser Arg Leu Leu Lys Asp
      15                20                25

CGC ATT GTT TTA TTG AGC GGT GAA ATT AAT GAC AGC GTG GCG TCT TCT      207
Arg Ile Val Leu Leu Ser Gly Glu Ile Asn Asp Ser Val Ala Ser Ser
      30                35                40

ATC GTG GCC CAA CTC TTG TTT TTG GAA GCT GAA GAC CCT GAA AAA GAC      255
Ile Val Ala Gln Leu Leu Phe Leu Glu Ala Glu Asp Pro Glu Lys Asp
      45                50                55                60

ATT GGT TTG TAT ATC AAT TCT CCC GGT GGG GTG ATA ACA AGC GGT CTT      303
Ile Gly Leu Tyr Ile Asn Ser Pro Gly Gly Val Ile Thr Ser Gly Leu
      65                70                75

AGT ATT TAT GAC ACC ATG AAT TTT ATC CGC CCT GAT GTT TCC ACG ATT      351
Ser Ile Tyr Asp Thr Met Asn Phe Ile Arg Pro Asp Val Ser Thr Ile
      80                85                90

TGC ATC GGT CAA GCG GCT TCT ATG GGG GCG TTT TTA CTG AGC TGT GGG      399
Cys Ile Gly Gln Ala Ala Ser Met Gly Ala Phe Leu Leu Ser Cys Gly
      95                100                105

GCT AAG GGC AAG CGC TTT TCG CTA CCC CAT TCA AGG ATT ATG ATC CAC      447
Ala Lys Gly Lys Arg Phe Ser Leu Pro His Ser Arg Ile Met Ile His
      110                115                120

CAG CCT TTA GGG GGG GCT CAA GGG CAA GCG AGC GAT ATT GAA ATC ATT      495
Gln Pro Leu Gly Gly Ala Gln Gly Gln Ala Ser Asp Ile Glu Ile Ile
      125                130                135                140

TCT AAT GAG ATT CTC AGG CTT AAA GGC TTG ATG AAT TCT ATT CTA GCT      543
Ser Asn Glu Ile Leu Arg Leu Lys Gly Leu Met Asn Ser Ile Leu Ala
      145                150                155

CAA AAC TCA GGG CAG AGT TTG GAG CAA ATC GCT AAA GAC ACG GAC AGG      591
Gln Asn Ser Gly Gln Ser Leu Glu Gln Ile Ala Lys Asp Thr Asp Arg
      160                165                170

GAT TTT TAT ATG AGT GCT AAA GAA GCT AAA GAG TAT GGC TTG ATT GAT      639
Asp Phe Tyr Met Ser Ala Lys Glu Ala Lys Glu Tyr Gly Leu Ile Asp
      175                180                185

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

```

Met Leu Pro Phe Asp Val Phe Ile Lys Ser Tyr Pro Thr Pro Cys Tyr
 1             5             10             15
Phe Lys Gln Phe Leu Arg Leu Lys Lys Thr Tyr Pro Ser Lys Leu Asn
      20             25             30
Glu Ser Phe Leu Phe Arg Arg Ile Asp Ala Gly Phe Ile Ser Ser Ile
      35             40             45
Ala Gly Tyr Pro Phe Ala Leu His Ser His Ser Leu Gly Ile Val Ala
      50             55             60
Tyr Lys Glu Val Leu Ser Val Leu Val Val Asp Thr Lys Asn Ala Phe
65             70             75             80
Asp Lys Glu Ser Ala Ser Ser Asn Ala Leu Ser Gln Ala Leu Gly Leu
      85             90             95
Lys Gly Glu Val Leu Ile Gly Asn Lys Ala Leu Gln Phe Tyr Tyr Ser
      100            105            110
Asn Pro Lys Lys Asp Phe Ile Asp Leu Ala Ala Leu Trp Tyr Glu Lys
      115            120            125
Lys Arg Leu Pro Phe Val Phe Gly Arg Leu Cys Tyr Tyr Gln Asn Lys
      130            135            140
Asp Phe Tyr Lys Arg Leu Ser Leu Ala Phe Lys His Gln Lys Thr Lys
145            150            155            160
Ile Pro Tyr Tyr Ile Leu Lys Glu Ala Ala Leu Lys Thr Asn Leu Lys
      165            170            175
Arg Gln Asp Ile Leu Asn Tyr Leu Gln Lys Ile Tyr Tyr Thr Leu Gly
      180            185            190
Lys Lys Glu Gln Leu Gly Leu Lys Ala Phe Tyr Arg Glu Leu Leu Phe
      195            200            205
Lys Arg Ile Gln Lys Pro Lys Arg Phe
      210            215

```

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 76...663

10	15	20	
AAA AAA ACC TAC CCC TCC AAA CTC AAT GAG AGT TTT TTA TTC AGG CGT			211
Lys Lys Thr Tyr Pro Ser Lys Leu Asn Glu Ser Phe Leu Phe Arg Arg			
25	30	35	
ATT GAT GCG GGG TTT ATT TCT TCT ATC GCC GGC TAT CCA TTC GCT CTT			259
Ile Asp Ala Gly Phe Ile Ser Ser Ile Ala Gly Tyr Pro Phe Ala Leu			
40	45	50	55
CAT TCC CAT TCT CTA GGC ATT GTC GCT TAT AAG GAA GTT TTA AGC GTG			307
His Ser His Ser Leu Gly Ile Val Ala Tyr Lys Glu Val Leu Ser Val			
60	65	70	
CTG GTT GTG GAT ACA AAA AAC GCT TTT GAT AAA GAA AGC GCT TCT TCA			355
Leu Val Val Asp Thr Lys Asn Ala Phe Asp Lys Glu Ser Ala Ser Ser			
75	80	85	
AAC GCC CTC TCT CAA GCG CTA GGG TTA AAG GGC GAA GTG TTA ATC GGC			403
Asn Ala Leu Ser Gln Ala Leu Gly Leu Lys Gly Glu Val Leu Ile Gly			
90	95	100	
AAT AAA GCA CTG CAG TTT TAT TAT TCC AAC CCT AAA AAA GAT TTT ATA			451
Asn Lys Ala Leu Gln Phe Tyr Tyr Ser Asn Pro Lys Lys Asp Phe Ile			
105	110	115	
GAT TTA GCC GCT CTT TGG TAT GAA AAA AAA CGC TTG CCG TTT GTT TTT			499
Asp Leu Ala Ala Leu Trp Tyr Glu Lys Lys Arg Leu Pro Phe Val Phe			
120	125	130	135
GGG CGT TTG TGT TAT TAC CAA AAC AAG GAT TTT TAC AAG CGC TTG TCT			547
Gly Arg Leu Cys Tyr Tyr Gln Asn Lys Asp Phe Tyr Lys Arg Leu Ser			
140	145	150	
TTA GCT TTC AAA CAT CAA AAA ACA AAA ATC CCT TAC TAC ATC CTT AAA			595
Leu Ala Phe Lys His Gln Lys Thr Lys Ile Pro Tyr Tyr Ile Leu Lys			
155	160	165	
GAA GCC GCT TTA AAA ACC AAC TTA AAA CGC CAA GAT ATT TTA AAT TAC			643
Glu Ala Ala Leu Lys Thr Asn Leu Lys Arg Gln Asp Ile Leu Asn Tyr			
170	175	180	
TTG CAA AAA ATT TAC TAC ACT TTA GGC AAA AAG GAG CAA TTA GGT CTT			691
Leu Gln Lys Ile Tyr Tyr Thr Leu Gly Lys Lys Glu Gln Leu Gly Leu			
185	190	195	
AAA GCG TTC TAT CGT GAA TTG TTA TTC AAA CGC ATT CAA AAA CCC AAG			739
Lys Ala Phe Tyr Arg Glu Leu Leu Phe Lys Arg Ile Gln Lys Pro Lys			
200	205	210	215
CGT TTT TAGTGATTCTG CTGAGAATGT AGGCTTAAAA TTCAGAAAGG GTGTTTTTAA GC			797
Arg Phe			
AAGATTAGGT TACAATCACA AGTTTTATTA			827

(2) INFORMATION FOR SEO ID NO:419:

(A) LENGTH: 827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 95...745
(D) OTHER INFORMATION:

CTTTTACTT	TTAGTTAAGT	TGTAAGAAAC	TTTAGCTACC	ATGCGATACA	AAAAAGGATT	60
TTAAGTGC	GT	TTTGGTAAAA	TTGATTATTT	GAAC	ATG CTC CCT TTT GAT GTG TTT	115
				Met	Leu Pro Phe Asp Val Phe	
				1	5	
ATC AAA	TCC	TAC	CCC	ACC	CCT TGT TAT TTC AAA CAA TTC TTA CGG CTT	163
Ile	Lys	Ser	Tyr	Pro	Thr Pro Cys Tyr Phe Lys Gln Phe Leu Arg Leu	

Leu	Ala	Thr	Leu	Leu	Trp	Arg	Phe	Leu	Gly	Ala	Ser	Met	Lys	Gln	Ser		
				120					125					130			
TTC	TTG	CCC	TCT	ATG	AAT	ATT	TGC	ATC	GTG	TGG	GTT	TTT	GCT	TCT	TCT		489
Phe	Leu	Pro	Ser	Met	Asn	Ile	Cys	Ile	Val	Trp	Val	Phe	Ala	Ser	Ser		
			135				140					145					
TTA	CAG	AGT	TTT	AGG	TTT	TTA	AGC	GTG	TCT	GAT	TGC	GTG	GAT	TTT	TCC		537
Leu	Gln	Ser	Phe	Arg	Phe	Leu	Ser	Val	Ser	Asp	Cys	Val	Asp	Phe	Ser		
		150					155					160					
CTT	TTT	ACA	CTC	GCG	CTT	ATT	TTA	TTG	ATA	CTG	GTT	TTA	ATC	TAT	TGC		585
Leu	Phe	Thr	Leu	Ala	Leu	Ile	Leu	Leu	Ile	Leu	Val	Leu	Ile	Tyr	Cys		
	165					170				175							
AAA	CGC	CTT	TTT	GGG	TTG	TAT	GAA	TAC	GCT	AAC	ACG	CTC	ATT	TTG	ATC		633
Lys	Arg	Leu	Phe	Gly	Leu	Tyr	Glu	Tyr	Ala	Asn	Thr	Leu	Ile	Leu	Ile		
180				185				190					195				
GTG	GGG	CTT	AGC	GTG	GTG	GTG	CTA	TGC	TCT	AGC	ATG	TTC	ATT	CAA	ACT		681
Val	Gly	Leu	Ser	Val	Val	Val	Leu	Cys	Ser	Ser	Met	Phe	Ile	Gln	Thr		
			200					205					210				
AAA	GAA	TAC	TAT	GGC	ATG	CGA	TTG	GGT	TTT	TAT	TTT	TTA	GGC	CTG	TTA		729
Lys	Glu	Tyr	Tyr	Gly	Met	Arg	Leu	Gly	Phe	Tyr	Phe	Leu	Gly	Leu	Leu		
		215					220					225					
GGG	TGG	CTT	TTA	GAA	TAT	GTG	CAT	AAC	ACT	TTA	AGG	CGT	TTG	GAA	CAT		777
Gly	Trp	Leu	Leu	Glu	Tyr	Val	His	Asn	Thr	Leu	Arg	Arg	Leu	Glu	His		
	230					235					240						
CAA	ATT	TAAAGCTCAA	ATAGGAATAG	CTAAAGCCTT	TTGATTGAGT	GTTTTTTTAG	GG										835
Gln	Ile																
	245																
CTTAAAAGCG	GGTTTA																851

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met	Asn	Phe	Tyr	Gln	Lys	Ile	Tyr	Thr	His	Lys	Val	Val	Phe	Ser	Ser		
1				5				10					15				
Leu	Phe	Phe	Leu	Leu	Phe	Leu	Phe	Asn	Val	Glu	Thr	Leu	Leu	Leu	Ser		
			20				25					30					
His	Phe	Ser	Asp	Asp	Phe	Ser	Gln	Leu	Phe	Phe	Leu	Phe	Glu	Asn	His		

180

185

190

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...783
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

ATTGATAGTT TCTTCAGCAA GAATGATTAG GCAATGATTA GGTGTAG ATG AAT TTT      57
                                     Met Asn Phe
                                     1

TAT CAA AAA ATA TAC ACT CAT AAA GTC GTT TTT TCT TCA TTG TTT TTT      105
Tyr Gln Lys Ile Tyr Thr His Lys Val Val Phe Ser Ser Leu Phe Phe
    5              10              15

TTG TTG TTT TTG TTC AAT GTG GAA ACT TTG TTG CTT TCG CAT TTC AGC      153
Leu Leu Phe Leu Phe Asn Val Glu Thr Leu Leu Leu Ser His Phe Ser
20              25              30              35

GAT GAT TTT TCG CAA TTG TTT TTT TTG TTT GAA AAC CAT GTT TAT GAT      201
Asp Asp Phe Ser Gln Leu Phe Phe Leu Phe Glu Asn His Val Tyr Asp
              40              45              50

TTC ATT GTC AAA TTA GAT TAT TTG GGG CTA ATA GGC GTT TCT TTA ATT      249
Phe Ile Val Lys Leu Asp Tyr Leu Gly Leu Ile Gly Val Ser Leu Ile
    55              60              65

TAT CTG CTT GTG CTT ATT CTA AAG CCT TTC ACC CTC ACG CGC CAA AAA      297
Tyr Leu Leu Val Leu Ile Leu Lys Pro Phe Thr Leu Thr Arg Gln Lys
    70              75              80

TGC GCT TGC GTA GGG ATA TTA TGC CTT TCT TTC TAC GCT TGG AAT TTT      345
Cys Ala Cys Val Gly Ile Leu Cys Leu Ser Phe Tyr Ala Trp Asn Phe
    85              90              95

CCT GTT AAA GAT TCT TTA ATG GTG CTT TAT CTT TTC TAT TTT GCG CTG      393
Pro Val Lys Asp Ser Leu Met Val Leu Tyr Leu Phe Tyr Phe Ala Leu
100              105              110              115

TTA GCG ACT TTA TTG TGG CGT TTT TTA GGG GCT AGC ATG AAG CAA TCT      441

```

TTA GAA AAT TTA GGC TCA ATG ACT TTA GGG GCA AAG AGC CAG CCA AAT 540
 Leu Glu Asn Leu Gly Ser Met Thr Leu Gly Ala Lys Ser Gln Pro Asn
 145 150 155 160

TGC AAG ACA TTA GAT AAA AAC GCC ACC ACC ACT AAA ATG ATT AAA ATC 588
 Cys Lys Thr Leu Asp Lys Asn Ala Thr Thr Thr Lys Met Ile Lys Ile
 165 170 175

GGT AAA AGC AAT AAA AAA GTG TCT TTA GCC AGT TGG TTA AAC AGC TCT T 637
 Gly Lys Ser Asn Lys Lys Val Ser Leu Ala Ser Trp Leu Asn Ser Ser
 180 185 190

GAACGCTTTC TTTACTGAAA TCTAGGGAAA AATCTTTCAA CACATGGCGA TACATTTTCGC 697
 TAAAGCCATC CACCCACCAT ATAAAAAATA CAAAAATACT AATTAGCCCG GCCAATAACC 757
 CCAAAACCCC CACCACTTCC ATGCTCTTAG GCACATTGCC TTCTTCTCTG GCTTTTTGGA 817
 TTTTTTTTCGC GCTAGGGAGT TCGGTTTTTTT CTTCTTCAGC CATTGGCCCT CTTTTTTAAA 877
 ATTTGAACGG CTAATTCATA GTCTTTTAGG GTGTTTAGGT TTAAAAATTC TTCTTCTTTG 937
 TCAAATT 945

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Val Gly Leu Val Thr Thr Thr Leu Ala Leu Gly Ile Ser Cys Ile Ile
 1 5 10 15
 Leu Phe Val Ala Phe Phe Ser Ile Ile Trp Arg Ile Leu Ala Leu Ile
 20 25 30
 Ser Gly Phe Pro Ser Cys Cys Leu Tyr Ser Ser Leu Thr Ser Cys Leu
 35 40 45
 Val Ile Phe Lys Glu Leu Val Tyr Trp Arg Arg Leu Ile Ala Lys Ser
 50 55 60
 Ile Lys Ala Lys Thr Lys Asn Lys Asn Lys Ser Glu Glu Met Ser His
 65 70 75 80
 Asn Ala Leu Phe Leu Asn His Asn Asn Trp Pro Cys Lys Phe Lys Arg
 85 90 95
 Ala Ala Trp Phe Asn Ser Pro Lys Asn Lys Glu Lys Met Lys Asn Pro
 100 105 110
 Arg Lys Lys Ala Lys Lys Thr Phe Lys Val Ile Lys Leu Pro Ser Arg
 115 120 125
 Ser Phe Phe Lys Glu Lys Arg Phe Leu Thr Pro Leu Ile Gly Leu Ile
 130 135 140
 Leu Glu Asn Leu Gly Ser Met Thr Leu Gly Ala Lys Ser Gln Pro Asn
 145 150 155 160
 Cys Lys Thr Leu Asp Lys Asn Ala Thr Thr Thr Lys Met Ile Lys Ile
 165 170 175
 Gly Lys Ser Asn Lys Lys Val Ser Leu Ala Ser Trp Leu Asn Ser Ser

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 61...636
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

TTAGCCACTA CCACAGGCAC AGGGTGTCTC TCATCAAATT TGAGAGCGAC GCGTAATGG      60
GTG GGG TTA GTA ACC ACG ACA TTG GCT TTA GGG ATT TCT TGC ATC ATT      108
Val Gly Leu Val Thr Thr Thr Leu Ala Leu Gly Ile Ser Cys Ile Ile
  1              5              10              15

TTA TTC GTG GCG TTT TTT AGC ATC ATT TGG CGG ATT TTG GCT TTG ATT      156
Leu Phe Val Ala Phe Phe Ser Ile Ile Trp Arg Ile Leu Ala Leu Ile
          20              25              30

TCT GGG TTC CCT TCT TGC TGT TTG TAT TCG TCC TTA ACT TCT TGT TTA      204
Ser Gly Phe Pro Ser Cys Cys Leu Tyr Ser Ser Leu Thr Ser Cys Leu
          35              40              45

GTC ATT TTT AAA GAG TTG GTG TAT TGG CGG CGT TTG ATC GCT AAA TCT      252
Val Ile Phe Lys Glu Leu Val Tyr Trp Arg Arg Leu Ile Ala Lys Ser
          50              55              60

ATA AAA GCC AAG ACA AAA AAT AAA AAT AAA AGC GAA GAA ATG AGC CAT      300
Ile Lys Ala Lys Thr Lys Asn Lys Asn Lys Ser Glu Glu Met Ser His
          65              70              75              80

AAC GCC TTA TTT TTA AAC CAC AAC AAC TGG CCT TGT AAA TTC AAA AGA      348
Asn Ala Leu Phe Leu Asn His Asn Asn Trp Pro Cys Lys Phe Lys Arg
          85              90              95

GCC GCA TGG TTT AAT TCC CCT AAA AAC AAA GAA AAG ATG AAA AAC CCC      396
Ala Ala Trp Phe Asn Ser Pro Lys Asn Lys Glu Lys Met Lys Asn Pro
          100              105              110

AGA AAA AAA GCT AAA AAA ACT TTT AAG GTG ATC AAA CTC CCA TCA AGG      444
Arg Lys Lys Ala Lys Lys Thr Phe Lys Val Ile Lys Leu Pro Ser Arg
          115              120              125

AGC TTT TTT AAA GAA AAA AGG TTT TTG ACG CCA TTG ATA GGG TTG ATT      492
Ser Phe Phe Lys Glu Lys Arg Phe Leu Thr Pro Leu Ile Gly Leu Ile
          130              135              140

```

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

Met Leu Glu Asn Ser Ser Ile Trp Ser Asn Pro Ala Phe Val Ala Ile
 1              5              10              15
Ile Cys Met Cys Val Leu Ser Leu Leu Arg Leu Asn Val Met Leu Ser
      20              25              30
Met Ile Ser Ala Thr Leu Ile Ala Gly Leu Met Gly Gly Leu Gly Ile
      35              40              45
Thr Glu Ser Phe Asn Ala Met Ile Asp Gly Met Lys Gly Asn Leu Asn
      50              55              60
Ile Ala Leu Ser Tyr Ile Leu Leu Gly Ala Leu Ala Val Ala Ile Ala
      65              70              75              80
Lys Ser Asn Leu Ile Lys Val Ala Leu Ser Lys Leu Ile Gly Leu Met
      85              90              95
Asp Tyr Lys Arg Ser Thr Phe Cys Phe Leu Ile Ala Phe Ile Ala Cys
      100             105             110
Phe Ser Gln Asn Leu Val Pro Val His Ile Ala Phe Ile Pro Ile Leu
      115             120             125
Ile Pro Pro Leu Leu His Leu Met Asn Arg Leu Glu Leu Asp Arg Arg
      130             135             140
Ala Val Ala Cys Ala Leu Thr Phe Gly Leu Gln Ala Pro Tyr Leu Val
      145             150             155             160
Leu Pro Val Gly Phe Gly Leu Ile Phe Gln Thr Thr Ile Leu Glu Gln
      165             170             175
Leu Lys Ala Asn Gly Val Ser Thr Thr Ile Ala Gln Ile Thr Gly Val
      180             185             190
Met Trp Ile Ala Gly Leu Ala Met Val Val Gly Leu Leu Val Ala Val
      195             200             205
Leu Thr Leu Tyr Lys Lys Pro Arg His Tyr Lys Glu Lys Ser Phe Asn
      210             215             220
Ile Glu Asn Tyr Ala Ser Leu Gln Leu Asn Tyr His Asp Tyr Leu Thr
      225             230             235             240
Phe Ile Gly Ile Val Val Ala Phe Val Ile Gln Leu Ala Thr Asp Ser
      245             250             255
Met Pro Leu Ala Ala Phe Leu Ala Leu Ala Ile Ile Leu Leu Gly Arg
      260             265             270
Gly Ile Lys Phe Lys Glu Thr Asp Ser Leu Met Asp Asp Ser Val Lys
      275             280             285
Met Met Ala Phe Ile Ala Phe Val Met Leu Val Ala Ser Gly Phe Gly
      290             295             300
Glu Val Leu Gln Lys Val His Ala Ile Glu Gly Leu Val Asn Ala Ile
      305             310             315             320
Thr Ser Val Val Gln Gly Lys Leu Leu Gly Ala Phe Leu Met Leu Val
      325             330             335
Val Gly Leu Phe Ile Thr Met Gly Ile Gly Thr Ser Phe Gly Thr Ile
      340             345             350
Pro Ile Ile Ala Val Phe Tyr Val Pro Leu Cys Ala Lys Leu Gly Phe
      355             360             365
Ser Val Glu Ser Thr Ile Leu Leu Ile Ala
      370             375

```

(2) INFORMATION FOR SEQ ID NO:415:

CTA TAC AAA AAA CCC AGG CAC TAC AAA GAG AAA TCT TTT AAT ATA GAA	728
Leu Tyr Lys Lys Pro Arg His Tyr Lys Glu Lys Ser Phe Asn Ile Glu	
215 220 225	
AAT TAC GCC TCG CTT CAA TTA AAC TAC CAT GAC TAC TTG ACT TTT ATA	776
Asn Tyr Ala Ser Leu Gln Leu Asn Tyr His Asp Tyr Leu Thr Phe Ile	
230 235 240	
GGG ATT GTC GTA GCG TTT GTG ATC CAA TTA GCC ACC GAT TCG ATG CCC	824
Gly Ile Val Val Ala Phe Val Ile Gln Leu Ala Thr Asp Ser Met Pro	
245 250 255	
TTA GCC GCC TTT TTA GCG TTA GCG ATC ATC TTA TTA GGC CGT GGC ATT	872
Leu Ala Ala Phe Leu Ala Leu Ala Ile Ile Leu Leu Gly Arg Gly Ile	
260 265 270	
AAG TTT AAA GAA ACA GAC TCG CTT ATG GAT GAT AGC GTG AAA ATG ATG	920
Lys Phe Lys Glu Thr Asp Ser Leu Met Asp Asp Ser Val Lys Met Met	
275 280 285 290	
GCG TTT ATC GCT TTT GTG ATG TTG GTG GCT AGC GGG TTT GGA GAA GTG	968
Ala Phe Ile Ala Phe Val Met Leu Val Ala Ser Gly Phe Gly Glu Val	
295 300 305	
TTG CAA AAA GTG CAT GCG ATA GAG GGC TTA GTG AAT GCG ATT ACA AGC	1016
Leu Gln Lys Val His Ala Ile Glu Gly Leu Val Asn Ala Ile Thr Ser	
310 315 320	
GTA GTC CAA GGG AAG CTT TTA GGG GCT TTT TTA ATG CTT GTT GTA GGG	1064
Val Val Gln Gly Lys Leu Leu Gly Ala Phe Leu Met Leu Val Val Gly	
325 330 335	
CTT TTT ATC ACT ATG GGG ATA GGG ACT TCT TTT GGC ACT ATT CCT ATC	1112
Leu Phe Ile Thr Met Gly Ile Gly Thr Ser Phe Gly Thr Ile Pro Ile	
340 345 350	
ATC GCT GTG TTT TAT GTC CCT TTA TGC GCG AAA TTA GGT TTT AGC GTA	1160
Ile Ala Val Phe Tyr Val Pro Leu Cys Ala Lys Leu Gly Phe Ser Val	
355 360 365 370	
GAA TCT ACG ATT TTA CTC ATC GCA TAGCCGCAGC TTTAGGCGAT GCAGGCTCAC	1214
Glu Ser Thr Ile Leu Ile Ala	
375	
CGGCTAGCGA TAGCACCATG GGG	1237

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

AAAAATTCTA TCATTTTTCG GCGGTATTTT CATTTTAAACA AGGAGCAAAA	ATG CTA	56
	Met Leu	
	1	
GAA AAT AGC TCT ATA TGG AGC AAT CCT GCC TTT GTG GCT ATC ATT TGC		104
Glu Asn Ser Ser Ile Trp Ser Asn Pro Ala Phe Val Ala Ile Ile Cys		
5 10 15		
ATG TGC GTT CTT AGC CTT TTA AGG CTC AAT GTC ATG CTT TCT ATG ATT		152
Met Cys Val Leu Ser Leu Leu Arg Leu Asn Val Met Leu Ser Met Ile		
20 25 30		
AGT GCG ACT CTC ATA GCA GGA CTT ATG GGA GGG CTT GGG ATC ACG GAG		200
Ser Ala Thr Leu Ile Ala Gly Leu Met Gly Gly Leu Gly Ile Thr Glu		
35 40 45 50		
AGT TTT AAT GCA ATG ATA GAC GGC ATG AAA GGC AAT TTG AAC ATC GCT		248
Ser Phe Asn Ala Met Ile Asp Gly Met Lys Gly Asn Leu Asn Ile Ala		
55 60 65		
TTA AGC TAC ATC CTT TTA GGG GCT TTA GCG GTA GCG ATC GCT AAA AGC		296
Leu Ser Tyr Ile Leu Leu Gly Ala Leu Ala Val Ala Ile Ala Lys Ser		
70 75 80		
AAT CTC ATT AAA GTC GCT TTG AGT AAA TTA ATA GGT TTA ATG GAT TAC		344
Asn Leu Ile Lys Val Ala Leu Ser Lys Leu Ile Gly Leu Met Asp Tyr		
85 90 95		
AAG CGA TCC ACT TTT TGC TTT TTG ATC GCT TTC ATC GCA TGC TTT TCG		392
Lys Arg Ser Thr Phe Cys Phe Leu Ile Ala Phe Ile Ala Cys Phe Ser		
100 105 110		
CAA AAT TTA GTG CCG GTG CAT ATC GCT TTT ATC CCT ATT TTA ATC CCC		440
Gln Asn Leu Val Pro Val His Ile Ala Phe Ile Pro Ile Leu Ile Pro		
115 120 125 130		
CCT CTT TTG CAT TTA ATG AAC CGG CTA GAA TTG GAT AGA AGA GCG GTC		488
Pro Leu Leu His Leu Met Asn Arg Leu Glu Leu Asp Arg Arg Ala Val		
135 140 145		
GCT TGC GCT TTA ACC TTT GGC TTG CAA GCC CCC TAC TTG GTG CTT CCT		536
Ala Cys Ala Leu Thr Phe Gly Leu Gln Ala Pro Tyr Leu Val Leu Pro		
150 155 160		
GTA GGG TTT GGC TTG ATT TTT CAA ACC ACC ATT TTA GAG CAA TTA AAA		584
Val Gly Phe Gly Leu Ile Phe Gln Thr Thr Ile Leu Glu Gln Leu Lys		
165 170 175		
GCT AAT GGC GTT AGC ACC ACC ATA GCG CAA ATC ACA GGA GTG ATG TGG		632
Ala Asn Gly Val Ser Thr Thr Ile Ala Gln Ile Thr Gly Val Met Trp		
180 185 190		
ATA GCG GGG TTA GCG ATG GTC GTT GGA CTG CTT GTT GCT GTA TTA ACG		680
Ile Ala Gly Leu Ala Met Val Val Gly Leu Leu Val Ala Val Leu Thr		
195 200 205 210		

1				5				10					15				
Met	Val	Trp	Ile	Pro	Thr	Thr	Phe	Leu	Ala	Cys	Met	Leu	Thr	Ala	Phe		
			20					25					30				
Ile	Met	Gly	Phe	Thr	Asp	Leu	Lys	Leu	Asp	Ser	Asp	Pro	His	Tyr	Leu		
		35					40					45					
Glu	Arg	Leu	Lys	Ala	Gly	Lys	Ile	Ser	Pro	Pro	Lys	Ile	Lys	Glu	Glu		
	50					55					60						
Lys	Glu	Thr	Ser	Lys	Asn	Ala	Lys	Leu	Ser	Leu	Trp	Ile	Phe	Ile	Gly		
65					70					75					80		
Gly	Val	Val	Ala	Ile	Val	Phe	Tyr	Ala	Ser	Ala	Ile	Ser	Lys	Asn	Ile		
				85					90					95			
Ala	Phe	Val	Ser	Pro	Val	Val	Leu	Gly	Arg	Asp	His	Ala	Ile	Val	Ser		
			100					105					110				
Phe	Met	Leu	Ser	Val	Ala	Thr	Leu	Ile	Val	Leu	Phe	Cys	Lys	Ile	Asn		
	115						120					125					
Ala	Asn	Glu	Ile	Ala	His	Ser	Ser	Val	Phe	Lys	Ser	Gly	Met	Gln	Ala		
	130					135				140							
Cys	Val	Cys	Val	Leu	Gly	Val	Ala	Trp	Leu	Gly	Asp	Thr	Phe	Val	Ser		
145				150					155					160			
Asn	His	Ile	Asp	Glu	Ile	Lys	Arg	Tyr	Ala	Ser	Phe	Leu	Ile	Ala	Asp		
			165					170					175				
Tyr	Pro	Phe	Leu	Leu	Ala	Val	Ala	Leu	Phe	Leu	Ala	Ser	Met	Leu	Leu		
		180						185					190				
Tyr	Ser	Gln	Ala	Ala	Thr	Ser	Lys	Ala	Leu	Ile	Pro	Ser	Val	Ile	Thr		
	195					200						205					
Ala	Leu	Gly	Ile	Ser	Ala	Asn	His	Thr	Glu	His	Leu	Tyr	Ile	Ile	Val		
	210					215					220						
Ala	Ser	Phe	Ala	Ser	Val	Ser	Ala	Leu	Phe	Val	Leu	Pro	Thr	Tyr	Pro		
225				230					235					240			
Thr	Leu	Leu	Gly	Ala	Ile	Ala	Met	Asp	Asn	Thr	Gly	Thr	Thr	Lys	Met		
			245					250						255			
Gly	Arg	Tyr	Val	Phe	Asp	His	Ala	Phe	Leu	Ile	Pro	Gly	Val	Leu	Val		
		260					265					270					
Val	Ser	Leu	Ser	Val	Ala	Leu	Gly	Phe	Val	Val	Ala	Pro	Leu	Val	Leu		
	275						280					285					

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1184
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Glu Ile Ala His Ser Ser Val Phe Lys Ser Gly Met Gln Ala Cys Val	
135 140 145	
TGC GTG TTG GGC GTG GCG TGG TTG GGC GAT ACT TTT GTG AGC AAT CAT	536
Cys Val Leu Gly Val Ala Trp Leu Gly Asp Thr Phe Val Ser Asn His	
150 155 160	
ATA GAT GAG ATC AAA CGA TAC GCT TCT TTT TTG ATC GCA GAT TAT CCG	584
Ile Asp Glu Ile Lys Arg Tyr Ala Ser Phe Leu Ile Ala Asp Tyr Pro	
165 170 175	
TTT TTA TTA GCC GTA GCG CTC TTT TTG GCT TCC ATG CTT TTG TAT TCG	632
Phe Leu Leu Ala Val Ala Leu Phe Leu Ala Ser Met Leu Leu Tyr Ser	
180 185 190	
CAA GCC GCC ACC TCT AAA GCG CTC ATC CCA AGC GTG ATC ACA GCC TTA	680
Gln Ala Ala Thr Ser Lys Ala Leu Ile Pro Ser Val Ile Thr Ala Leu	
195 200 205 210	
GGC ATT AGC GCT AAT CAT ACG GAG CAT TTG TAT ATT ATC GTG GCT TCG	728
Gly Ile Ser Ala Asn His Thr Glu His Leu Tyr Ile Ile Val Ala Ser	
215 220 225	
TTT GCG AGC GTT TCG GCG TTG TTT GTG TTA CCC ACT TAC CCC ACT TTA	776
Phe Ala Ser Val Ser Ala Leu Phe Val Leu Pro Thr Tyr Pro Thr Leu	
230 235 240	
CTA GGA GCG ATC GCT ATG GAT AAC ACC GGC ACC ACT AAA ATG GGC CGT	824
Leu Gly Ala Ile Ala Met Asp Asn Thr Gly Thr Thr Lys Met Gly Arg	
245 250 255	
TAT GTG TTT GAT CAT GCG TTT TTG ATC CCT GGG GTT TTA GTC GTG TCT	872
Tyr Val Phe Asp His Ala Phe Leu Ile Pro Gly Val Leu Val Val Ser	
260 265 270	
TTG AGC GTA GCG TTA GGG TTT GTT GTC GCG CCG TTA GTT TTG TAGATTTTA	923
Leu Ser Val Ala Leu Gly Phe Val Val Ala Pro Leu Val Leu	
275 280 285	
TCACCAACGA TAAAAAGCTT GGCGTTGCGA TTTTCTCTAAA CCCC	967

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Ser Gly Ile Leu Glu Pro Leu Gly Ala Asn Tyr Leu Thr Leu Leu

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...914
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

TAGTCAAGTC GCTATTACTG CAAGCCCGGT GAGCGCAGCG GTNGGTGTTT	ATG AGC	56
	Met Ser	
	1	
GGC ATT TTA GAG CCT TTA GGA GCA AAT TAC TTG ACC CTT TTA ATG GTT		104
Gly Ile Leu Glu Pro Leu Gly Ala Asn Tyr Leu Thr Leu Leu Met Val		
5 10 15		
TGG ATC CCT ACG ACT TTT TTA GCA TGC ATG CTC ACG GCA TTT ATT ATG		152
Trp Ile Pro Thr Thr Phe Leu Ala Cys Met Leu Thr Ala Phe Ile Met		
20 25 30		
GGT TTT ACT GAT TTG AAA TTA GAC AGC GAT CCG CAT TAT TTA GAG CGC		200
Gly Phe Thr Asp Leu Lys Leu Asp Ser Asp Pro His Tyr Leu Glu Arg		
35 40 45 50		
TTG AAA GCG GGC AAA ATC TCG CCC CCT AAA ATC AAA GAA GAA AAA GAA		248
Leu Lys Ala Gly Lys Ile Ser Pro Pro Lys Ile Lys Glu Glu Lys Glu		
55 60 65		
ACC TCA AAA AAC GCG AAA TTA TCG TTA TGG ATT TTT ATC GGT GGG GTT		296
Thr Ser Lys Asn Ala Lys Leu Ser Leu Trp Ile Phe Ile Gly Gly Val		
70 75 80		
GTA GCG ATC GTT TTT TAT GCG AGC GCG ATT TCT AAA AAT ATC GCT TTT		344
Val Ala Ile Val Phe Tyr Ala Ser Ala Ile Ser Lys Asn Ile Ala Phe		
85 90 95		
GTT AGC CCG GTG GTT TTA GGC AGA GAT CAC GCG ATT GTG TCT TTC ATG		392
Val Ser Pro Val Val Leu Gly Arg Asp His Ala Ile Val Ser Phe Met		
100 105 110		
CTA AGC GTG GCG ACT TTA ATT GTG CTT TTT TGC AAA ATT AAC GCT AAT		440
Leu Ser Val Ala Thr Leu Ile Val Leu Phe Cys Lys Ile Asn Ala Asn		
115 120 125 130		
GAA ATC GCT CAT TCA AGC GTG TTT AAA TCC GGC ATG CAA GCG TGC GTG		488

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...165
(D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

```

AAGGTTTTTA GCGAAATAAG CCCCCACGCC AACACGCCC ATGCTCATTA G CAC AAT      57
                                   His Asn
                                   1

ATC GCA CAT AAA GCA CAA AGC GCA AAT CAA AAA CAC ATA ATT CCT AGC      105
Ile Ala His Lys Ala Gln Ser Ala Asn Gln Lys His Ile Ile Pro Ser
      5              10              15

CAT CCC CCT TTC CAC AAT AAA CAA GGA TTG CGC CCC CAC CGC CGC ACA      153
His Pro Pro Phe His Asn Lys Gln Gly Leu Arg Pro His Arg Arg Thr
      20              25              30

CAA AGA AAT CGC TAAACCAAAA CCTTCTATAA AAACCACAAA CATCTTGCTT AATCC      210
Gln Arg Asn Arg
35

TTTCACTC      218

```

- (2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```

His Asn Ile Ala His Lys Ala Gln Ser Ala Asn Gln Lys His Ile Ile
  1              5              10              15
Pro Ser His Pro Pro Phe His Asn Lys Gln Gly Leu Arg Pro His Arg
      20              25              30
Arg Thr Gln Arg Asn Arg
35

```

- (2) INFORMATION FOR SEQ ID NO:411:

35	40	45	50	
GCG TTT TTA GCT CTG TTA GCG CCT AAA ATC TAT TTA AGC AAT AAT ATC				248
Ala Phe Leu Ala Leu Leu Ala Pro Lys Ile Tyr Leu Ser Asn Asn Ile	55	60	65	
TAT TAT ATT AGC CGT AAA ATC AAC ACC CTA GAA GAT CAA AAA CGC CTG				296
Tyr Tyr Ile Ser Arg Lys Ile Asn Thr Leu Glu Asp Gln Lys Arg Leu	70	75	80	
CTT TTA GAA GAG CAA CAA ATC CTA AAA AAC GAA TTA GAA AAA GAG CGT				344
Leu Leu Glu Glu Gln Gln Ile Leu Lys Asn Glu Leu Glu Lys Glu Arg	85	90	95	
TTT AAA TAC TAC ATA GAA AAT AGT GAA AAT ATT GGC GAT ATT GCG TTT T				393
Phe Lys Tyr Tyr Ile Glu Asn Ser Glu Asn Ile Gly Asp Ile Ala Phe	100	105	110	
AAGTGAAAAA CCCCCTATCC CCTTAAGAGA GCTTAATTAA TGGTCAATCA TT				445

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Asn Ile Lys Thr His Ser Ser Asn Glu Lys Glu Arg Phe Val Arg			
1 5 10 15			
Ile Glu Glu Asp Glu Lys Lys Gly Leu Phe Ala Gly Thr Ala Asn Glu			
20 25 30			
Asn Ser His Gly Leu Ser Leu Met Ala Leu Ile Gly Val Leu Val Phe			
35 40 45			
Gly Gly Ala Phe Leu Ala Leu Leu Ala Pro Lys Ile Tyr Leu Ser Asn			
50 55 60			
Asn Ile Tyr Tyr Ile Ser Arg Lys Ile Asn Thr Leu Glu Asp Gln Lys			
65 70 75 80			
Arg Leu Leu Leu Glu Glu Gln Gln Ile Leu Lys Asn Glu Leu Glu Lys			
85 90 95			
Glu Arg Phe Lys Tyr Tyr Ile Glu Asn Ser Glu Asn Ile Gly Asp Ile			
100 105 110			
Ala Phe			

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid

```

Ser Ser Lys Asp Ala Lys Ala Ile Glu Glu Leu Gln Asp Lys Leu Arg
    195                200                205
Phe Ser Ala Pro Lys Leu Gly Val Ser Ile Gln Ala His His Leu Lys
    210                215                220
Asn Leu Leu Glu Ala Phe Tyr His Gln Asn Lys Glu Ser Leu Gly Phe
    225                230                235                240
Phe Ser Pro Tyr Phe Ser Leu Arg Ser Gln Thr Pro Ser Val Ser Tyr
    245                250                255
Glu Ser Ala Leu Ala Ser Leu Glu Asn Tyr Phe Met Ala Leu Phe Gln
    260                265                270
Ser His Phe Lys Asp Asp Thr Ala Leu Gln Gln Asn Phe Lys Gly Leu
    275                280                285
Leu Gln Ala Phe Val Ser Met Ala Lys Asp Lys Arg Ser Gln Ile Ala
    290                295                300
Leu Asn Ala Gln Ala Lys Asp Asn Ala Lys Leu Thr Phe Asn Ala Leu
    305                310                315                320
Leu Glu Ser Leu Ser Val Asn Phe Phe Gln Ser Tyr Lys Ile Ser His
    325                330                335
Glu

```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...392
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

AAAATGAGGG TGTTC AATT CAAGCCATGA GTAAGTTATA TGAGTAAGCC ATG AAT      56
                                     Met Asn
                                     1

ATC AAA ACC CAT TCT TCA AAT GAA AAA GAA CGC TTT GTG CGC ATA GAA      104
Ile Lys Thr His Ser Ser Asn Glu Lys Glu Arg Phe Val Arg Ile Glu
    5                10                15

GAG GAC GAA AAG AAA GGA TTA TTT GCT GGA ACT GCA AAT GAA AAT TCG      152
Glu Asp Glu Lys Lys Gly Leu Phe Ala Gly Thr Ala Asn Glu Asn Ser
    20                25                30

CAC GGC CTT TCT TTA ATG GCT TTA ATA GGG GTA TTG GTT TTT GGG GGC      200
His Gly Leu Ser Leu Met Ala Leu Ile Gly Val Leu Val Phe Gly Gly

```

```

TTT AAA GAC GAT ACC GCA CTC CAA CAG AAT TTT AAA GGA TTG TTG CAA      920
Phe Lys Asp Asp Thr Ala Leu Gln Gln Asn Phe Lys Gly Leu Leu Gln
275                      280                      285                      290

GCC TTT GTT TCT ATG GCT AAA GAC AAA CGA TCC CAA ATC GCT CTT AAC      968
Ala Phe Val Ser Met Ala Lys Asp Lys Arg Ser Gln Ile Ala Leu Asn
                295                      300                      305

GCC CAA GCT AAA GAC AAC GCC AAG CTA ACT TTT AAC GCC TTG TTA GAA      1016
Ala Gln Ala Lys Asp Asn Ala Lys Leu Thr Phe Asn Ala Leu Leu Glu
                310                      315                      320

AGC CTT AGC GTG AAT TTC TTT CAA TCT TAC AAA ATA AGC CAT GAG TGATT      1066
Ser Leu Ser Val Asn Phe Phe Gln Ser Tyr Lys Ile Ser His Glu
                325                      330                      335

TCGAAGTCCC CCCCAAAGCT AAAGGGTTTA AACGCCTTTT TAAAGCCC      1114

```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

Met Ser Trp Met Val Val Ile Gly Ala Leu Ile Cys Met Leu Leu Gly
 1                      5                      10                      15
Val Phe Ile Phe Phe Thr Ser Met Ser Val Lys Lys Phe Leu Ser Ala
                20                      25                      30
Tyr Leu Asn Ala Tyr Leu Asp Gln Arg Pro His Ile Lys Gly Met Gly
                35                      40                      45
Ile Ala Gly Thr Pro Phe Glu Cys Glu Gly Phe Phe Lys Ile Ala Cys
                50                      55                      60
Val Ser Lys Glu Leu Ser Phe Leu Asp Ser Gln Asn Ser Pro Ile Val
65                      70                      75                      80
Asn Phe Lys Asn Leu Ser Ile Lys Leu Arg Ser Leu Asp Lys Ser Ser
                85                      90                      95
Leu Thr Leu Ser Val His Ser Gln Ile Lys Ser Pro Ile Leu Glu Gln
                100                      105                      110
Asp Met Gln Gln Lys Ile Ser Gln Ile Pro Leu Lys Asp Leu Asn Ala
                115                      120                      125
Leu Leu Glu Lys Met Lys Pro Thr Arg Leu Asn Cys Ser Leu Thr Phe
                130                      135                      140
Asn Ala Leu Asp Glu Lys Thr Leu Asn Asp Asn Leu Lys Cys Asp Leu
145                      150                      155                      160
Thr Asn Ala Glu Asn Ile Leu Ala Tyr Thr Phe Phe Gln Glu Gly Leu
                165                      170                      175
Met Glu Ala Gln Glu Asn Leu Ser Leu Lys Asn Ile Phe Lys Thr Leu
                180                      185                      190

```

GGC	ACT	CCC	TTT	GAA	TGC	GAA	GGG	TTT	TTT	AAA	ATC	GCA	TGC	GTT	TCT	248
Gly	Thr	Pro	Phe	Glu	Cys	Glu	Gly	Phe	Phe	Lys	Ile	Ala	Cys	Val	Ser	
			55						60					65		
AAA	GAG	CTC	AGT	TTT	TTA	GAC	TCT	CAA	AAC	TCC	CCT	ATT	GTG	AAT	TTT	296
Lys	Glu	Leu	Ser	Phe	Leu	Asp	Ser	Gln	Asn	Ser	Pro	Ile	Val	Asn	Phe	
			70					75					80			
AAA	AAT	TTG	AGT	ATT	AAG	CTC	CGT	TCT	TTA	GAT	AAA	AGC	TCT	CTT	ACT	344
Lys	Asn	Leu	Ser	Ile	Lys	Leu	Arg	Ser	Leu	Asp	Lys	Ser	Ser	Leu	Thr	
		85					90					95				
CTT	TCT	GTC	CAT	TCT	CAA	ATC	AAA	TCC	CCT	ATT	TTA	GAA	CAA	GAT	ATG	392
Leu	Ser	Val	His	Ser	Gln	Ile	Lys	Ser	Pro	Ile	Leu	Glu	Gln	Asp	Met	
	100					105					110					
CAG	CAA	AAA	ATC	AGC	CAA	ATC	CCC	CTA	AAA	GAC	TTG	AAT	GCC	TTA	TTA	440
Gln	Gln	Lys	Ile	Ser	Gln	Ile	Pro	Leu	Lys	Asp	Leu	Asn	Ala	Leu	Leu	
115					120					125				130		
GAA	AAA	ATG	AAA	CCC	ACG	CGC	TTG	AAT	TGC	TCT	TTA	ACA	TTC	AAC	GCT	488
Glu	Lys	Met	Lys	Pro	Thr	Arg	Leu	Asn	Cys	Ser	Leu	Thr	Phe	Asn	Ala	
				135					140					145		
CTA	GAT	GAA	AAA	ACC	TTA	AAC	GAC	AAC	TTA	AAA	TGC	GAT	TTG	ACT	AAT	536
Leu	Asp	Glu	Lys	Thr	Leu	Asn	Asp	Asn	Leu	Lys	Cys	Asp	Leu	Thr	Asn	
			150					155					160			
GCG	GAA	AAT	ATC	CTT	GCT	TAC	ACT	TTT	TTT	CAA	GAG	GGT	TTA	ATG	GAG	584
Ala	Glu	Asn	Ile	Leu	Ala	Tyr	Thr	Phe	Phe	Gln	Glu	Gly	Leu	Met	Glu	
	165						170					175				
GCT	CAA	GAA	AAT	CTA	TCC	CTT	AAA	AAT	ATT	TTT	AAA	ACC	TTG	AGT	TCT	632
Ala	Gln	Glu	Asn	Leu	Ser	Leu	Lys	Asn	Ile	Phe	Lys	Thr	Leu	Ser	Ser	
	180					185					190					
AAA	GAC	GCT	AAA	GCC	ATA	GAA	GAG	TTG	CAA	GAC	AAA	CTG	CGT	TTT	TCA	680
Lys	Asp	Ala	Lys	Ala	Ile	Glu	Glu	Leu	Gln	Asp	Lys	Leu	Arg	Phe	Ser	
195				200						205				210		
GCG	CCA	AAG	TTG	GGC	GTT	TCT	ATC	CAA	GCG	CAC	CAT	CTT	AAA	AAC	CTT	728
Ala	Pro	Lys	Leu	Gly	Val	Ser	Ile	Gln	Ala	His	His	Leu	Lys	Asn	Leu	
				215					220					225		
TTG	GAA	GCC	TTT	TAT	CAC	CAA	AAT	AAA	GAG	AGT	TTG	GGC	TTT	TTT	TCC	776
Leu	Glu	Ala	Phe	Tyr	His	Gln	Asn	Lys	Glu	Ser	Leu	Gly	Phe	Phe	Ser	
			230					235					240			
CCT	TAT	TTT	AGT	TTG	CGA	TCT	CAA	ACC	CCT	AGC	GTC	TCT	TAT	GAA	AGC	824
Pro	Tyr	Phe	Ser	Leu	Arg	Ser	Gln	Thr	Pro	Ser	Val	Ser	Tyr	Glu	Ser	
		245					250					255				
GCG	TTA	GCT	TCT	TTA	GAA	AAC	TAT	TTT	ATG	GCT	TTG	TTC	CAA	TCC	CAT	872
Ala	Leu	Ala	Ser	Leu	Glu	Asn	Tyr	Phe	Met	Ala	Leu	Phe	Gln	Ser	His	
	260					265					270					

```

Tyr Ala Gly Ile Met Gly Met Met Ala Ser His Ser Val Gly Gly His
          325                      330                      335
Ser Leu Ala Gln Met Leu Ser Leu Ala Phe Thr His Ile Ala Asn Glu
          340                      345                      350
Lys Thr Phe Val Leu Met Thr Phe Leu Ser Ala Gly Ile Val Asn Ile
          355                      360                      365
Phe Ile Pro Ser Gly Gly Gly Gln Trp Ala Ile Gln Ala Pro Ile Met
          370                      375                      380
Leu Pro Ala Gly Gln Ser Leu Gly Val Asp Pro Gly Val Val Ser Met
385                      390                      395                      400
Ala Ile Ala Trp Gly Asp Ala Trp Thr Asn Met Ile Gln Pro Phe Trp
          405                      410                      415
Ala Leu Pro Ala Leu Ala Ile Ala Gly Leu Gly Ala Lys Asp Ile Met
          420                      425                      430
Gly Tyr Cys Val Leu Thr Leu Ile Phe Val Gly Leu Val Val Cys Gly
          435                      440                      445
Val Phe Tyr Phe Leu Val
          450

```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1061
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

TATCACTATA CTTTCAATAA AATAAGGGGT TTTTTTTGAC TAAAAAATTC ATG TCT      56
                                     Met Ser
                                     1

TGG ATG GTG GTT ATT GGG GCT TTA ATT TGC ATG CTT TTA GGG GTG TTT      104
Trp Met Val Val Ile Gly Ala Leu Ile Cys Met Leu Leu Gly Val Phe
      5                      10                      15

ATC TTC TTC ACT AGC ATG TCG GTT AAA AAA TTT TTA AGC GCT TAT CTT      152
Ile Phe Phe Thr Ser Met Ser Val Lys Lys Phe Leu Ser Ala Tyr Leu
      20                      25                      30

AAC GCT TAT TTG GAT CAA CGC CCC CAT ATT AAG GGC ATG GGG ATT GCA      200
Asn Ala Tyr Leu Asp Gln Arg Pro His Ile Lys Gly Met Gly Ile Ala
      35                      40                      45                      50

```


TTTTCTCT

1465

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```

Met Phe Leu Leu Arg His Leu Thr Ser Ala Cys Val Phe Leu Ala Ser
 1             5             10             15
Lys Cys Leu Pro Asp Ser Phe Val Leu Val Ala Leu Leu Ser Phe Val
      20             25             30
Val Phe Val Leu Val Tyr Cys Leu Thr Gly Gln Asp Ala Phe Ser Val
      35             40             45
Ile Ser Ser Trp Gly Asn Gly Ala Trp Thr Leu Leu Gly Phe Ser Met
      50             55             60
Gln Met Ala Leu Ile Leu Val Leu Gly Gln Ala Leu Ala Asn Ala Lys
      65             70             75             80
Leu Val Gln Lys Leu Leu Lys Tyr Leu Ala Ser Leu Pro Lys Gly Tyr
      85             90             95
Tyr Thr Ala Leu Trp Leu Val Thr Phe Leu Ser Leu Ile Ala Asn Trp
      100            105            110
Ile Asn Trp Gly Phe Gly Leu Val Ile Ser Ala Ile Phe Ala Lys Glu
      115            120            125
Ile Ala Lys Asn Val Lys Gly Val Asp Tyr Arg Leu Leu Ile Ala Ser
      130            135            140
Ala Tyr Ser Gly Phe Val Ile Trp His Gly Gly Leu Ser Gly Ser Ile
      145            150            155            160
Pro Leu Ser Val Ala Thr Gln Asn Glu Asn Leu Ser Lys Ile Ser Ala
      165            170            175
Gly Val Ile Glu Lys Ala Ile Pro Ile Ser Gln Thr Ile Phe Ser Ser
      180            185            190
Tyr Asn Leu Ile Ile Ile Gly Ile Ile Leu Val Gly Leu Pro Phe Leu
      195            200            205
Met Ala Met Ile His Pro Lys Lys Glu Glu Ile Val Glu Ile Asp Ser
      210            215            220
Lys Leu Leu Lys Asp Glu Tyr Lys Glu Ile Glu Leu Ile Ser His Gln
      225            230            235            240
Gln Asp Lys Thr Ile Ala His Phe Leu Glu Asn Ser Ala Leu Leu Ser
      245            250            255
Tyr Leu Leu Val Phe Leu Gly Phe Gly Tyr Leu Gly Val Tyr Phe Phe
      260            265            270
Lys Gly Gly Gly Ile Ser Leu Asn Ile Val Asn Thr Ile Phe Leu Phe
      275            280            285
Leu Gly Ile Leu Leu His Lys Thr Pro Leu Ala Tyr Val Lys Ala Ile
      290            295            300
Asp Arg Ser Ala Xaa Ser Val Ala Gly Ile Leu Leu Gln Phe Pro Phe
      305            310            315            320

```

Lys Thr Ile Ala His Phe Leu Glu Asn Ser Ala Leu Leu Ser Tyr Leu	
245 250 255	
TTG GTT TTT TTG GGT TTT GGG TAT CTT GGT GTT TAT TTT TTT AAA GGG	872
Leu Val Phe Leu Gly Phe Gly Tyr Leu Gly Val Tyr Phe Phe Lys Gly	
260 265 270	
GGA GGG ATT AGT TTA AAC ATT GTC AAT ACG ATT TTC CTT TTT TTA GGG	920
Gly Gly Ile Ser Leu Asn Ile Val Asn Thr Ile Phe Leu Phe Leu Gly	
275 280 285 290	
ATT TTA CTG CAT AAA ACC CCT TTA GCT TAT GTG AAA GCG ATC GAT CGT	968
Ile Leu Leu His Lys Thr Pro Leu Ala Tyr Val Lys Ala Ile Asp Arg	
295 300 305	
TCC GCT ANG AGC GTG GCT GGG ATT TTA TTG CAA TTC CCT TTT TAC GCT	1016
Ser Ala Xaa Ser Val Ala Gly Ile Leu Leu Gln Phe Pro Phe Tyr Ala	
310 315 320	
GGG ATT ATG GGG ATG ATG GCA AGC CAT AGC GTG GGG GGT CAT TCT TTA	1064
Gly Ile Met Gly Met Met Ala Ser His Ser Val Gly Gly His Ser Leu	
325 330 335	
GCG CAA ATG CTT TCT TTA GCT TTC ACG CAC ATC GCT AAT GAA AAA ACT	1112
Ala Gln Met Leu Ser Leu Ala Phe Thr His Ile Ala Asn Glu Lys Thr	
340 345 350	
TTC GTG CTC ATG ACT TTT TTG AGC GCA GGG ATT GTC AAT ATT TTT ATT	1160
Phe Val Leu Met Thr Phe Leu Ser Ala Gly Ile Val Asn Ile Phe Ile	
355 360 365 370	
CCG TCT GGC GGA GGG CAA TGG GCG ATT CAA GCT CCT ATC ATG CTT CCG	1208
Pro Ser Gly Gly Gly Gln Trp Ala Ile Gln Ala Pro Ile Met Leu Pro	
375 380 385	
GCT GGG CAA AGC TTA GGG GTG GAT CCG GGA GTG GTT TCT ATG GCT ATC	1256
Ala Gly Gln Ser Leu Gly Val Asp Pro Gly Val Val Ser Met Ala Ile	
390 395 400	
GCT TGG GGA GAT GCT TGG ACG AAT ATG ATA CAG CCT TTT TGG GCT TTG	1304
Ala Trp Gly Asp Ala Trp Thr Asn Met Ile Gln Pro Phe Trp Ala Leu	
405 410 415	
CCC GCT TTA GCC ATT GCG GGT TTG GGC GCT AAA GAT ATT ATG GGC TAT	1352
Pro Ala Leu Ala Ile Ala Gly Leu Gly Ala Lys Asp Ile Met Gly Tyr	
420 425 430	
TGC GTT TTG ACT TTA ATT TTT GTA GGC TTA GTC GTG TGT GGG GTG TTT	1400
Cys Val Leu Thr Leu Ile Phe Val Gly Leu Val Val Cys Gly Val Phe	
435 440 445 450	
TAT TTT TTA GTG TGAGTTTTTT ATGCCTAAAA CCATGCTCTT TTCAATGGGG TAAGG	1457
Tyr Phe Leu Val	

20	25	30	
GTT CTT GTT TAT TGC TTG ACA GGG CAA GAC GCT TTT TCT GTC ATT TCT			200
Val Leu Val Tyr Cys Leu Thr Gly Gln Asp Ala Phe Ser Val Ile Ser			
35	40	45	50
AGT TGG GGG AAT GGC GCT TGG ACG CTT TTA GGT TTT TCT ATG CAA ATG			248
Ser Trp Gly Asn Gly Ala Trp Thr Leu Leu Gly Phe Ser Met Gln Met			
	55	60	65
GCC CTT ATT TTG GTG TTG GGT CAG GCT CTG GCT AAC GCT AAA TTA GTC			296
Ala Leu Ile Leu Val Leu Gly Gln Ala Leu Ala Asn Ala Lys Leu Val			
	70	75	80
CAA AAG CTT TTA AAA TAT CTA GCG TCT TTA CCT AAA GGG TAT TAT ACG			344
Gln Lys Leu Leu Lys Tyr Leu Ala Ser Leu Pro Lys Gly Tyr Tyr Thr			
	85	90	95
GCT TTA TGG TTG GTT ACT TTT TTA TCG TTA ATC GCT AAT TGG ATC AAC			392
Ala Leu Trp Leu Val Thr Phe Leu Ser Leu Ile Ala Asn Trp Ile Asn			
	100	105	110
TGG GGT TTT GGC TTG GTG ATT AGT GCG ATT TTT GCA AAA GAG ATC GCC			440
Trp Gly Phe Gly Leu Val Ile Ser Ala Ile Phe Ala Lys Glu Ile Ala			
	115	120	125
AAA AAT GTT AAG GGG GTG GAT TAC AGG CTG CTC ATT GCT AGC GCT TAT			488
Lys Asn Val Lys Gly Val Asp Tyr Arg Leu Leu Ile Ala Ser Ala Tyr			
	135	140	145
TCG GGT TTT GTC ATC TGG CAT GGG GGT TTA TCA GGC TCT ATC CCT TTA			536
Ser Gly Phe Val Ile Trp His Gly Gly Leu Ser Gly Ser Ile Pro Leu			
	150	155	160
AGC GTT GCC ACC CAA AAT GAA AAT CTA TCC AAA ATA AGC GCT GGG GTG			584
Ser Val Ala Thr Gln Asn Glu Asn Leu Ser Lys Ile Ser Ala Gly Val			
	165	170	175
ATT GAA AAA GCT ATC CCT ATC AGT CAG ACG ATT TTT TCT TCT TAT AAT			632
Ile Glu Lys Ala Ile Pro Ile Ser Gln Thr Ile Phe Ser Ser Tyr Asn			
	180	185	190
TTA ATC ATT ATA GGG ATC ATT CTT GTA GGG TTA CCC TTT TTA ATG GCA			680
Leu Ile Ile Ile Gly Ile Ile Leu Val Gly Leu Pro Phe Leu Met Ala			
	195	200	205
ATG ATC CAC CCT AAA AAA GAA GAA ATC GTT GAG ATT GAT TCA AAG CTT			728
Met Ile His Pro Lys Lys Glu Glu Ile Val Glu Ile Asp Ser Lys Leu			
	215	220	225
TTA AAA GAC GAG TAC AAA GAG ATT GAA CTC ATT AGC CAC CAA CAA GAC			776
Leu Lys Asp Glu Tyr Lys Glu Ile Glu Leu Ile Ser His Gln Gln Asp			
	230	235	240
AAA ACG ATC GCG CAT TTT TTG GAA AAC AGC GCT TTG CTT TCT TAT CTT			824

```

Ile His Asp Ser Val Gly Val Leu Asp Glu Tyr Phe Ala Gln Ser Glu
      35              40              45
Phe Phe Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys
      50              55              60
Asp Met Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His
      65              70              75              80
Thr His Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val
      85              90              95
Ile Cys Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu
      100             105             110
Lys Asp Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro
      115             120             125
Leu Arg Leu His Cys Asp Thr Leu Ala Leu Lys Glu Lys Ile Lys Ser
      130             135             140
Glu Leu Asp Lys Asn Pro Ser Lys Val Phe Asp Ile Thr Leu Thr Tyr
      145             150             155             160
Ile Ser Val Gln Gly Lys Trp Tyr Phe Ser Ser Trp Arg Ala Asp Val
      165             170             175
Asn Arg Ser Gly Gly Leu Ala Thr Gln Met Gly Val Asn Ile Phe Asp
      180             185             190
Thr Leu Ile Tyr Leu Phe Gly Ser Val Lys Asp Lys Val Ile Asn Lys
      195             200             205
Glu Glu Pro Asp Cys Val Gly Gly Tyr Ser Phe
      210             215

```

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1412
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

```

GACAGAAGCT GAATTTGAGG TGC GCTTATA GCTTGTA AAA GGGGGTGT TT ATG TTT      56
                                     Met Phe
                                     1

TTA TTA AGG CAT TTG ACT TCA GCG TGC GTG TTT TTG GCG TCT AAA TGT      104
Leu Leu Arg His Leu Thr Ser Ala Cys Val Phe Leu Ala Ser Lys Cys
      5              10              15

TTG CCG GAC TCC TTT GTC TTG GTC GCT CTT TTA TCG TTT GTC GTG TTT      152
Leu Pro Asp Ser Phe Val Leu Val Ala Leu Leu Ser Phe Val Val Phe

```

TTT GAT CAC ATC CGT TTC GGG TTA AGA AAC GGC ATG CAT GTG ATT TGT	346
Phe Asp His Ile Arg Phe Gly Leu Arg Asn Gly Met His Val Ile Cys	
85 90 95	
GAA AAA CCC TTA GTT TTA GAC CCT GGC GAA ATA CAA GAA TTG AAA GAT	394
Glu Lys Pro Leu Val Leu Asp Pro Gly Glu Ile Gln Glu Leu Lys Asp	
100 105 110	
TTA GAG GTG AAA CAC CAA AAA AGG GTG TTT AGT CTT TTA CCC TTG CGC	442
Leu Glu Val Lys His Gln Lys Arg Val Phe Ser Leu Leu Pro Leu Arg	
115 120 125 130	
TTG CAT TGC GAC ACG CTG GCT TTG AAA GAA AAA ATT AAG AGC GAA TTA	490
Leu His Cys Asp Thr Leu Ala Leu Lys Glu Lys Ile Lys Ser Glu Leu	
135 140 145	
GAC AAA AAC CCT AGC AAG GTG TTT GAC ATC ACG CTC ACT TAT ATC AGC	538
Asp Lys Asn Pro Ser Lys Val Phe Asp Ile Thr Leu Thr Tyr Ile Ser	
150 155 160	
GTT CAA GGG AAA TGG TAT TTT TCT TCA TGG CGA GCG GAT GTG AAT AGG	586
Val Gln Gly Lys Trp Tyr Phe Ser Ser Trp Arg Ala Asp Val Asn Arg	
165 170 175	
AGC GGA GGG TTA GCC ACT CAA ATG GGG GTG AAT ATT TTT GAC ACT TTA	634
Ser Gly Gly Leu Ala Thr Gln Met Gly Val Asn Ile Phe Asp Thr Leu	
180 185 190	
ATC TAT TTG TTT GGA AGC GTT AAA GAC AAG GTT ATC AAT AAA GAA GAG	682
Ile Tyr Leu Phe Gly Ser Val Lys Asp Lys Val Ile Asn Lys Glu Glu	
195 200 205 210	
CCT GAT TGC GTA GGG GGA TAC TCT TTT TAGAGCATGC CAAAATAAGA TGGTTTT	736
Pro Asp Cys Val Gly Gly Tyr Ser Phe	
215	
TTTCCATCAA TCCAGAACAC ATGGGAG	763

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met	Leu	Phe	Ala	Met	Ile	Gly	Ser	Gly	Gly	Phe	Ile	Ala	Pro	Lys	His
1				5					10					15	
Leu	Gln	Ala	Ile	Arg	Asp	Thr	Gly	His	Phe	Leu	Asp	Cys	Ser	Phe	Asp
			20					25						30	

```

Thr Gln Gly Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met
      355                      360                      365
Gly Leu Lys Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu
      370                      375                      380
Leu Lys Val Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp
      385                      390                      395                      400
Pro Ser Trp Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys
      405                      410                      415
Leu Lys Phe

```

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...709
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

AAATAAGCTA ATCTTTGCTA AAATGAGATT TAAAATTATT TAAGGAAGAT GA ATG CTT      58
                                     Met Leu
                                     1

TTT GCG ATG ATT GGT TCA GGG GGG TTT ATC GCT CCC AAG CAC TTG CAA      106
Phe Ala Met Ile Gly Ser Gly Gly Phe Ile Ala Pro Lys His Leu Gln
      5                      10                      15

GCG ATT AGA GAT ACA GGG CAT TTT TTG GAT TGC TCT TTT GAT ATT CAT      154
Ala Ile Arg Asp Thr Gly His Phe Leu Asp Cys Ser Phe Asp Ile His
      20                      25                      30

GAT AGC GTG GGG GTT TTA GAT GAG TAT TTC GCG CAA TCA GAG TTT TTT      202
Asp Ser Val Gly Val Leu Asp Glu Tyr Phe Ala Gln Ser Glu Phe Phe
      35                      40                      45                      50

ACG AAT ATT GAA GAT TTT GAA AAG CAT TTA GAG CAA TCT AAG GAT ATG      250
Thr Asn Ile Glu Asp Phe Glu Lys His Leu Glu Gln Ser Lys Asp Met
      55                      60                      65

GGT AAA GAA ATC AAC TAT TTG AGT GTT TGC ACG CCT ACG CAC ACG CAT      298
Gly Lys Glu Ile Asn Tyr Leu Ser Val Cys Thr Pro Thr His Thr His
      70                      75                      80

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

Met Lys Glu Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp
 1           5           10           15
Ile Arg Lys Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro
          20           25           30
Asp Val Leu Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys
          35           40           45
Asn Ile Gly Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr
          50           55           60
Thr Asn Glu Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser
65           70           75           80
Asp Phe Ser Met His Glu Tyr Asp Lys Phe Phe Ser Gln Pro Ile Lys
          85           90           95
Leu Leu Ala Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg
          100          105          110
Asn Ile Tyr Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln
          115          120          125
Arg Glu Thr Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val
          130          135          140
Leu Met Asp Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys
145          150          155          160
Gln Asp Thr Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe
          165          170          175
Thr Ile Asn Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile
          180          185          190
Phe Thr Lys Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly
          195          200          205
Thr Arg Lys Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu
          210          215          220
Asn Tyr Asn Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr
225          230          235          240
Thr Arg Gln Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser
          245          250          255
Asn Tyr Leu Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp
          260          265          270
Arg Phe Asn Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser
          275          280          285
Gln Ala Thr Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile
          290          295          300
Ile Ala Asn Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His
305          310          315          320
Phe Ile Tyr Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp
          325          330          335
Phe Gln Tyr Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp
          340          345          350

```

GGG TAT TTG TCC AAC ACT ATA ATT ACA AAA GAT GAG CTT AAT TAT AAT	729
Gly Tyr Leu Ser Asn Thr Ile Ile Thr Lys Asp Glu Leu Asn Tyr Asn	
215 220 225	
CGT ATC AAT TGG CGA GAT ATA GGA AAA GAT AAA AAT ACC ACC AGA CAA	777
Arg Ile Asn Trp Arg Asp Ile Gly Lys Asp Lys Asn Thr Thr Arg Gln	
230 235 240	
GAA TAC GAT CTT ATA AAC TCT AAA AGG ATT GCT AAT TCT AAC TAT CTT	825
Glu Tyr Asp Leu Ile Asn Ser Lys Arg Ile Ala Asn Ser Asn Tyr Leu	
245 250 255	
ATT TCA AAA GCT AAG AAA GTG GTG AAA CGA TAT AAT GAT AGA TTT AAT	873
Ile Ser Lys Ala Lys Lys Val Val Lys Arg Tyr Asn Asp Arg Phe Asn	
260 265 270 275	
AAT TCT CTC TCT GAA GTA AAA CAA GAA AAA GAA GAG TCG CAA GCC ACA	921
Asn Ser Leu Ser Glu Val Lys Gln Glu Lys Glu Glu Ser Gln Ala Thr	
280 285 290	
CAA ATA CAC CAT ATT TTT CCC ATC CAA GAC TTT CCC ATT ATT GCT AAC	969
Gln Ile His His Ile Phe Pro Ile Gln Asp Phe Pro Ile Ile Ala Asn	
295 300 305	
TAT ATA GAG AAT CTT ATC GCA CTC ACT CCT AAT CAA CAT TTT ATT TAC	1017
Tyr Ile Glu Asn Leu Ile Ala Leu Thr Pro Asn Gln His Phe Ile Tyr	
310 315 320	
GCC CAC CCT AAT AAT CAA ACC CGC TTG ATT GAT AAA GAT TTT CAA TAT	1065
Ala His Pro Asn Asn Gln Thr Arg Leu Ile Asp Lys Asp Phe Gln Tyr	
325 330 335	
ATC TGC TTA TTA GCT AAA ACG ACC ACA ATT CTT AAT GAC ACT CAA GGC	1113
Ile Cys Leu Leu Ala Lys Thr Thr Thr Ile Leu Asn Asp Thr Gln Gly	
340 345 350 355	
GTA TAT GAT TGG AAT GAT TAT ATT GTT GTG TTG AAT ATG GGC CTC AAA	1161
Val Tyr Asp Trp Asn Asp Tyr Ile Val Val Leu Asn Met Gly Leu Lys	
360 365 370	
ACA ACT ATC TTT TCT CAA GTC AAG AAC GAA TGG GAA TTA TTA AAA GTA	1209
Thr Thr Ile Phe Ser Gln Val Lys Asn Glu Trp Glu Leu Leu Lys Val	
375 380 385	
ATA GAT GCT TTT TAT TTT GAT TTT AAC AAG AGC AAA GAT CCA AGT TGG	1257
Ile Asp Ala Phe Tyr Phe Asp Phe Asn Lys Ser Lys Asp Pro Ser Trp	
390 395 400	
TCA TAC TTG CTA GAT AAA AAC GAT TTA AGA GCT TTC AAG CTA AAA TTT T	1306
Ser Tyr Leu Leu Asp Lys Asn Asp Leu Arg Ala Phe Lys Leu Lys Phe	
405 410 415	
AATAAGTTTT ATTGAACTG GCTATAAAAA CCCGCTTGAC TTATCTTATC CTTTT	1361

(2) INFORMATION FOR SEQ ID NO:400:

TATTGATAGC ATGAGTTGTT TTTGGTTTGG AATTTTAAGG AGTAGCTT ATG AAA GAG	57
Met Lys Glu	
1	
CAA TCA ATG ATT GAT TTT TTA AAA CTT AGA GAT TAT GAC ATT AGA AAA	105
Gln Ser Met Ile Asp Phe Leu Lys Leu Arg Asp Tyr Asp Ile Arg Lys	
5 10 15	
ACA CAA AAT GCG CGA TGG ATA GAT CAA AAA TGC ACC CCT GAT GTG TTG	153
Thr Gln Asn Ala Arg Trp Ile Asp Gln Lys Cys Thr Pro Asp Val Leu	
20 25 30 35	
TCT CTT GTT GCT GAT TGT ATT TTA GAG TTT ACG CAA TGT AAT ATT GGA	201
Ser Leu Val Ala Asp Cys Ile Leu Glu Phe Thr Gln Cys Asn Ile Gly	
40 45 50	
AAA TCA TTT TCT ATT AGG GAT ATT TGG GAT AGC CCT TAC ACC AAT GAA	249
Lys Ser Phe Ser Ile Arg Asp Ile Trp Asp Ser Pro Tyr Thr Asn Glu	
55 60 65	
AAT GTT AAA ATG ATT TTT TCT AAA CCT GAT TTA AAT TCT GAC TTT TCC	297
Asn Val Lys Met Ile Phe Ser Lys Pro Asp Leu Asn Ser Asp Phe Ser	
70 75 80	
ATG CAT GAA TAC GAT AAG TTT TTT TCT CAG CCT ATT AAA TTA TTA GCC	345
Met His Glu Tyr Asp Lys Phe Ser Gln Pro Ile Lys Leu Leu Ala	
85 90 95	
TAT AGC GGT ATT TTA TTT GAA ACA AAA ACT GGC AAT AGA AAT ATT TAT	393
Tyr Ser Gly Ile Leu Phe Glu Thr Lys Thr Gly Asn Arg Asn Ile Tyr	
100 105 110 115	
ACC ATA CAA AAC ATA GAG CTA TTA GAA TAT CTC ATG CAA AGA GAA ACA	441
Thr Ile Gln Asn Ile Glu Leu Leu Glu Tyr Leu Met Gln Arg Glu Thr	
120 125 130	
AAC GCT TTG AAA TTC CTT ATT TTA TAT ATT CAA AAG GTA TTA ATG GAT	489
Asn Ala Leu Lys Phe Leu Ile Leu Tyr Ile Gln Lys Val Leu Met Asp	
135 140 145	
AGT GGG ATT TAT CCT TTA TTT GAC AAC TTT TTA CAA AAA CAA GAC ACA	537
Ser Gly Ile Tyr Pro Leu Phe Asp Asn Phe Leu Gln Lys Gln Asp Thr	
150 155 160	
GAA AGT TTT AAG CAA CTA AAA GAT GGT TTC ACT CAT TTT ACT ATC AAT	585
Glu Ser Phe Lys Gln Leu Lys Asp Gly Phe Thr His Phe Thr Ile Asn	
165 170 175	
AAC ACA GCA ATC AAT AAC GCT ACG GAA TGT TTT AGG ATT TTT ACT AAA	633
Asn Thr Ala Ile Asn Asn Ala Thr Glu Cys Phe Arg Ile Phe Thr Lys	
180 185 190 195	
ATT ATC AAT CCT TTA GCT TTT TAT TAT GGT AAA AAA GGC ACA AGA AAA	681
Ile Ile Asn Pro Leu Ala Phe Tyr Tyr Gly Lys Lys Gly Thr Arg Lys	
200 205 210	

1				5					10					15				
Cys	Val	Lys	Cys	Ala	Lys	Cys	Val	Pro	Gly	Cys	Thr	Ile	Tyr	Arg	Ile			
			20					25					30					
His	Lys	Asp	Glu	Ala	Thr	Ser	Pro	Arg	Gly	Phe	Leu	Asp	Leu	Met	Arg			
		35					40					45						
Leu	Asn	Ala	Gln	Asn	Lys	Leu	Gln	Leu	Asp	Thr	Asn	Leu	Lys	His	Leu			
	50					55					60							
Leu	Glu	Thr	Cys	Phe	Leu	Cys	Thr	Ala	Cys	Val	Glu	Ile	Cys	Pro	Phe			
65					70					75					80			
His	Leu	Pro	Ile	Asp	Thr	Leu	Ile	Glu	Lys	Ala	Arg	Glu	Lys	Ile	Ala			
			85					90					95					
Gln	Lys	His	Gly	Ile	Ala	Trp	Tyr	Lys	Lys	Ser	Tyr	Phe	Ser	Leu	Leu			
			100					105					110					
Lys	Asn	Arg	Lys	Lys	Met	Asp	Arg	Val	Phe	Ser	Thr	Ala	His	Phe	Leu			
		115					120					125						
Ala	Pro	Cys	Val	Phe	Lys	Gln	Val	Gly	Asp	Ser	Leu	Glu	Pro	Arg	Ala			
	130					135					140							
Val	Phe	Lys	Gly	Leu	Phe	Lys	Arg	Phe	Lys	Lys	Ser	Ala	Leu	Pro	Pro			
145					150					155					160			
Leu	Asn	Gln	Lys	Ser	Phe	Leu	Gln	Lys	His	Ala	Glu	Met	Lys	Leu	Leu			
				165				170					175					
Glu	Asn	Pro	Ile	Gln	Lys	Val	Ala	Ile	Phe	Ile	Gly	Cys	Leu	Ser	Asn			
			180					185					190					
Tyr	His	Tyr	Gln	Gln	Val	Gly	Glu	Ser	Leu	Leu	Tyr	Ile	Leu	Glu	Lys			
		195				200					205							
Leu	Asn	Ile	Gln	Ala	Ile	Ile	Pro	Lys	Gln	Glu	Cys	Cys	Ser	Ala	Pro			
	210					215					220							
Ala	Tyr	Phe	Thr	Gly	Asp	Lys	Asp	Thr	Thr	Leu	Phe	Leu	Val	Lys	Lys			
225					230					235					240			
Asn	Ile	Glu	Trp	Phe	Glu	Ser	Tyr	Leu	Asp	Lys	Val	Asp	Ala	Ile	Ile			
				245				250					255					
Val	Pro	Glu	Ala	Thr	Cys	Ala	Thr	Cys	Ser	Ser	Thr	Ile	Ile	Thr	Arg			
		260					265						270					
Cys	Phe	Trp	Ala	Lys	Lys	Ile	Arg	Ile	Cys	Met								
		275					280											

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1305
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Cys	Val	Phe	Lys	Gln	Val	Gly	Asp	Ser	Leu	Glu	Pro	Arg	Ala	Val	Phe		
				135					140					145			
AAA	GGT	TTG	TTC	AAA	CGC	TTT	AAA	AAA	AGC	GCG	CTG	CCT	CCT	TTA	AAT		536
Lys	Gly	Leu	Phe	Lys	Arg	Phe	Lys	Lys	Ser	Ala	Leu	Pro	Pro	Leu	Asn		
				150				155						160			
CAA	AAA	AGT	TTT	TTA	CAA	AAG	CAT	GCA	GAA	ATG	AAG	CTT	TTA	GAA	AAC		584
Gln	Lys	Ser	Phe	Leu	Gln	Lys	His	Ala	Glu	Met	Lys	Leu	Leu	Glu	Asn		
				165			170							175			
CCC	ATT	CAA	AAA	GTG	GCC	ATT	TTT	ATA	GGG	TGC	TTG	AGC	AAT	TAC	CAT		632
Pro	Ile	Gln	Lys	Val	Ala	Ile	Phe	Ile	Gly	Cys	Leu	Ser	Asn	Tyr	His		
				180			185							190			
TAC	CAG	CAA	GTG	GGG	GAA	AGC	TTG	TTG	TAT	ATT	TTA	GAA	AAA	CTC	AAC		680
Tyr	Gln	Gln	Val	Gly	Glu	Ser	Leu	Leu	Tyr	Ile	Leu	Glu	Lys	Leu	Asn		
					200					205					210		
ATT	CAA	GCG	ATC	ATC	CCT	AAG	CAA	GAA	TGC	TGC	TCA	GCG	CCT	GCG	TAT		728
Ile	Gln	Ala	Ile	Ile	Pro	Lys	Gln	Glu	Cys	Cys	Ser	Ala	Pro	Ala	Tyr		
					215				220					225			
TTT	ACC	GGC	GAT	AAA	GAC	ACC	ACG	CTT	TTT	TTA	GTG	AAA	AAA	AAC	ATA		776
Phe	Thr	Gly	Asp	Lys	Asp	Thr	Thr	Leu	Phe	Leu	Val	Lys	Lys	Asn	Ile		
				230				235						240			
GAA	TGG	TTT	GAA	AGC	TAT	TTA	GAT	AAA	GTG	GAT	GCG	ATC	ATT	GTG	CCT		824
Glu	Trp	Phe	Glu	Ser	Tyr	Leu	Asp	Lys	Val	Asp	Ala	Ile	Ile	Val	Pro		
				245				250						255			
GAA	GCC	ACA	TGC	GCT	ACA	TGC	TCA	TCA	ACG	ATT	ATT	ACA	AGG	TGT	TTT		872
Glu	Ala	Thr	Cys	Ala	Thr	Cys	Ser	Ser	Thr	Ile	Ile	Thr	Arg	Cys	Phe		
				260			265							270			
TGG	GCG	AAA	AAG	ATA	AGG	ATT	TGT	ATG	TGAAGCGCTT	GGAAAAAATC	ACGCCTA						926
Trp	Ala	Lys	Lys	Ile	Arg	Ile	Cys	Met									
				275			280										
AAATCTATCT	GGCGAGCGTG	TTTTTA															952

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met Asn Glu Asn Ile Asn Glu Asn Ile Phe Glu Glu Val Gly Asp Ala

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...899
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAGTTTGACG CGTATTTGCG TGGGGGCGAA AAACATTTC	GTAAAACGCT	ATG AAT	56
		Met Asn	
		1	
GAA AAT ATT AAT GAA AAT ATT TTT GAA GAA GTA GGG GAC GCT TGC GTT			104
Glu Asn Ile Asn Glu Asn Ile Phe Glu Glu Val Gly Asp Ala Cys Val			
5 10 15			
AAA TGC GCT AAG TGC GTG CCA GGC TGC ACC ATA TAC CGC ATT CAT AAA			152
Lys Cys Ala Lys Cys Val Pro Gly Cys Thr Ile Tyr Arg Ile His Lys			
20 25 30			
GAC GAG GCG ACT TCG CCT AGA GGC TTT TTA GAT TTG ATG CGC TTA AAC			200
Asp Glu Ala Thr Ser Pro Arg Gly Phe Leu Asp Leu Met Arg Leu Asn			
35 40 45 50			
GCT CAA AAC AAG CTC CAA TTA GAC ACG AAT TTA AAA CAC CTT TTA GAA			248
Ala Gln Asn Lys Leu Gln Leu Asp Thr Asn Leu Lys His Leu Leu Glu			
55 60 65			
ACT TGC TTT TTA TGC ACC GCT TGC GTG GAA ATT TGC CCT TTT CAT TTG			296
Thr Cys Phe Leu Cys Thr Ala Cys Val Glu Ile Cys Pro Phe His Leu			
70 75 80			
CCC ATA GAC ACC TTA ATA GAA AAA GCC AGA GAA AAA ATC GCT CAA AAG			344
Pro Ile Asp Thr Leu Ile Glu Lys Ala Arg Glu Lys Ile Ala Gln Lys			
85 90 95			
CAT GGC ATC GCT TGG TAT AAA AAA TCC TAT TTT TCC CTT TTA AAA AAC			392
His Gly Ile Ala Trp Tyr Lys Lys Ser Tyr Phe Ser Leu Leu Lys Asn			
100 105 110			
CGC AAA AAA ATG GAT AGG GTG TTT TCA ACT GCG CAT TTT TTA GCC CCT			440
Arg Lys Lys Met Asp Arg Val Phe Ser Thr Ala His Phe Leu Ala Pro			
115 120 125 130			
TGC GTT TTC AAG CAA GTA GGG GAT AGT TTA GAG CCT AGG GCG GTG TTT			488

```

AAT TTA CGC CAA AAA GAT GGG AAT TTG CCT AAT ATC AAC ACC TTA AAC      440
Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr Leu Asn
115                      120                      125                      130

TTT GTC AAA CAA ATC AAA AAA GAA CAC CCT AAT TTA TTC TTT AAT TTT      488
Phe Val Lys Gln Ile Lys Lys Glu His Pro Asn Leu Phe Phe Asn Phe
                      135                      140                      145

GAC AAC ATG TTC AAA CAA CCC CCT TTT AAT GAG AAT AAT TTT GAA AAT      536
Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe Glu Asn
                      150                      155                      160

TTT GAC AAT AGC GAT GAG GAA AAT TTT TAATGCAAAC CATTGATTTT GAAAAAT      590
Phe Asp Asn Ser Asp Glu Glu Asn Phe
                      165                      170

TTTCACAATA TTCCAAGCCC GGCCCA .                                     616

```

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```

Val Glu Lys Leu Pro Lys Lys Arg Val Ser Lys Thr Lys Ser Gln Lys
 1              5              10              15
Leu Ile His Ser Leu Thr Thr Gln Lys Asn Arg Ala Phe Leu Lys Lys
              20              25              30
Ile Ser Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys
              35              40              45
Lys Asn Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val
              50              55              60
Leu Val Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys
65              70              75              80
Ala Phe Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr
              85              90              95
Gln Ala Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu
              100              105              110
Leu Glu Asn Leu Arg Gln Lys Asp Gly Asn Leu Pro Asn Ile Asn Thr
              115              120              125
Leu Asn Phe Val Lys Gln Ile Lys Lys Glu His Pro Asn Leu Phe Phe
              130              135              140
Asn Phe Asp Asn Met Phe Lys Gln Pro Pro Phe Asn Glu Asn Asn Phe
145              150              155              160
Glu Asn Phe Asp Asn Ser Asp Glu Glu Asn Phe
              165              170

```

(2) INFORMATION FOR SEQ ID NO:397:

Leu Tyr Asn Phe Ile Gln Lys Phe
355 360

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...563
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

TAATGAGAAT TAAACGAAAT TGGATACAAT CAGCTTAAAA AGGATATAAA GTG GAA	56
Val Glu	
1	
AAA TTA CCT AAA AAA CGA GTT TCT AAA ACC AAA TCA CAA AAA CTT ATC	104
Lys Leu Pro Lys Lys Arg Val Ser Lys Thr Lys Ser Gln Lys Leu Ile	
5 10 15	
CAT AGC TTA ACC ACC CAA AAA AAC AGA GCC TTT CTC AAA AAA ATC AGC	152
His Ser Leu Thr Thr Gln Lys Asn Arg Ala Phe Leu Lys Lys Ile Ser	
20 25 30	
GCT AAT GAA ATG CTT TTA GAA TTA GAA AAA GGG GCG TTT AAA AAA AAT	200
Ala Asn Glu Met Leu Leu Glu Leu Glu Lys Gly Ala Phe Lys Lys Asn	
35 40 45 50	
GAA GCT TAT TTT ATT TCT GAT GAA GAA GAT AAA AAT TAT GTT TTG GTG	248
Glu Ala Tyr Phe Ile Ser Asp Glu Glu Asp Lys Asn Tyr Val Leu Val	
55 60 65	
CCA GAT AAC GTG ATC TCT CTT TTG GCA GAA AAC GCC AGA AAG GCT TTT	296
Pro Asp Asn Val Ile Ser Leu Leu Ala Glu Asn Ala Arg Lys Ala Phe	
70 75 80	
GAA GCC AGG CTT AGG GCG GAA TTA GAA AGG GAT ATT ATC ACC CAA GCG	344
Glu Ala Arg Leu Arg Ala Glu Leu Glu Arg Asp Ile Ile Thr Gln Ala	
85 90 95	
CCG ATT GAT TTT GAA GAC GTG CGC GAA GTT TCC TTG CAA CTA TTG GAA	392
Pro Ile Asp Phe Glu Asp Val Arg Glu Val Ser Leu Gln Leu Leu Glu	
100 105 110	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

```

Met Asp Phe Leu Glu Lys Val Leu Asp Asn Gln Val Thr Glu Ser Lys
 1           5           10           15
Glu Leu Val Arg Leu Tyr Asp Tyr Asp Leu Tyr Thr Leu Gly Glu Val
          20           25           30
Ala Asp Arg Met Arg Gln Asn Met His Gln Lys Ile Val Tyr Phe Asn
          35           40           45
Val Asn Arg His Leu Asn Pro Ser Asn Ile Cys Ala Asp Ala Cys Lys
          50           55           60
Phe Cys Ala Phe Ser Ala His Arg Lys Asn Pro Asn Pro Tyr Glu Met
65           70           75           80
Ser Leu Glu Glu Ile Leu Glu Lys Val Lys Asn Ser Tyr Asn Lys Gly
          85           90           95
Ile Lys Glu Val His Ile Val Ser Ala His Asn Pro Asn Tyr Ser Tyr
          100          105          110
Glu Trp Tyr Leu Lys Val Phe Glu Thr Ile Lys Gln Glu Met Pro Asn
          115          120          125
Leu His Leu Lys Ala Met Thr Ala Ala Glu Val His Phe Leu Ser Val
          130          135          140
Lys Phe Asn Lys Pro Phe Glu Leu Val Leu Glu Asp Met Leu Lys Ala
145          150          155          160
Gly Val Asp Ser Met Pro Gly Gly Gly Ala Glu Ile Phe Asp Glu Glu
          165          170          175
Ile Arg Arg Lys Ile Cys Asn Gly Lys Val Gly Ser Ser Arg Trp Leu
          180          185          190
Glu Ile His Ala Tyr Trp His Lys Leu Gly Lys Met Ser Asn Ala Thr
          195          200          205
Met Leu Phe Gly His Ile Glu Asn Lys Ile His Arg Ile Asp His Met
210          215          220
Leu Arg Ile Lys Lys Ile Gln Ser Pro Lys Asn Gln Val Glu Asn Lys
225          230          235          240
Glu Gly Gly Phe Asn Ala Phe Ile Pro Leu Leu Tyr Gln Lys Glu Asn
          245          250          255
Asn Tyr Leu Asn Val Glu Lys Ser Pro Ser Ala Ile Glu Ile Leu Lys
          260          265          270
Thr Ile Ala Ile Ser Arg Ile Leu Leu Asn Asn Ile Pro His Ile Lys
          275          280          285
Ala Tyr Trp Ala Thr Leu Gly Leu Asn Leu Ala Leu Val Ala Gln Glu
290          295          300
Phe Gly Ala Asn Asp Leu Asp Gly Thr Ile Glu Ile Glu Ser Ile Gln
305          310          315          320
Ser Ala Ala Gly Ala Lys Ser Arg His Gly Leu Glu Lys Glu Asp Leu
          325          330          335
Ile Phe Lys Ile Lys Asp Ala Gly Phe Val Ala Val Glu Arg Asp Ser
          340          345          350

```

GAT TCC ATG CCT GGT GGG GGG GCG GAG ATT TTT GAT GAA GAA ATC AGG	584
Asp Ser Met Pro Gly Gly Gly Ala Glu Ile Phe Asp Glu Glu Ile Arg	
165 170 175	
CGT AAA ATC TGT AAT GGT AAG GTG GGA TCT TCT CGG TGG TTA GAA ATC	632
Arg Lys Ile Cys Asn Gly Lys Val Gly Ser Ser Arg Trp Leu Glu Ile	
180 185 190	
CAT GCT TAT TGG CAC AAA TTA GGC AAA ATG AGT AAC GCT ACC ATG CTT	680
His Ala Tyr Trp His Lys Leu Gly Lys Met Ser Asn Ala Thr Met Leu	
195 200 205 210	
TTT GGG CAT ATT GAA AAT AAA ATC CAT CGC ATC GAT CAC ATG CTA AGA	728
Phe Gly His Ile Glu Asn Lys Ile His Arg Ile Asp His Met Leu Arg	
215 220 225	
ATC AAA AAA ATC CAA AGC CCT AAA AAT CAA GTA GAA AAC AAA GAA GGG	776
Ile Lys Lys Ile Gln Ser Pro Lys Asn Gln Val Glu Asn Lys Glu Gly	
230 235 240	
GGT TTT AAC GCT TTT ATC CCC TTG TTG TAT CAA AAA GAA AAC AAT TAT	824
Gly Phe Asn Ala Phe Ile Pro Leu Leu Tyr Gln Lys Glu Asn Asn Tyr	
245 250 255	
TTG AAT GTG GAA AAA TCC CCC AGT GCG ATA GAA ATC TTA AAA ACC ATC	872
Leu Asn Val Glu Lys Ser Pro Ser Ala Ile Glu Ile Leu Lys Thr Ile	
260 265 270	
GCC ATA TCT CGC ATT CTT TTA AAC AAT ATC CCT CAC ATT AAA GCT TAT	920
Ala Ile Ser Arg Ile Leu Leu Asn Asn Ile Pro His Ile Lys Ala Tyr	
275 280 285 290	
TGG GCG ACT TTG GGC TTG AAT TTG GCT TTA GTG GCT CAA GAA TTT GGC	968
Trp Ala Thr Leu Gly Leu Asn Leu Ala Leu Val Ala Gln Glu Phe Gly	
295 300 305	
GCT AAC GAT TTA GAC GGC ACG ATA GAG ATA GAG AGC ATT CAA AGC GCG	1016
Ala Asn Asp Leu Asp Gly Thr Ile Glu Ile Glu Ser Ile Gln Ser Ala	
310 315 320	
GCA GGC GCA AAG AGC CGG CAT GGT TTA GAA AAA GAA GAT TTG ATA TTT	1064
Ala Gly Ala Lys Ser Arg His Gly Leu Glu Lys Glu Asp Leu Ile Phe	
325 330 335	
AAA ATC AAG GAC GCT GGT TTT GTT GCG GTA GAA AGG GAT AGT TTG TAT	1112
Lys Ile Lys Asp Ala Gly Phe Val Ala Val Glu Arg Asp Ser Leu Tyr	
340 345 350	
AAT TTT ATA CAG AAA TTT TAATAATTTT TAGCGTTTTT AAGAATGATT AGTTATAA	1168
Asn Phe Ile Gln Lys Phe	
355 360	
TAACGCTACT AACAA	1183

(2) INFORMATION FOR SEQ ID NO:394:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1130
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

ATCTAAAAAT GCTACAATGT TTATCTTTAA AACGAAAGGG CAATTTAACC	ATG GAC	56
	Met Asp	
	1	
TTT TTA GAA AAA GTA TTA GAC AAT CAA GTT ACT GAA AGT AAA GAA TTG		104
Phe Leu Glu Lys Val Leu Asp Asn Gln Val Thr Glu Ser Lys Glu Leu		
5 10 15		
GTC AGG CTT TAT GAT TAT GAT TTA TAC ACG CTA GGG GAA GTA GCG GAT		152
Val Arg Leu Tyr Asp Tyr Asp Leu Tyr Thr Leu Gly Glu Val Ala Asp		
20 25 30		
CGC ATG CGC CAA AAC ATG CAC CAA AAA ATC GTG TAT TTT AAT GTC AAT		200
Arg Met Arg Gln Asn Met His Gln Lys Ile Val Tyr Phe Asn Val Asn		
35 40 45 50		
AGG CAT TTA AAC CCT AGC AAT ATT TGC GCG GAC GCT TGC AAA TTT TGC		248
Arg His Leu Asn Pro Ser Asn Ile Cys Ala Asp Ala Cys Lys Phe Cys		
55 60 65		
GCT TTT TCA GCC CAC AGA AAA AAC CCA AAC CCT TAT GAA ATG AGC TTA		296
Ala Phe Ser Ala His Arg Lys Asn Pro Asn Pro Tyr Glu Met Ser Leu		
70 75 80		
GAA GAA ATC CTA GAA AAG GTT AAA AAC TCC TAC AAC AAG GGG ATT AAA		344
Glu Glu Ile Leu Glu Lys Val Lys Asn Ser Tyr Asn Lys Gly Ile Lys		
85 90 95		
GAA GTC CAT ATC GTG AGC GCT CAT AAC CCT AAT TAC TCC TAT GAA TGG		392
Glu Val His Ile Val Ser Ala His Asn Pro Asn Tyr Ser Tyr Glu Trp		
100 105 110		
TAT TTA AAG GTG TTT GAA ACC ATC AAG CAA GAA ATG CCT AAC TTG CAT		440
Tyr Leu Lys Val Phe Glu Thr Ile Lys Gln Glu Met Pro Asn Leu His		
115 120 125 130		
TTA AAG GCC ATG ACC GCT GCA GAA GTG CAT TTT TTA AGC GTT AAA TTC		488
Leu Lys Ala Met Thr Ala Ala Glu Val His Phe Leu Ser Val Lys Phe		
135 140 145		
AAC AAA CCT TTT GAA TTG GTG CTA GAA GAC ATG CTC AAA GCC GGG GTG		536
Asn Lys Pro Phe Glu Leu Val Leu Glu Asp Met Leu Lys Ala Gly Val		
150 155 160		

```

TTA GAA GAC GCT ATT AAT TTT GGG CAA GAA TTA GAA AAC GCT AAC CCT      392
Leu Glu Asp Ala Ile Asn Phe Gly Gln Glu Leu Glu Asn Ala Asn Pro
    100                      105                      110

AAT TAC CAA CAA AAA ATC GCT AAC GCT ACC GGC TTA GCC CTT AAG AAT      440
Asn Tyr Gln Gln Lys Ile Ala Asn Ala Thr Gly Leu Ala Leu Lys Asn
    115                      120                      125                      130

AAA AAA GAA AAA GGA TAGAATTGGA TTTTITAGAG ATTGTAGGAC AAGTCCCTTT A    496
Lys Lys Glu Lys Gly
                      135

AAAGGAGAGG TA                                                              508

```

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

```

Met Gly Asn Leu Thr Tyr Tyr Ala Tyr Met Tyr Leu Ile Leu Phe Val
 1           5           10           15
Cys Leu Leu Pro Val Leu Leu Met Gly Leu Val Trp Arg Leu Thr Arg
    20           25           30
Pro Pro Leu Lys Gln Asn Ile Pro Asn Lys Ser Leu Ser Leu Glu Asn
    35           40           45
Leu Asn Glu Gln Ile Lys Asn Leu Lys Ser Val Pro Ala Leu Glu Lys
    50           55           60
Leu Lys Asn Asp Phe Asn Glu Arg Phe Lys Ile Cys Pro Lys Asp Lys
    65           70           75           80
Glu Thr Leu Trp Leu Glu Thr Ile Gln Lys Leu Val Ala Ser Glu Phe
    85           90           95
Phe Glu Leu Glu Asp Ala Ile Asn Phe Gly Gln Glu Leu Glu Asn Ala
    100          105          110
Asn Pro Asn Tyr Gln Gln Lys Ile Ala Asn Ala Thr Gly Leu Ala Leu
    115          120          125
Lys Asn Lys Lys Glu Lys Gly
    130          135

```

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

130		135		140	
Leu	Lys	Ala	Ile	Glu	Thr
145		150		155	
Arg	Thr	Asp	His	Ile	Ala
		165		170	
Gly	Phe				

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...455
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

ATTGAAGCGA	GTAACGCTTA	TTATAAAAAA	CGCTTATAAA	TCTTATCAAC	ATG GGC	56
					Met Gly	
					1	
AAT TTG ACT	TAT TAC GCT	TAC ATG TAT	TTG ATC CTC	TTT GTA TGC	TTG	104
Asn Leu Thr	Tyr Tyr Ala	Tyr Met Tyr	Leu Ile Leu	Phe Val Cys	Leu	
5		10		15		
CTG CCT GTG	TTA TTA ATG	GGG CTT GTT	TGG AGG CTT	ACT CGC CCC	CCC	152
Leu Pro Val	Leu Leu Met	Gly Leu Val	Trp Arg Leu	Thr Arg Pro	Pro	
20		25		30		
TTA AAG CAA	AAT ATT CCT	AAT AAA AGC	CTC TCT TTA	GAA AAT TTA	AAC	200
Leu Lys Gln	Asn Ile Pro	Asn Lys Ser	Leu Ser Leu	Glu Asn Leu	Asn	
35		40		45	50	
GAA CAA ATC	AAA AAC CTT	AAA AGC GTA	CCA GCT TTA	GAA AAA CTG	AAA	248
Glu Gln Ile	Lys Asn Leu	Lys Ser Val	Pro Ala Leu	Glu Lys Leu	Lys	
	55		60		65	
AAC GAC TTC	AAT GAG CGT	TTT AAA ATT	TGC CCC AAA	GAT AAA GAA	ACT	296
Asn Asp Phe	Asn Glu Arg	Phe Lys Ile	Cys Pro Lys	Asp Lys Glu	Thr	
	70		75		80	
CTG TGG TTA	GAA ACG ATC	CAA AAA TTA	GTC GCT TCA	GAA TTT TTT	GAA	344
Leu Trp Leu	Glu Thr Ile	Gln Lys Leu	Val Ala Ser	Glu Phe Phe	Glu	
85		90		95		

95	100	105	
TTT TTA GGG GAT TTG CCT AAA ACT TTT ATC GTG GGG CTT GTG CCT TTT			448
Phe Leu Gly Asp Leu Pro Lys Thr Phe Ile Val Gly Leu Val Pro Phe			
110	115	120	
GTG ATA GGG AGC GAG ACC ACT TTC AAG CTT TCA AGC AAA ATT TTA AAC			496
Val Ile Gly Ser Glu Thr Thr Phe Lys Leu Ser Ser Lys Ile Leu Asn			
125	130	135	
GCT TTA GAA ACC GCC TTA AAA GCC ATA GAA ACC CAA CTC AAC GCA TGG			544
Ala Leu Glu Thr Ala Leu Lys Ala Ile Glu Thr Gln Leu Asn Ala Trp			
140	145	150	155
GGG GTT AAA ATG CAA CGC ACC GAT CAT ATC GCT TTA GAA TGT ATC GCT			592
Gly Val Lys Met Gln Arg Thr Asp His Ile Ala Leu Glu Cys Ile Ala			
160	165	170	
GAA CTT TCT TAT AAG GGT TTT TGAATTGGTT TTTGTTTTTC TTTTAAATG CGTT			647
Glu Leu Ser Tyr Lys Gly Phe			
175			
AATGAAGAAA CAAGCCTGAA TTTTACGCCC CTTTGTAGAGC GAATGGCATG CAATTTGCAA			707
GCGCGTTTTT ATA			720

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met	Ser	Gln	Lys	Ile	Leu	Ile	Leu	Gly	Ile	Gly	Asn	Ile	Leu	Phe	Gly
1				5				10					15		
Asp	Glu	Gly	Ile	Gly	Val	His	Leu	Ala	His	Tyr	Leu	Lys	Lys	Asn	Phe
		20						25					30		
Ser	Phe	Phe	Pro	Ser	Val	Asp	Ile	Ile	Asp	Gly	Gly	Thr	Met	Ala	Gln
		35					40					45			
Gln	Leu	Ile	Pro	Leu	Ile	Thr	Ser	Tyr	Glu	Lys	Val	Leu	Ile	Leu	Asp
	50					55					60				
Cys	Val	Ser	Ala	Glu	Gly	Val	Glu	Ile	Gly	Ser	Val	Tyr	Ala	Phe	Asp
65				70					75					80	
Phe	Lys	Asp	Ala	Pro	Lys	Glu	Ile	Thr	Trp	Ala	Gly	Ser	Ala	His	Glu
			85					90						95	
Val	Glu	Met	Leu	His	Thr	Leu	Arg	Leu	Thr	Glu	Phe	Leu	Gly	Asp	Leu
		100						105					110		
Pro	Lys	Thr	Phe	Ile	Val	Gly	Leu	Val	Pro	Phe	Val	Ile	Gly	Ser	Glu
		115					120					125			
Thr	Thr	Phe	Lys	Leu	Ser	Ser	Lys	Ile	Leu	Asn	Ala	Leu	Glu	Thr	Ala

```

      530              535              540
Ile His Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp
545              550              555              560
Phe Lys Gly Gln Ser Leu Asn Glu Phe Lys Val Glu Pro Asn Phe Ala
      565              570              575
Lys Phe

```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 80...613
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```

ATATGGTGTT TTTCCATTCT ATCAGGTATG AAAGTTCGGG GCGCGATTCT ATGATTAATG      60
GCTATGGTTA TACCAAAGA ATG AGT CAA AAA ATC CTA ATT CTA GGT ATT GGC      112
      Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly
              1              5              10

AAT ATC CTT TTT GGC GAT GAA GGG ATT GGG GTG CAT TTA GCC CAC TAC      160
Asn Ile Leu Phe Gly Asp Glu Gly Ile Gly Val His Leu Ala His Tyr
              15              20              25

CTC AAA AAA AAT TTT TCT TTT TTC CCT AGC GTG GAT ATT ATA GAT GGG      208
Leu Lys Lys Asn Phe Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly
              30              35              40

GGG ACA ATG GCC CAG CAG CTC ATT CCT TTA ATC ACT TCG TAT GAA AAG      256
Gly Thr Met Ala Gln Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys
              45              50              55

GTT TTG ATT TTG GAT TGC GTG AGC GCT GAA GGC GTT GAG ATA GGA TCA      304
Val Leu Ile Leu Asp Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser
        60              65              70              75

GTC TAT GCT TTT GAT TTT AAG GAC GCT CCT AAA GAA ATC ACA TGG GCT      352
Val Tyr Ala Phe Asp Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala
              80              85              90

GGG AGC GCT CAT GAA GTG GAA ATG CTA CAC ACT TTA AGG CTC ACG GAG      400
Gly Ser-Ala His Glu Val Glu Met Leu His Thr Leu Arg Leu Thr Glu

```

```

Asn Met Ala Leu Leu Phe His Asp His Val Val His Phe Tyr Thr Leu
      100      105      110
His Gly Leu Asp Trp Cys Asp Ile Met Ser Ala Leu Lys Ala Asp Pro
      115      120      125
Ile Gln Ala Ala Lys Leu Ser Phe Lys Tyr Ser Pro Tyr Pro Ile Asn
      130      135      140
Thr Gly Ala Gly Glu Leu Lys Ala Val Gln Lys Arg Leu Ser Asp Phe
145      150      155      160
Ala Lys Ser Gly Ser Leu Gly Pro Phe Ser Asn Gly Tyr Tyr Gly His
      165      170      175
Lys Thr Tyr Arg Leu Ser Pro Glu Gln Asn Leu Ile Val Leu Ser His
      180      185      190
Tyr Leu Lys Leu Leu Glu Ile Gln Arg Glu Ala Ala Lys Met Thr Ala
      195      200      205
Ile Phe Gly Ala Lys Gln Pro His Pro Gln Ser Leu Thr Val Gly Gly
      210      215      220
Val Thr Ser Val Met Asp Ile Leu Asp Pro Thr Arg Leu Ala Glu Trp
225      230      235      240
Lys Ser Lys Phe Glu Val Val Ala Asn Phe Ile Asn His Ala Tyr Tyr
      245      250      255
Pro Asp Leu Val Met Ala Gly Glu Met Phe Ala Asn Glu Gln Ser Val
      260      265      270
Ile Lys Gly Cys Gly Leu Arg Asn Phe Ile Ala Tyr Glu Glu Val Leu
      275      280      285
Leu Gly Arg Asp Lys Tyr Leu Leu Ser Ser Gly Val Val Leu Asp Gly
      290      295      300
Asp Ile Ser Lys Leu His Pro Ile Asp Glu Ser Leu Ile Lys Glu Glu
305      310      315      320
Val Thr His Ser Trp Tyr Gln Tyr Glu Asp Thr Lys Glu Val Gln Leu
      325      330      335
His Pro Tyr Asp Gly Gln Thr Asn Pro His Tyr Thr Gly Leu Lys Asp
      340      345      350
Gly Glu Ser Val Gly Ile Glu Asn Lys Ile Ile Pro Ala Lys Val Leu
      355      360      365
Asp Thr Lys Asn Lys Tyr Ser Trp Ile Lys Ser Pro Arg Tyr Asp Ser
      370      375      380
Lys Pro Met Glu Val Gly Pro Leu Ser Ser Val Val Val Gly Leu Ala
385      390      395      400
Ala Lys Asn Pro Tyr Val Thr Glu Val Ala Thr Lys Phe Leu Lys Asp
      405      410      415
Thr Lys Leu Pro Leu Glu Ala Leu Phe Ser Thr Leu Gly Arg Thr Ala
      420      425      430
Ala Arg Cys Ile Glu Ala Lys Thr Ile Ala Asp Asn Gly Leu Leu Ala
      435      440      445
Phe Asp Ala Leu Val Glu Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala
      450      455      460
Pro Tyr His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly
465      470      475      480
Gln Val Pro Arg Gly Met Leu Ser His Trp Val Arg Ile Lys Asn Gly
      485      490      495
Val Val Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly
      500      505      510
Pro Arg Asp Ser Gln Asn Gln Arg Gly Ala Tyr Glu Met Ser Leu Ile
      515      520      525
Gly Thr Lys Ile Ala Asp Leu Thr Gln Pro Leu Glu Ile Ile Arg Thr

```

CAC ATT GAT AAA AAT CAA GAA TAT AAA GGG CGC TAC ATT GGT CAA GTG 1496
His Ile Asp Lys Asn Gln Glu Tyr Lys Gly Arg Tyr Ile Gly Gln Val
470 475 480

CCA AGG GGC ATG CTA AGC CAT TGG GTG CGT ATT AAA AAC GGC GTG GTG 1544
Pro Arg Gly Met Leu Ser His Trp Val Arg Ile Lys Asn Gly Val Val
485 490 495

GAA AAT TAT CAA GCG GTG GTG CCT TCT ACT TGG AAT GCA GGG CCT AGA 1592
Glu Asn Tyr Gln Ala Val Val Pro Ser Thr Trp Asn Ala Gly Pro Arg
500 505 510

GAT TCT CAA AAT CAA AGG GGG GCT TAT GAA ATG AGC TTG ATT GGC ACT 1640
Asp Ser Gln Asn Gln Arg Gly Ala Tyr Glu Met Ser Leu Ile Gly Thr
515 520 525 530

AAA ATC GCT GAT TTA ACC CAG CCT TTA GAA ATC ATT AGG ACT ATC CAT 1688
Lys Ile Ala Asp Leu Thr Gln Pro Leu Glu Ile Ile Arg Thr Ile His
535 540 545

TCT TTT GAC CCA TGC ATC GCA TGC TCG GTG CAT GTG ATG GAT TTT AAA 1736
Ser Phe Asp Pro Cys Ile Ala Cys Ser Val His Val Met Asp Phe Lys
550 555 560

GGG CAG TCT TTA AAC GAG TTT AAA GTA GAG CCT AAT TTC GCT AAA TTC T 1785
Gly Gln Ser Leu Asn Glu Phe Lys Val Glu Pro Asn Phe Ala Lys Phe
565 570 575

AAAAAGGGTT ACGCATGGAT AAAATGAATA AGGTCGTTTT ACACAAAGAA TA 1837

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Ser Lys Lys Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His
1 5 10 15
Leu Arg Ile Glu Val Ile Val Asp Asp Asn Val Ile Thr Asp Ala
20 25 30
Phe Ser Ser Ser Thr Leu Phe Arg Gly Leu Glu Thr Ile Ile Lys Gly
35 40 45
Arg Asp Pro Arg Asp Ala Gly Phe Ile Ala Gln Arg Ile Cys Gly Val
50 55 60
Cys Thr Tyr Ser His Tyr Lys Ala Gly Ile Thr Ala Val Glu Asn Ala
65 70 75 80
Leu Gly Ile Thr Pro Pro Leu Asn Ala Gln Leu Val Arg Ser Leu Met
85 90 95

AAG TTT GAA GTG GTG GCC AAT TTC ATC AAC CAT GCT TAC TAC CCT GAT	824
Lys Phe Glu Val Val Ala Asn Phe Ile Asn His Ala Tyr Tyr Pro Asp	
245 250 255	
TTG GTG ATG GCA GGC GAA ATG TTC GCT AAC GAA CAA TCC GTT ATC AAA	872
Leu Val Met Ala Gly Glu Met Phe Ala Asn Glu Gln Ser Val Ile Lys	
260 265 270	
GGC TGT GGC TTA AGG AAT TTT ATC GCT TAT GAA GAA GTG CTG CTT GGG	920
Gly Cys Gly Leu Arg Asn Phe Ile Ala Tyr Glu Glu Val Leu Leu Gly	
275 280 285 290	
AGG GAT AAA TAC CTT TTG AGT AGT GGG GTG GTG CTT GAT GGG GAT ATT	968
Arg Asp Lys Tyr Leu Leu Ser Ser Gly Val Val Leu Asp Gly Asp Ile	
295 300 305	
TCT AAA TTA CAC CCC ATT GAT GAA AGT TTG ATT AAA GAA GAA GTT ACG	1016
Ser Lys Leu His Pro Ile Asp Glu Ser Leu Ile Lys Glu Glu Val Thr	
310 315 320	
CAT TCT TGG TAT CAA TAC GAA GAC ACT AAA GAA GTG CAA CTC CAC CCT	1064
His Ser Trp Tyr Gln Tyr Glu Asp Thr Lys Glu Val Gln Leu His Pro	
325 330 335	
TAT GAC GGG CAA ACG AAC CCG CAT TAT ACC GGT TTA AAA GAC GGC GAG	1112
Tyr Asp Gly Gln Thr Asn Pro His Tyr Thr Gly Leu Lys Asp Gly Glu	
340 345 350	
AGC GTG GGG ATT GAA AAT AAA ATC ATC CCT GCT AAA GTG CTT GAC ACT	1160
Ser Val Gly Ile Glu Asn Lys Ile Ile Pro Ala Lys Val Leu Asp Thr	
355 360 365 370	
AAA AAT AAA TAT TCT TGG ATA AAA TCG CCC AGA TAC GAT AGT AAG CCC	1208
Lys Asn Lys Tyr Ser Trp Ile Lys Ser Pro Arg Tyr Asp Ser Lys Pro	
375 380 385	
ATG GAA GTA GGT CCT TTA AGT TCC GTA GTG GTA GGT TTA GCG GCG AAA	1256
Met Glu Val Gly Pro Leu Ser Ser Val Val Val Gly Leu Ala Ala Lys	
390 395 400	
AAC CCT TAT GTT ACT GAA GTG GCT ACG AAG TTT TTA AAA GAC ACT AAA	1304
Asn Pro Tyr Val Thr Glu Val Ala Thr Lys Phe Leu Lys Asp Thr Lys	
405 410 415	
CTG CCT TTA GAG GCG TTG TTT TCA ACG CTT GGG CGA ACA GCT GCA AGG	1352
Leu Pro Leu Glu Ala Leu Phe Ser Thr Leu Gly Arg Thr Ala Ala Arg	
420 425 430	
TGT ATT GAA GCT AAA ACG ATC GCT GAT AAT GGC CTT TTG GCG TTT GAT	1400
Cys Ile Glu Ala Lys Thr Ile Ala Asp Asn Gly Leu Leu Ala Phe Asp	
435 440 445 450	
GCG TTA GTG GAA AAT CTA AAA AGC GAT CAA AGC ACT TGT GCT CCT TAT	1448
Ala Leu Val Glu Asn Leu Lys Ser Asp Gln Ser Thr Cys Ala Pro Tyr	
455 460 465	

Ile	Glu	Val	Ile	Val	Asp	Asp	Asp	Asn	Val	Ile	Thr	Asp	Ala	Phe	Ser		
20						25					30						
TCT	TCT	ACG	CTT	TTT	AGG	GGG	CTA	GAA	ACC	ATT	ATT	AAA	GGC	AGA	GAT	200	
Ser	Ser	Thr	Leu	Phe	Arg	Gly	Leu	Glu	Thr	Ile	Ile	Lys	Gly	Arg	Asp	50	
35					40					45							
CCA	CGA	GAT	GCA	GGC	TTC	ATC	GCT	CAA	AGG	ATT	TGC	GGG	GTA	TGC	ACT	248	
Pro	Arg	Asp	Ala	Gly	Phe	Ile	Ala	Gln	Arg	Ile	Cys	Gly	Val	Cys	Thr	65	
				55					60								
TAT	TCG	CAT	TAT	AAG	GCC	GGT	ATC	ACG	GCG	GTA	GAA	AAC	GCT	CTA	GGC	296	
Tyr	Ser	His	Tyr	Lys	Ala	Gly	Ile	Thr	Ala	Val	Glu	Asn	Ala	Leu	Gly	80	
			70					75									
ATC	ACT	CCC	CCA	TTA	AAC	GCG	CAA	TTG	GTG	CGA	TCT	TTG	ATG	AAC	ATG	344	
Ile	Thr	Pro	Pro	Leu	Asn	Ala	Gln	Leu	Val	Arg	Ser	Leu	Met	Asn	Met	95	
		85					90										
GCG	CTG	CTT	TTT	CAT	GAC	CAT	GTG	GTG	CAT	TTC	TAT	ACT	TTG	CAT	GGG	392	
Ala	Leu	Leu	Phe	His	Asp	His	Val	Val	His	Phe	Tyr	Thr	Leu	His	Gly	110	
	100					105											
CTT	GAT	TGG	TGC	GAT	ATC	ATG	AGC	GCT	TTA	AAA	GCC	GAT	CCC	ATT	CAA	440	
Leu	Asp	Trp	Cys	Asp	Ile	Met	Ser	Ala	Leu	Lys	Ala	Asp	Pro	Ile	Gln	130	
	115				120					125							
GCG	GCA	AAA	CTT	TCT	TTT	AAA	TAC	AGC	CCT	TAC	CCT	ATT	AAT	ACC	GGT	488	
Ala	Ala	Lys	Leu	Ser	Phe	Lys	Tyr	Ser	Pro	Tyr	Pro	Ile	Asn	Thr	Gly	145	
				135					140								
GCC	GGT	GAA	TTA	AAA	GCG	GTT	CAA	AAA	CGC	TTG	AGC	GAT	TTC	GCT	AAA	536	
Ala	Gly	Glu	Leu	Lys	Ala	Val	Gln	Lys	Arg	Leu	Ser	Asp	Phe	Ala	Lys	160	
			150					155									
AGC	GGA	TCT	TTG	GGG	CCT	TTC	AGT	AAC	GGC	TAT	TAC	GGG	CAT	AAA	ACT	584	
Ser	Gly	Ser	Leu	Gly	Pro	Phe	Ser	Asn	Gly	Tyr	Tyr	Gly	His	Lys	Thr	175	
		165					170										
TAT	CGT	TTA	AGT	CCG	GAG	CAA	AAT	TTA	ATC	GTC	TTA	AGC	CAC	TAC	CTC	632	
Tyr	Arg	Leu	Ser	Pro	Glu	Gln	Asn	Leu	Ile	Val	Leu	Ser	His	Tyr	Leu	190	
	180					185											
AAG	CTT	TTA	GAA	ATC	CAA	AGG	GAA	GCG	GCG	AAA	ATG	ACC	GCT	ATT	TTT	680	
Lys	Leu	Leu	Glu	Ile	Gln	Arg	Glu	Ala	Ala	Lys	Met	Thr	Ala	Ile	Phe	210	
	195				200					205							
GGG	GCC	AAA	CAG	CCT	CAC	CCA	CAA	AGC	CTA	ACG	GTG	GGG	GGT	GTT	ACG	728	
Gly	Ala	Lys	Gln	Pro	His	Pro	Gln	Ser	Leu	Thr	Val	Gly	Gly	Val	Thr	225	
				215					220								
AGT	GTT	ATG	GAT	ATA	TTG	GAT	CCG	ACG	AGA	TTG	GCT	GAA	TGG	AAG	AGC	776	
Ser	Val	Met	Asp	Ile	Leu	Asp	Pro	Thr	Arg	Leu	Ala	Glu	Trp	Lys	Ser	240	
			230					235									

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

Met Val Met Arg Pro Gly Val Leu Gln Val Gly Ala Met Tyr Ala Asn
 1             5             10             15
Gly Val Gly Ile Gln Thr Asn Arg Leu Lys Ala Ala Arg Tyr Tyr Glu
      20             25             30
Trp Val Ala Ala Gly Ala Met Arg Pro Leu Ala Arg Ile Trp Leu Arg
      35             40             45
Cys Met Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu
      50             55             60
Cys Asn Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala
65             70             75             80
Ile Ile Trp Gly Gly Cys Leu Leu Thr Glu Val Gly Ser Gln Lys Ile
      85             90             95
Ile Thr Lys Arg
      100

```

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1784
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```

CGCATGCGCT CCTTTCTAAA GCGATCAAAA ACAAAGAGTA AGGGATTAAC  ATG TCA      56
                                     Met Ser
                                     1

AAA AAA ATC GTA GTC GAT CCT ATC ACT AGG ATT GAG GGG CAT TTA AGG      104
Lys Lys Ile Val Val Asp Pro Ile Thr Arg Ile Glu Gly His Leu Arg
      5             10             15

ATT GAA GTG ATC GTA GAT GAT GAT AAC GTG ATC ACT GAT GCG TTT TCT      152

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...350
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

AAAGGGCGAT TATCAAGGGG CTTTCAAGCT TTTTCCCAA TCGTGCGATA	ATG GTA	56
	Met Val	
	1	
ATG CGG CCG GGT GTT TTG CAA GTG GGG GCG ATG TAT GCT AAT GGG GTA		104
Met Arg Pro Gly Val Leu Gln Val Gly Ala Met Tyr Ala Asn Gly Val		
5 10 15		
GGG ATC CAA ACC AAC AGA TTA AAA GCC GCT CGC TAT TAT GAA TGG GTT		152
Gly Ile Gln Thr Asn Arg Leu Lys Ala Ala Arg Tyr Tyr Glu Trp Val		
20 25 30		
GCA GCG GGG GCG ATG CGA CCG CTT GCG CGA ATC TGG CTC AGA TGT ATG		200
Ala Ala Gly Ala Met Arg Pro Leu Ala Arg Ile Trp Leu Arg Cys Met		
35 40 45 50		
AAA ACA AGA AAA ATG CGG ATT CAA ACG ATA AAG AAA ACG CTT TGC AAT		248
Lys Thr Arg Lys Met Arg Ile Gln Thr Ile Lys Lys Thr Leu Cys Asn		
55 60 65		
TGT ATG CGG TGG CTT GTC AAG GGG GGG ATA TGC TCG CAT GCA ATA ATT		296
Cys Met Arg Trp Leu Val Lys Gly Gly Ile Cys Ser His Ala Ile Ile		
70 75 80		
TGG GGT GGA TGT TTG CTA ACG GAA GTG GGG TCC CAA AAG ATT ATT ACA		344
Trp Gly Gly Cys Leu Leu Thr Glu Val Gly Ser Gln Lys Ile Ile Thr		
85 90 95		
AAG CGA TAAGTTATTA TAAATTTTCA TGCGAGAATG GGAATGATAT GGGGTGTTAT AA		402
Lys Arg		
100		
T		403

(2) INFORMATION FOR SEQ ID NO:386:

```

Leu Met Arg Leu Asp Lys Phe Lys Ile Lys Lys Ala Gln Asn Leu Leu
      130                      135                      140

GAC GCT ATT TTA AAA AGC AAA AAC CCT CCC TTA TGG CGT TTG ATT AAC      600
Asp Ala Ile Leu Lys Ser Lys Asn Pro Pro Leu Trp Arg Leu Ile Asn
      145                      150                      155

GCT TTA GGG ATT GAG CAT ATT GGT AAG GGA GCG AGT AAA ACG CTG GCC      648
Ala Leu Gly Ile Glu His Ile Gly Lys Gly Ala Ser Lys Thr Leu Ala
      160                      165                      170                      175

AAA TAC GGC TTA AAT GTG TTA GAA AAA AGC GAA SCG AGT TTT TAGAAATGG      699
Lys Tyr Gly Leu Asn Val Leu Glu Lys Ser Glu Xaa Ser Phe
      180                      185

AAGGCTTTGG GGTGGAAATG GCGCGCTCTT TAGTCAATTT TTATGCGAGC AATCAA      755

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

Met Ile Asn Arg Ala Thr Leu His Asn Tyr Ser Glu Ile Glu Lys Lys
 1           5           10           15
Asn Ile Met Leu Ser Asp Arg Val Val Val Ile Arg Ser Gly Asp Val
      20           25           30
Ile Pro Lys Ile Ile Lys Pro Leu Glu Ser Tyr Arg Asp Gly Ser Gln
      35           40           45
His Lys Ile Glu Arg Pro Lys Val Cys Pro Ile Cys Ser His Glu Leu
      50           55           60
Leu Cys Glu Glu Ile Phe Thr Tyr Cys Gln Asn Leu Asn Cys Pro Ala
      65           70           75           80
Arg Leu Lys Glu Ser Leu Ile His Phe Ala Ser Lys Asp Ala Leu Asn
      85           90           95
Ile Gln Gly Leu Gly Asp Lys Val Ile Glu Gln Leu Phe Glu Glu Lys
      100          105          110
Leu Ile Phe Asn Ala Leu Asp Leu Tyr Ala Leu Lys Leu Glu Asp Leu
      115          120          125
Met Arg Leu Asp Lys Phe Lys Ile Lys Lys Ala Gln Asn Leu Leu Asp
      130          135          140
Ala Ile Leu Lys Ser Lys Asn Pro Pro Leu Trp Arg Leu Ile Asn Ala
      145          150          155          160
Leu Gly Ile Glu His Ile Gly Lys Gly Ala Ser Lys Thr Leu Ala Lys
      165          170          175
Tyr Gly Leu Asn Val Leu Glu Lys Ser Glu Xaa Ser Phe
      180          185

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 124...690
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

TTGCGCTTAT AAATTCCCGG CTTAGAAAA ACACACCAAA ATTGTAGGAG TCATTAACCA      60
AGTGGGGCGC ASSGGGCGAT CACACCGGTC GCTCTTTTAG AGCCTGTGGA AATTGCTGGA      120
GCT ATG ATT AAT AGA GCG ACC TTA CAC AAT TAT TCT GAA ATT GAA AAA      168
  Met Ile Asn Arg Ala Thr Leu His Asn Tyr Ser Glu Ile Glu Lys
    1             5             10             15

AAG AAT ATC ATG CTC AGT GAT AGG GTC GTT GTC ATT AGA AGC GGC GAT      216
Lys Asn Ile Met Leu Ser Asp Arg Val Val Ile Arg Ser Gly Asp
          20             25             30

GTG ATC CCT AAA ATC ATC AAG CCT TTA GAA TCT TAT AGA GAC GGC TCG      264
Val Ile Pro Lys Ile Ile Lys Pro Leu Glu Ser Tyr Arg Asp Gly Ser
          35             40             45

CAA CAT AAA ATT GAA CGC CCC AAG GTT TGC CCT ATA TGT TCG CAT GAG      312
Gln His Lys Ile Glu Arg Pro Lys Val Cys Pro Ile Cys Ser His Glu
          50             55             60

CTT TTG TGC GAA GAG ATT TTT ACT TAT TGT CAA AAC CTT AAT TGC CCG      360
Leu Leu Cys Glu Glu Ile Phe Thr Tyr Cys Gln Asn Leu Asn Cys Pro
          65             70             75

GCA AGG TTG AAA GAA AGC TTG ATT CAT TTC GCT TCT AAA GAC GCT TTA      408
Ala Arg Leu Lys Glu Ser Leu Ile His Phe Ala Ser Lys Asp Ala Leu
          80             85             90             95

AAC ATT CAA GGC TTG GGC GAT AAA GTC ATA GAG CAA CTT TTT GAA GAA      456
Asn Ile Gln Gly Leu Gly Asp Lys Val Ile Glu Gln Leu Phe Glu Glu
          100            105            110

AAG CTC ATT TTT AAC GCT CTG GAT TTG TAT GCT TTA AAA TTA GAA GAT      504
Lys Leu Ile Phe Asn Ala Leu Asp Leu Tyr Ala Leu Lys Leu Glu Asp
          115            120            125

TTA ATG CGG CTA GAC AAA TTT AAA ATT AAA AAA GCT CAA AAT CTA TTA      552

```

1540 1545 1550
 Ser Asp Lys Pro Met Asp Ile His Ala Pro Ser Leu Glu Tyr Tyr Ile
 1555 1560 1565
 Lys Tyr Ile Gln Gly Ser Ala Gly Leu Asp Ala Ile Lys Ser Ala Gly
 1570 1575 1580
 Asn Asn Ser Ile Leu Trp Leu Asn Glu Leu Phe Val Ala Lys Gly Gly
 585 1590 1595 1600
 Asn Pro Leu Phe Ala Pro Tyr Tyr Leu Gln Asp Asn Pro Thr Glu His
 1605 1610 1615
 Ile Val Thr Leu Met Lys Asp Ile Thr Ser Ala Leu Gly Met Leu Ser
 1620 1625 1630
 Lys Pro Asn Leu Lys Asn Asn Ser Thr Asp Ala Leu Gln Leu Asn Thr
 1635 1640 1645
 Tyr Thr Gln Gln Met Ser Arg Leu Ala Lys Leu Ser Asn Phe Ala Ser
 1650 1655 1660
 Phe Asp Ser Thr Asp Phe Ser Glu Arg Leu Ser Ser Leu Lys Asn Gln
 665 1670 1675 1680
 Arg Phe Ala Asp Ala Ile Pro Asn Ala Met Asp Val Ile Leu Lys Tyr
 1685 1690 1695
 Ser Gln Arg Asp Lys Leu Lys Asn Asn Leu Trp Ala Thr Gly Val Gly
 1700 1705 1710
 Gly Val Ser Phe Val Glu Asn Gly Thr Gly Thr Leu Tyr Gly Val Asn
 1715 1720 1725
 Val Gly Tyr Asp Arg Phe Ile Lys Gly Val Ile Val Gly Gly Tyr Ala
 1730 1735 1740
 Ala Tyr Gly Tyr Ser Gly Phe Tyr Glu Arg Ile Thr Asn Ser Lys Ser
 745 1750 1755 1760
 Asp Asn Val Asp Val Gly Leu Tyr Ala Arg Ala Phe Ile Lys Lys Ser
 1765 1770 1775
 Glu Leu Thr Phe Ser Val Asn Glu Thr Trp Gly Ala Asn Lys Asn Gln
 1780 1785 1790
 Ile Ser Ser Asn Asp Thr Leu Leu Ser Met Ile Asn Gln Ser Tyr Lys
 1795 1800 1805
 Tyr Ser Thr Trp Thr Thr Asn Ala Lys Val Asn Tyr Gly Tyr Asp Phe
 1810 1815 1820
 Met Phe Lys Asn Lys Ser Ile Ile Leu Lys Pro Gln Ile Gly Leu Arg
 825 1830 1835 1840
 Tyr Tyr Tyr Ile Gly Met Thr Gly Leu Glu Gly Val Met His Asn Ala
 1845 1850 1855
 Leu Tyr Asn Gln Phe Lys Ala Asn Ala Asp Pro Ser Lys Lys Ser Val
 1860 1865 1870
 Leu Thr Ile Glu Leu Ala Leu Glu Asn Arg His Tyr Phe Asn Thr Asn
 1875 1880 1885
 Ser Tyr Phe Tyr Ala Ile Gly Gly Phe Gly Arg Asp Leu Leu Val Asn
 1890 1895 1900
 Ser Met Gly Asp Lys Leu Val Arg Phe Ile Gly Asn Asn Thr Leu Ser
 905 1910 1915 1920
 Tyr Arg Lys Gly Glu Leu Tyr Asn Thr Phe Ala Ser Ile Thr Thr Gly
 1925 1930 1935
 Gly Glu Val Arg Leu Phe Lys Ser Phe Tyr Ala Asn Ala Gly Val Gly
 1940 1945 1950
 Ala Arg Phe Gly Leu Asp Tyr Lys Met Ile Asn Ile Thr Gly Asn Ile
 1955 1960 1965
 Gly Met Arg Leu Ala Phe
 1970 1

Leu Ile Asn Lys Leu Ile Ser Trp Leu Gly Pro Gln Asp Leu Ser Val
 105 1110 1115 1120
 Leu Val Asn Ile Ala Leu Asn Ser Ile Thr Asn Pro Ser Lys Glu Leu
 1125 1130 1135
 Thr Ser Thr Ile Ser Ser Ile Gly Glu Lys Ala Leu Asn Asp Leu Leu
 1140 1145 1150
 Gly Asp Gly Val Val Asn Lys Ile Met Ser Asn Gln Val Leu Gly Gln
 1155 1160 1165
 Met Ile Asn Lys Ile Ile Ala Asp Lys Gly Phe Gly Gly Val Tyr Gln
 1170 1175 1180
 Gln Gly Leu Gly Ser Ile Leu Pro Gln Ser Leu Gln Asp Glu Leu Lys
 185 1190 1195 1200
 Lys Leu Gly Met Gly Ser Leu Leu Gly Ser Arg Gly Leu His Asn Leu
 1205 1210 1215
 Trp Gln Arg Gly Asn Phe Asn Phe Val Ala Lys Asp Tyr Leu Phe Thr
 1220 1225 1230
 Asn Asn Ser Ser Phe Ser Asn Ala Thr Gly Gly Glu Leu Asn Phe Val
 1235 1240 1245
 Ala Gly Lys Ser Ile Ile Phe Asn Gly Lys Asn Thr Ile Asn Phe Thr
 1250 1255 1260
 Gln Tyr Gln Gly Lys Leu Ser Phe Ile Ser Lys Asp Phe Ser Asn Ile
 265 1270 1275 1280
 Ser Leu Asp Thr Leu Asn Ala Thr Asn Gly Leu Thr Leu Asn Ala Pro
 1285 1290 1295
 Lys Asn Asp Ile Ser Val Gln Lys Gly Gln Ile Cys Val Asn Val Leu
 1300 1305 1310
 Asn Cys Met Gly Glu Lys Lys Ala His Ser Ser Ser Ala Thr Ala Pro
 1315 1320 1325
 Thr Asn Glu Thr Leu Glu Ala Asn Ala Asn Asn Phe Ala Phe Leu Gly
 1330 1335 1340
 Ala Ile Lys Ala Asn Gly Leu Val Asp Phe Ser Lys Val Leu Gln Asn
 345 1350 1355 1360
 Thr Thr Ile Gly Thr Leu Asp Leu Gly Pro Asn Ala Thr Phe Lys Ala
 1365 1370 1375
 Asn His Leu Ile Val Asn Asn Ala Phe Asn Asn Asn Ser Asn Tyr Arg
 1380 1385 1390
 Ala Asp Ile Ser Gly Asn Leu Asn Val Val Lys Gly Ala Ala Leu Ser
 1395 1400 1405
 Thr Asn Glu Asn Gly Leu Asn Val Gly Gly Asp Phe Lys Ser Glu Gly
 1410 1415 1420
 Ser Leu Ile Phe Asn Leu Asn Asn Lys Thr Asn Gln Thr Ile Ile Asn
 425 1430 1435 1440
 Val Ala Gly Asn Ser Thr Ile Met Ser Tyr Asn Asn Gln Ala Leu Ile
 1445 1450 1455
 His Phe Asn Thr Gln Leu Lys Gln Gly Ala Tyr Thr Leu Ile Asn Ala
 1460 1465 1470
 Lys Arg Met Leu Tyr Gly Tyr Asp Asn Gln Ile Ile Arg Gly Gly Ser
 1475 1480 1485
 Leu Ser Asp Tyr Leu Lys Leu Tyr Thr Leu Ile Asp Phe Asn Gly Lys
 1490 1495 1500
 Arg Met Gln Leu Asn Gly Asp Ser Leu Ser Tyr Asp Asn Gln Pro Val
 505 1510 1515 1520
 Asn Ile Lys Asp Gly Gly Leu Val Val Ser Phe Lys Asp Asn Gln Gly
 1525 1530 1535
 Gln Met Val Tyr Ser Ser Ile Leu Tyr Asp Lys Val Gln Val Ser Val

				660					665					670	
Glu	Asn	Ser	Tyr	Asn	Tyr	Thr	Ser	Asp	Lys	Val	Gly	Thr	Tyr	Tyr	Leu
				675					680					685	
Thr	Ser	Asn	Ile	Lys	Gly	Phe	Asn	Gln	Asn	Asn	Lys	Thr	Pro	Gly	Thr
				690					695					700	
Tyr	Asn	Ala	Gln	Asn	Gln	Pro	Leu	Gln	Ala	Leu	His	Ile	Tyr	Asn	Gln
705					710					715					720
Ala	Ile	Thr	Lys	Gln	Asp	Leu	Asn	Met	Ile	Ala	Ser	Leu	Gly	Lys	Glu
				725					730					735	
Phe	Leu	Pro	Lys	Ile	Ala	Asn	Leu	Leu	Ser	Ser	Gly	Ala	Leu	Asp	Asn
				740					745					750	
Leu	Asn	Ser	Pro	Asn	Ser	Phe	Glu	Thr	Leu	Phe	Gly	Ile	Phe	Glu	Lys
				755					760					765	
Tyr	Gly	Ile	Thr	Leu	Asn	Gln	Glu	Asn	Trp	Lys	Ser	Leu	Leu	Lys	Ile
				770					775					780	
Ile	Asn	Asn	Phe	Ser	Asn	Thr	Thr	Asn	Tyr	Asp	Phe	Ser	Gln	Gly	Asn
785					790					795					800
Leu	Val	Val	Gly	Ala	Ile	Lys	Glu	Gly	Gln	Thr	Asn	Thr	Lys	Ser	Val
				805					810					815	
Val	Trp	Phe	Gly	Gly	Glu	Gly	Tyr	Lys	Glu	Pro	Cys	Ala	Val	Gly	Asp
				820					825					830	
Asn	Thr	Cys	Gln	Met	Phe	Arg	Gln	Thr	Asn	Leu	Gly	Gln	Leu	Leu	His
				835					840					845	
Ser	Ser	Thr	Pro	Tyr	Leu	Gly	Tyr	Ile	Asn	Ala	Asn	Phe	Arg	Ala	Lys
				850					855					860	
Asn	Ile	Tyr	Ile	Thr	Gly	Thr	Ile	Gly	Ser	Gly	Asn	Ala	Trp	Gly	Ser
865					870					875					880
Gly	Gly	Ser	Ala	Asn	Val	Ser	Phe	Glu	Ser	Gly	Thr	Asn	Leu	Val	Leu
				885					890					895	
Asn	Gln	Ala	Lys	Ile	Asp	Ala	Gln	Gly	Thr	Asp	Lys	Ile	Phe	Ser	Tyr
				900					905					910	
Leu	Gly	Gln	Gly	Gly	Ile	Glu	Lys	Leu	Phe	Gly	Glu	Lys	Gly	Leu	Gly
				915					920					925	
Asn	Ala	Leu	Ser	Asn	Ile	Ile	Tyr	Glu	Glu	Ser	Leu	Asn	Asp	Asn	Ala
				930					935					940	
Ile	Pro	Lys	Asp	Leu	Ala	Asn	Met	Ile	Pro	Lys	Asp	Phe	Gly	Ser	Lys
945					950					955					960
Thr	Leu	Ser	Ser	Leu	Leu	Ser	Pro	Thr	Glu	Val	Asn	Asn	Leu	Leu	Gly
				965					970					975	
Val	Ser	Ala	Phe	Lys	Asn	Ala	Ile	Met	Glu	Ile	Leu	Asn	Ser	Lys	Thr
				980					985					990	
Val	Gly	Asp	Val	Phe	Gly	Glu	Asn	Gly	Leu	Leu	Asn	Ala	Leu	Asp	Pro
				995					1000					1005	
Thr	Glu	Arg	Lys	Lys	Ile	Asp	Gln	Met	Leu	Leu	Glu	Gln	Ile	Gln	Ala
				1010					1015					1020	
His	Ser	Ser	Gly	Phe	Glu	Lys	Phe	Ile	Val	Lys	Thr	Leu	Gly	Ile	Glu
025					1030					1035					1040
Asn	Val	Glu	Asn	Phe	Ile	Asn	Asn	Trp	Tyr	Gly	Lys	Gln	Ser	Leu	Ser
				1045					1050					1055	
Ser	Phe	Ala	Asn	Asn	Phe	Val	Pro	Gly	Gly	Leu	Asn	Gln	Ala	Leu	Asp
				1060					1065					1070	
Lys	Ile	Gly	Ser	Ser	Ser	Asp	Ala	Lys	Asp	Leu	Gln	Asn	Phe	Leu	Asp
				1075					1080					1085	
Lys	Thr	Thr	Phe	Gly	Asp	Ile	Leu	Asn	Gln	Met	Ile	Glu	Gln	Ala	Pro
				1090					1095					1100	


```

Ile Lys Asn Ser Asn Phe Arg Asp Phe Thr Trp Gly Gly Phe Asn Phe
225                230                235                240
Asn Ser Gly Arg Ile Thr Phe Glu Asn Thr Thr Phe Ser Gly Trp Thr
                245                250                255
Asn Ile Asn Gly Ala Thr Glu Ser Gly Ser Ser Tyr Val Asn Met Val
                260                265                270
Ala Asn Thr Asp Leu Ile Phe Ser Asn Ser Ile Leu Gly Gly Gly Ile
                275                280                285
Arg Tyr Asp Leu Lys Ala Asn Asn Ile Ile Phe Asn Asn Ser Gln Met
                290                295                300
Val Ile Asp Val Ser Lys Asn Val Asn Gln Ser Ser Leu Asn Gly Asn
305                310                315                320
Val Thr Phe Asn Asn Ser Arg Leu Ser Val Lys Pro Asn Ala Ala Ile
                325                330                335
Asn Ile Gly Asp Ser Gln Thr Gln Thr Ala Leu Glu Asn Ala Ser Ser
                340                345                350
Leu Ser Phe Tyr Asn Asn Ser Val Ala Asn Phe Asn Gly Thr Thr Ala
                355                360                365
Phe Asn Gly Val Ser Tyr Leu Asn Leu Asn Pro Asn Ala Gln Val Ser
370                375                380
Phe Asn Gln Val Asn Phe Asn Asn Ala Asn Val Thr Phe Tyr Gly Ile
385                390                395                400
Pro Leu Phe Gly Lys Thr Pro Asp Phe Gly Asn Ser Ala Arg Leu Ile
                405                410                415
Asn Phe Lys Gly Asn Thr Asn Phe Asn Gln Ala Thr Leu Asn Leu Arg
                420                425                430
Ala Lys Asn Ile His Ile Asn Phe Gln Gly Val Ser Thr Phe Lys Gln
435                440                445
Asn Ser Thr Met Asn Leu Ala Glu Ser Ser Gln Ala Ser Phe Asn Ala
450                455                460
Leu Lys Val Glu Gly Glu Thr Asn Phe Asn Leu Asn Asn Ser Ser Leu
465                470                475                480
Leu Asn Phe Asn Gly Asn Ser Val Phe Asn Ala Pro Val Ser Phe Tyr
                485                490                495
Ala Asn His Ser Gln Ile Ser Phe Thr Lys Leu Ala Thr Phe Asn Ser
500                505                510
Asp Ala Ser Phe Asp Leu Ser Asn Asn Ser Thr Leu Asn Phe Gln Ser
515                520                525
Val Leu Leu Asn Gly Ala Leu Asn Leu Leu Gly Asn Gly Ser Asn Asn
530                535                540
Leu Ala Ile Asn Ala Lys Gly Asn Phe Ser Phe Gly Ser Lys Gly Ile
545                550                555                560
Leu Asn Leu Ser Tyr Met Asn Leu Phe Gly Gly Asp Lys Lys Thr Ser
565                570                575
Val Tyr Asp Val Leu Gln Ala Gln Asn Ile Asp Gly Leu Met Gly Asn
580                585                590
Asn Gly Tyr Glu Lys Ile Arg Phe Tyr Gly Ile Gln Ile Asp Lys Ala
595                600                605
Asp Tyr Ser Phe Asp Asn Gly Val His Ser Trp Arg Phe Thr Asn Pro
610                615                620
Leu Asn Thr Thr Glu Thr Ile Thr Glu Thr Leu His Asn Asn Arg Leu
625                630                635                640
Lys Val Gln Ile Ser Gln Asn Gly Val Ser Asn Asn Lys Met Phe Asn
645                650                655
Leu Ala Pro Ser Leu Tyr Asp Tyr Gln Lys Asn Pro Tyr Asn Glu Thr

```

GTG AGG TTG TTT AAA AGC TTT TAT GCG AAT GCT GGG GTG GGG GCT AGG 5912
 Val Arg Leu Phe Lys Ser Phe Tyr Ala Asn Ala Gly Val Gly Ala Arg
 1940 1945 1950

TTT GGA TTG GAC TAT AAA ATG ATC AAC ATT ACC GGA AAT ATT GGA ATG 5960
 Phe Gly Leu Asp Tyr Lys Met Ile Asn Ile Thr Gly Asn Ile Gly Met
 1955 1960 1965 1970

CGT TTA GCG TTT TAAAAGGTGG GGGCTTACCC CTTTTTGTGAG CCATTAAATA AATCA 6017
 Arg Leu Ala Phe
 1

ATGGTG GGG 6025

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1974 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Arg Asp Asn Ala Phe Ser Lys Asn Leu Trp Asn Leu Ile His Tyr Gly
 1 5 10 15
 Gly Glu Gln Gly Thr Leu Leu Arg Ala Asp Asn Asn Thr Phe Phe Val
 20 25 30
 Gln Phe Thr Gln Ser Asn Gly Gln Lys Phe Val Phe Glu Glu Thr Phe
 35 40 45
 Asn Pro Gly Ser Ile Thr Tyr Lys Tyr Phe Thr Ile His Ser Ser Leu
 50 55 60
 Phe His Thr Asp Ala Asp Ser Lys Asp Ile Trp Ser Gln Val Arg Lys
 65 70 75 80
 Gln Phe Asp Phe Ile Pro Gly Lys Thr Pro Val Cys Val Gly Val Cys
 85 90 95
 Tyr Ile Ala Pro Tyr Lys Asn Gln Asp Leu Ile Gly Ser Ser Ala Phe
 100 105 110
 Ala Trp Ser Leu Asn Phe Gly Ala Thr Val Val Gly Thr Leu Leu Leu
 115 120 125
 Gly Ser Ala Gln Glu Lys Ala Asn Asn Asn Gly Gly Ser Ile Trp Phe
 130 135 140
 Gly Lys Asn Asn Leu Leu Tyr Leu His Gly Asn Phe Asn Ala Thr Asn
 145 150 155 160
 Ile Phe Leu Thr Asn Asn Phe Asn Val Gly Asn Pro Asn Ala Gly Gly
 165 170 175
 Gly Ala Thr Ile Asn Phe Asn Ala Asp Glu Thr Leu Asn Ala Asp Gly
 180 185 190
 Leu Asn Tyr Thr Asn Phe Gln Thr Val Ala Leu Gly Leu Gln Thr Ser
 195 200 205
 Ala Ser Gln His Ser Trp Ala Asn Phe Asn Ser Lys Leu Ser Met Glu
 210 215 220

-632-

GAT TAC CTC AAG CTT TAC ACC CTC ATT GAT TTT AAC GGC AAA CGC ATG Asp Tyr Leu Lys Leu Tyr Thr Leu Ile Asp Phe Asn Gly Lys Arg Met	4568
1495 1500 1505	
CAA TTA AAC GGC GAT TCA CTA AGC TAT GAC AAC CAA CCG GTC AAT ATT Gln Leu Asn Gly Asp Ser Leu Ser Tyr Asp Asn Gln Pro Val Asn Ile	4616
1510 1515 1520	
AAA GAT GGG GGT CTT GTG GTA AGC TTT AAA GAC AAT CAG GGG CAA ATG Lys Asp Gly Gly Leu Val Val Ser Phe Lys Asp Asn Gln Gly Gln Met	4664
1525 1530 1535	
GTG TAT TCA TCT ATC CTT TAT GAT AAA GTT CAA GTT AGC GTC TCT GAT Val Tyr Ser Ser Ile Leu Tyr Asp Lys Val Gln Val Ser Val Ser Asp	4712
1540 1545 1550	
AAG CCC ATG GAT ATT CAT GCC CCT AGT TTG GAG TAT TAC ATT AAA TAC Lys Pro Met Asp Ile His Ala Pro Ser Leu Glu Tyr Tyr Ile Lys Tyr	4760
1555 1560 1565 1570	
ATT CAA GGC AGT GCT GGT TTG GAT GCG ATC AAA TCT GCA GGC AAT AAT Ile Gln Gly Ser Ala Gly Leu Asp Ala Ile Lys Ser Ala Gly Asn Asn	4808
1575 1580 1585	
TCC ATT CTG TGG TTG AAT GAG CTT TTT GTG GCT AAA GGG GGT AAT CCC Ser Ile Leu Trp Leu Asn Glu Leu Phe Val Ala Lys Gly Gly Asn Pro	4856
1590 1595 1600	
TTG TTC GCT CCT TAT TAT TTG CAA GAC AAT CCC ACT GAA CAC ATT GTT Leu Phe Ala Pro Tyr Tyr Leu Gln Asp Asn Pro Thr Glu His Ile Val	4904
1605 1610 1615	
ACT TTA ATG AAA GAT ATT ACT AGC GCT TTA GGC ATG CTT TCT AAA CCC Thr Leu Met Lys Asp Ile Thr Ser Ala Leu Gly Met Leu Ser Lys Pro	4952
1620 1625 1630	
AAT CTT AAA AAC AAT TCC ACC GAT GCT TTA CAG CTC AAC ACT TAC ACG Asn Leu Lys Asn Asn Ser Thr Asp Ala Leu Gln Leu Asn Thr Tyr Thr	5000
1635 1640 1645 1650	
CAA CAA ATG AGC CGT TTA GCC AAG CTT TCT AAT TTC GCT TCC TTT GAT Gln Gln Met Ser Arg Leu Ala Lys Leu Ser Asn Phe Ala Ser Phe Asp	5048
1655 1660 1665	
TCA ACG GAT TTT AGC GAA CGC TTG AGC AGT CTT AAA AAC CAA AGA TTT Ser Thr Asp Phe Ser Glu Arg Leu Ser Ser Leu Lys Asn Gln Arg Phe	5096
1670 1675 1680	
GCT GAT GCA ATC CCT AAT GCG ATG GAT GTG ATT TTA AAA TAC TCT CAA Ala Asp Ala Ile Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser Gln	5144
1685 1690 1695	
AGG GAT AAA CTA AAA AAC AAC CTT TGG GCG ACC GGC GTT GGG GGC GTG Arg Asp Lys Leu Lys Asn Asn Leu Trp Ala Thr Gly Val Gly Gly Val	5192
1700 1705 1710	

CAG GGT AAG CTT TCG TTT ATT TCT AAA GAT TTT TCT AAC ATT TCA TTA	3896
Gln Gly Lys Leu Ser Phe Ile Ser Lys Asp Phe Ser Asn Ile Ser Leu	
1270 1275 1280	
GAT ACC TTA AAC GCT ACT AAC GGA TTA ACG CTT AAT GCT CCT AAA AAT	3944
Asp Thr Leu Asn Ala Thr Asn Gly Leu Thr Leu Asn Ala Pro Lys Asn	
1285 1290 1295	
GAC ATT AGC GTT CAA AAA GGT CAG ATT TGC GTG AAT GTT TTA AAT TGC	3992
Asp Ile Ser Val Gln Lys Gly Gln Ile Cys Val Asn Val Leu Asn Cys	
1300 1305 1310	
ATG GGC GAG AAA AAA GCT CAT TCT TCA AGC GCG ACA GCC CCA ACC AAT	4040
Met Gly Glu Lys Lys Ala His Ser Ser Ser Ala Thr Ala Pro Thr Asn	
1315 1320 1325 1330	
GAA ACA CTA GAA GCG AAT GCG AAT AAT TTC GCT TTT TTA GGT GCA ATT	4088
Glu Thr Leu Glu Ala Asn Ala Asn Asn Phe Ala Phe Leu Gly Ala Ile	
1335 1340 1345	
AAG GCT AAT GGA TTA GTG GAT TTT TCA AAA GTT TTA CAA AAT ACT ACG	4136
Lys Ala Asn Gly Leu Val Asp Phe Ser Lys Val Leu Gln Asn Thr Thr	
1350 1355 1360	
ATC GGG ACT TTA GAT TTA GGG CCA AAC GCT ACT TTT AAA GCG AAT CAT	4184
Ile Gly Thr Leu Asp Leu Gly Pro Asn Ala Thr Phe Lys Ala Asn His	
1365 1370 1375	
TTG ATC GTG AAT AAC GCT TTT AAC AAT AAC TCT AAT TAC AGG GCT GAT	4232
Leu Ile Val Asn Asn Ala Phe Asn Asn Asn Ser Asn Tyr Arg Ala Asp	
1380 1385 1390	
ATT AGC GGT AAT CTC AAT GTG GTT AAA GGA GCG GCT CTC AGC ACG AAT	4280
Ile Ser Gly Asn Leu Asn Val Val Lys Gly Ala Ala Leu Ser Thr Asn	
1395 1400 1405 1410	
GAA AAT GGT TTG AAT GTG GGG GGC GAT TTC AAG AGC GAA GGG TCA TTA	4328
Glu Asn Gly Leu Asn Val Gly Gly Asp Phe Lys Ser Glu Gly Ser Leu	
1415 1420 1425	
ATC TTT AAT CTT AAC AAT AAA ACC AAT CAA ACG ATT ATT AAT GTG GCT	4376
Ile Phe Asn Leu Asn Asn Lys Thr Asn Gln Thr Ile Ile Asn Val Ala	
1430 1435 1440	
GGC AAT TCT ACG ATC ATG TCT TAT AAC AAT CAA GCT TTA ATC CAT TTT	4424
Gly Asn Ser Thr Ile Met Ser Tyr Asn Asn Gln Ala Leu Ile His Phe	
1445 1450 1455	
AAT ACC CAA CTC AAG CAA GGC GCT TAC ACG CTT ATT AAT GCG AAA CGC	4472
Asn Thr Gln Leu Lys Gln Gly Ala Tyr Thr Leu Ile Asn Ala Lys Arg	
1460 1465 1470	
ATG CTT TAT GGT TAT GAC AAT CAA ATC ATT CGT GGA GGG AGC TTG AGC	4520
Met Leu Tyr Gly Tyr Asp Asn Gln Ile Ile Arg Gly Gly Ser Leu Ser	
1475 1480 1485 1490	

GAG AAT TTC ATC AAT AAC TGG TAT GGC AAG CAA AGC TTG AGT TCT TTT	3224
Glu Asn Phe Ile Asn Asn Trp Tyr Gly Lys Gln Ser Leu Ser Ser Phe	
1045 1050 1055	
GCC AAT AAT TTT GTG CCT GGA GGC TTG AAT CAA GCC CTT GAT AAA ATA	3272
Ala Asn Asn Phe Val Pro Gly Gly Leu Asn Gln Ala Leu Asp Lys Ile	
1060 1065 1070	
GGC TCT AGC TCT GAT GCC AAA GAC TTA CAG AAC TTC TTG GAT AAA ACG	3320
Gly Ser Ser Ser Asp Ala Lys Asp Leu Gln Asn Phe Leu Asp Lys Thr	
1075 1080 1085 1090	
ACT TTT GGG GAT ATT TTA AAT CAA ATG ATT GAA CAA GCC CCC TTA ATC	3368
Thr Phe Gly Asp Ile Leu Asn Gln Met Ile Glu Gln Ala Pro Leu Ile	
1095 1100 1105	
AAT AAA CTC ATT TCT TGG CTG GGT CCG CAG GAT TTG AGC GTT TTA GTG	3416
Asn Lys Leu Ile Ser Trp Leu Gly Pro Gln Asp Leu Ser Val Leu Val	
1110 1115 1120	
AAT ATC GCT TTA AAT AGC ATC ACT AAC CCT AGT AAA GAG CTG ACT AGC	3464
Asn Ile Ala Leu Asn Ser Ile Thr Asn Pro Ser Lys Glu Leu Thr Ser	
1125 1130 1135	
ACC ATT TCT AGC ATA GGT GAA AAA GCG TTA AAT GAC TTA TTA GGC GAT	3512
Thr Ile Ser Ser Ile Gly Glu Lys Ala Leu Asn Asp Leu Leu Gly Asp	
1140 1145 1150	
GGC GTA GTG AAT AAA ATC ATG AGC AAT CAA GTC TTA GGG CAA ATG ATC	3560
Gly Val Val Asn Lys Ile Met Ser Asn Gln Val Leu Gly Gln Met Ile	
1155 1160 1165 1170	
AAT AAA ATC ATT GCT GAT AAG GGC TTT GGA GGC GTT TAT CAG CAA GGT	3608
Asn Lys Ile Ile Ala Asp Lys Gly Phe Gly Gly Val Tyr Gln Gln Gly	
1175 1180 1185	
TTA GGC TCC ATA CTG CCT CAA TCT TTA CAA GAT GAA TTG AAG AAA TTG	3656
Leu Gly Ser Ile Leu Pro Gln Ser Leu Gln Asp Glu Leu Lys Lys Leu	
1190 1195 1200	
GGC ATG GGC TCT TTA CTA GGA TCT AGG GGG TTG CAC AAT CTT TGG CAA	3704
Gly Met Gly Ser Leu Leu Gly Ser Arg Gly Leu His Asn Leu Trp Gln	
1205 1210 1215	
AGA GGG AAT TTC AAT TTT GTG GCT AAA GAT TAT TTA TTC ACT AAT AAC	3752
Arg Gly Asn Phe Asn Phe Val Ala Lys Asp Tyr Leu Phe Thr Asn Asn	
1220 1225 1230	
AGC TCG TTT AGT AAC GCC ACA GGG GGG GAA TTG AAT TTT GTG GCG GGC	3800
Ser Ser Phe Ser Asn Ala Thr Gly Gly Glu Leu Asn Phe Val Ala Gly	
1235 1240 1245 1250	
AAG TCT ATT ATT TTT AAC GGG AAA AAT ACG ATC AAT TTC ACG CAG TAT	3848
Lys Ser Ile Ile Phe Asn Gly Lys Asn Thr Ile Asn Phe Thr Gln Tyr	
1255 1260 1265	

TTT GGA GGC GAA GGC TAT AAA GAG CCA TGT GCG GTT GGG GAT AAC ACT	2552
Phe Gly Gly Glu Gly Tyr Lys Glu Pro Cys Ala Val Gly Asp Asn Thr	
820 825 830	
TGC CAG ATG TTC AGA CAG ACT AAT TTA GGG CAA TTG CTC CAT TCT AGT	2600
Cys Gln Met Phe Arg Gln Thr Asn Leu Gly Gln Leu Leu His Ser Ser	
835 840 845 850	
ACG CCT TAT TTA GGC TAC ATT AAC GCT AAT TTT AGG GCT AAA AAC ATT	2648
Thr Pro Tyr Leu Gly Tyr Ile Asn Ala Asn Phe Arg Ala Lys Asn Ile	
855 860 865	
TAC ATT ACC GGA ACC ATC GGC AGC GGG AAC GCT TGG GGG AGT GGA GGG	2696
Tyr Ile Thr Gly Thr Ile Gly Ser Gly Asn Ala Trp Gly Ser Gly Gly	
870 875 880	
AGT GCG AAT GTG TCT TTT GAA AGC GGC ACT AAT TTA GTG CTT AAT CAA	2744
Ser Ala Asn Val Ser Phe Glu Ser Gly Thr Asn Leu Val Leu Asn Gln	
885 890 895	
GCT AAG ATT GAC GCT CAA GGG ACC GAT AAA ATC TTT TCT TAC TTG GGG	2792
Ala Lys Ile Asp Ala Gln Gly Thr Asp Lys Ile Phe Ser Tyr Leu Gly	
900 905 910	
CAA GGG GGT ATT GAA AAG CTT TTT GGA GAA AAA GGT TTA GGG AAT GCG	2840
Gln Gly Gly Ile Glu Lys Leu Phe Gly Glu Lys Gly Leu Gly Asn Ala	
915 920 925 930	
CTT TCT AAT ATC ATT TAT GAA GAG AGC TTG AAT GAT AAC GCT ATC CCT	2888
Leu Ser Asn Ile Ile Tyr Glu Glu Ser Leu Asn Asp Asn Ala Ile Pro	
935 940 945	
AAA GAT TTA GCC AAC ATG ATC CCT AAA GAT TTT GGA TCT AAG ACT TTA	2936
Lys Asp Leu Ala Asn Met Ile Pro Lys Asp Phe Gly Ser Lys Thr Leu	
950 955 960	
AGC TCA TTG CTT AGC CCT ACT GAA GTG AAT AAC CTC TTA GGC GTG AGC	2984
Ser Ser Leu Leu Ser Pro Thr Glu Val Asn Asn Leu Leu Gly Val Ser	
965 970 975	
GCA TTC AAA AAC GCG ATC ATG GAA ATT TTA AAT TCT AAA ACG GTG GGC	3032
Ala Phe Lys Asn Ala Ile Met Glu Ile Leu Asn Ser Lys Thr Val Gly	
980 985 990	
GAT GTT TTT GGT GAA AAC GGG CTT TTA AAC GCG CTA GAT CCT ACG GAA	3080
Asp Val Phe Gly Glu Asn Gly Leu Leu Asn Ala Leu Asp Pro Thr Glu	
995 1000 1005 1010	
AGA AAA AAA ATT GAT CAA ATG CTT TTA GAG CAA ATC CAA GCC CAT TCT	3128
Arg Lys Lys Ile Asp Gln Met Leu Leu Glu Gln Ile Gln Ala His Ser	
1015 1020 1025	
TCA GGG TTT GAA AAA TTC ATC GTG AAA ACT TTA GGG ATT GAA AAT GTA	3176
Ser Gly Phe Glu Lys Phe Ile Val Lys Thr Leu Gly Ile Glu Asn Val	
1030 1035 1040	

TAT GAG AAG ATC CGT TTT TAT GGC ATA CAG ATT GAC AAG GCT GAT TAC	1880
Tyr Glu Lys Ile Arg Phe Tyr Gly Ile Gln Ile Asp Lys Ala Asp Tyr	
595 600 605 610	
TCG TTT GAT AAC GGC GTT CAT TCT TGG AGA TTC ACT AAC CCG CTC AAT	1928
Ser Phe Asp Asn Gly Val His Ser Trp Arg Phe Thr Asn Pro Leu Asn	
615 620 625	
ACG ACT GAA ACG ATT ACA GAA ACC TTG CAT AAC AAC CGC TTG AAA GTG	1976
Thr Thr Glu Thr Ile Thr Glu Thr Leu His Asn Asn Arg Leu Lys Val	
630 635 640	
CAG ATC TCT CAA AAC GGC GTT TCT AAT AAT AAG ATG TTC AAT CTC GCT	2024
Gln Ile Ser Gln Asn Gly Val Ser Asn Asn Lys Met Phe Asn Leu Ala	
645 650 655	
CCT AGC TTG TAT GAT TAC CAA AAA AAC CCT TAT AAT GAA ACC GAG AAT	2072
Pro Ser Leu Tyr Asp Tyr Gln Lys Asn Pro Tyr Asn Glu Thr Glu Asn	
660 665 670	
TCC TAT AAT TAC ACA AGC GAT AAG GTT GGC ACT TAT TAT TTA ACG AGC	2120
Ser Tyr Asn Tyr Thr Ser Asp Lys Val Gly Thr Tyr Tyr Leu Thr Ser	
675 680 685 690	
AAT ATC AAA GGC TTT AAT CAA AAC AAT AAA ACA CCC GGG ACT TAT AAC	2168
Asn Ile Lys Gly Phe Asn Gln Asn Asn Lys Thr Pro Gly Thr Tyr Asn	
695 700 705	
GCG CAA AAC CAA CCC TTA CAA GCC TTA CAC ATT TAC AAT CAG GCT ATC	2216
Ala Gln Asn Gln Pro Leu Gln Ala Leu His Ile Tyr Asn Gln Ala Ile	
710 715 720	
ACT AAG CAA GAT TTG AAC ATG ATC GCC AGT TTG GGT AAG GAG TTT TTG	2264
Thr Lys Gln Asp Leu Asn Met Ile Ala Ser Leu Gly Lys Glu Phe Leu	
725 730 735	
CCT AAA ATA GCC AAT CTT TTA TCT TCA GGG GCT TTG GAT AAT CTC AAT	2312
Pro Lys Ile Ala Asn Leu Leu Ser Ser Gly Ala Leu Asp Asn Leu Asn	
740 745 750	
AGC CCG AAT AGT TTT GAA ACT CTT TTT GGT ATC TTT GAA AAG TAT GGT	2360
Ser Pro Asn Ser Phe Glu Thr Leu Phe Gly Ile Phe Glu Lys Tyr Gly	
755 760 765 770	
ATC ACT TTA AAC CAA GAA AAT TGG AAG AGC TTA TTA AAG ATT ATC AAT	2408
Ile Thr Leu Asn Gln Glu Asn Trp Lys Ser Leu Leu Lys Ile Ile Asn	
775 780 785	
AAT TTT TCC AAC ACA ACT AAT TAT GAT TTC TCT CAA GGC AAT CTC GTT	2456
Asn Phe Ser Asn Thr Thr Asn Tyr Asp Phe Ser Gln Gly Asn Leu Val	
790 795 800	
GTA GGA GCG ATC AAA GAG GGG CAA ACG AAC ACT AAA AGC GTG GTG TGG	2504
Val Gly Ala Ile Lys Glu Gly Gln Thr Asn Thr Lys Ser Val Val Trp	
805 810 815	

GGG GTG TCT TAT TTG AAT TTG AAC CCT AAC GCT CAA GTA AGC TTC AAT	1208
Gly Val Ser Tyr Leu Asn Leu Asn Pro Asn Ala Gln Val Ser Phe Asn	
375 380 385	
CAA GTA AAT TTC AAT AAC GCT AAT GTA ACT TTT TAT GGC ATT CCT TTA	1256
Gln Val Asn Phe Asn Asn Ala Asn Val Thr Phe Tyr Gly Ile Pro Leu	
390 395 400	
TTT GGT AAA ACG CCT GAT TTT GGC AAC TCT GCA CGC CTT ATC AAT TTC	1304
Phe Gly Lys Thr Pro Asp Phe Gly Asn Ser Ala Arg Leu Ile Asn Phe	
405 410 415	
AAA GGG AAT ACG AAT TTT AAT CAA GCC ACG CTC AAT TTA AGG GCT AAA	1352
Lys Gly Asn Thr Asn Phe Asn Gln Ala Thr Leu Asn Leu Arg Ala Lys	
420 425 430	
AAT ATC CAT ATC AAT TTC CAA GGC GTT TCT ACT TTT AAA CAA AAC TCT	1400
Asn Ile His Ile Asn Phe Gln Gly Val Ser Thr Phe Lys Gln Asn Ser	
435 440 445 450	
ACG ATG AAT TTA GCT GAA AGT TCC CAA GCG AGC TTT AAC GCT CTT AAA	1448
Thr Met Asn Leu Ala Glu Ser Ser Gln Ala Ser Phe Asn Ala Leu Lys	
455 460 465	
GTG GAA GGG GAA ACG AAT TTC AAT CTC AAT AAC TCA AGC TTG TTG AAT	1496
Val Glu Gly Glu Thr Asn Phe Asn Leu Asn Asn Ser Ser Leu Leu Asn	
470 475 480	
TTC AAT GGC AAT AGC GTT TTC AAC GCT CCT GTG AGT TTT TAT GCT AAT	1544
Phe Asn Gly Asn Ser Val Phe Asn Ala Pro Val Ser Phe Tyr Ala Asn	
485 490 495	
CAT TCT CAA ATT TCT TTC ACT AAA TTA GCG ACT TTT AAT TCT GAC GCT	1592
His Ser Gln Ile Ser Phe Thr Lys Leu Ala Thr Phe Asn Ser Asp Ala	
500 505 510	
TCT TTT GAT TTA AGC AAC AAC AGC ACC CTG AAT TTT CAA AGC GTT CTT	1640
Ser Phe Asp Leu Ser Asn Asn Ser Thr Leu Asn Phe Gln Ser Val Leu	
515 520 525 530	
TTA AAT GGT GCT CTA AAC CTT TTA GGC AAT GGC AGT AAC AAT CTA GCG	1688
Leu Asn Gly Ala Leu Asn Leu Leu Gly Asn Gly Ser Asn Asn Leu Ala	
535 540 545	
ATC AAC GCT AAA GGG AAT TTT AGT TTT GGG TCT AAA GGG ATT TTG AAT	1736
Ile Asn Ala Lys Gly Asn Phe Ser Phe Gly Ser Lys Gly Ile Leu Asn	
550 555 560	
CTG TCT TAT ATG AAT CTA TTT GGG GGG GAT AAA AAA ACT TCC GTT TAT	1784
Leu Ser Tyr Met Asn Leu Phe Gly Gly Asp Lys Lys Thr Ser Val Tyr	
565 570 575	
GAT GTG TTG CAA GCC CAA AAT ATT GAT GGC TTA ATG GGG AAT AAC GGC	1832
Asp Val Leu Gln Ala Gln Asn Ile Asp Gly Leu Met Gly Asn Asn Gly	
580 585 590	

AAT AAT TTG CTG TAT TTG CAT GGC AAT TTC AAC GCG ACT AAT ATC TTT	536
Asn Asn Leu Leu Tyr Leu His Gly Asn Phe Asn Ala Thr Asn Ile Phe	
150 155 160	
TTA ACG AAT AAT TTT AAT GTC GGC AAC CCT AAC GCT GGC GGT GGG GCG	584
Leu Thr Asn Asn Phe Asn Val Gly Asn Pro Asn Ala Gly Gly Ala	
165 170 175	
ACG ATT AAT TTT AAC GCT GAT GAA ACC TTG AAC GCT GAC GGG TTA AAT	632
Thr Ile Asn Phe Asn Ala Asp Glu Thr Leu Asn Ala Asp Gly Leu Asn	
180 185 190	
TAC ACG AAT TTC CAA ACC GTG GCT TTG GGC TTA CAA ACC AGT GCG AGC	680
Tyr Thr Asn Phe Gln Thr Val Ala Leu Gly Leu Gln Thr Ser Ala Ser	
195 200 205 210	
CAG CAT TCA TGG GCG AAT TTT AAT TCC AAG CTT TCT ATG GAG ATT AAA	728
Gln His Ser Trp Ala Asn Phe Asn Ser Lys Leu Ser Met Glu Ile Lys	
215 220 225	
AAT TCT AAC TTT AGG GAT TTC ACA TGG GGA GGC TTT AAT TTT AAT TCA	776
Asn Ser Asn Phe Arg Asp Phe Thr Trp Gly Gly Phe Asn Phe Asn Ser	
230 235 240	
GGG CGT ATC ACT TTT GAA AAC ACC ACT TTT AGC GGC TGG ACC AAT ATT	824
Gly Arg Ile Thr Phe Glu Asn Thr Thr Phe Ser Gly Trp Thr Asn Ile	
245 250 255	
AAC GGA GCG ACT GAG AGC GGC TCA TCG TAT GTG AAT ATG GTT GCG AAT	872
Asn Gly Ala Thr Glu Ser Gly Ser Ser Tyr Val Asn Met Val Ala Asn	
260 265 270	
ACG GAT TTG ATA TTT TCT AAT TCC ATT TTA GGA GGG GGC ATT CGC TAT	920
Thr Asp Leu Ile Phe Ser Asn Ser Ile Leu Gly Gly Gly Ile Arg Tyr	
275 280 285 290	
GAT TTG AAA GCT AAT AAC ATT ATT TTC AAT AAC TCT CAA ATG GTT ATT	968
Asp Leu Lys Ala Asn Asn Ile Ile Phe Asn Asn Ser Gln Met Val Ile	
295 300 305	
GAT GTG TCT AAG AAT GTG AAT CAG TCA TCA TTG AAT GGG AAT GTT ACT	1016
Asp Val Ser Lys Asn Val Asn Gln Ser Ser Leu Asn Gly Asn Val Thr	
310 315 320	
TTC AAT AAT TCC AGG CTT TCA GTC AAG CCC AAT GCG GCT ATT AAT ATT	1064
Phe Asn Asn Ser Arg Leu Ser Val Lys Pro Asn Ala Ala Ile Asn Ile	
325 330 335	
GGG GAT AGC CAA ACC CAA ACG GCT TTA GAA AAC GCT TCA AGC CTT TCT	1112
Gly Asp Ser Gln Thr Gln Thr Ala Leu Glu Asn Ala Ser Ser Leu Ser	
340 345 350	
TTT TAC AAC AAC AGC GTG GCG AAT TTT AAC GGC ACA ACC GCT TTT AAC	1160
Phe Tyr Asn Asn Ser Val Ala Asn Phe Asn Gly Thr Thr Ala Phe Asn	
355 360 365 370	

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...5972
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

TTACACGCTT TTAAGCGGAA ATAGTATCAA ATACAATAAC CAAGCTTTAG	CGG GAC	56
	Arg Asp	
	1	
AAT GCT TTT TCA AAA AAT TTA TGG AAT TTA ATC CAT TAT GGT GGC GAA	104	
Asn Ala Phe Ser Lys Asn Leu Trp Asn Leu Ile His Tyr Gly Gly Glu		
5 10 15		
CAA GGG ACT CTA TTA AGA GCG GAT AAC AAC ACC TTT TTT GTG CAA TTC	152	
Gln Gly Thr Leu Leu Arg Ala Asp Asn Asn Thr Phe Phe Val Gln Phe		
20 25 30		
ACC CAA AGC AAC GGC CAA AAA TTT GTT TTT GAA GAA ACT TTT AAT CCG	200	
Thr Gln Ser Asn Gly Gln Lys Phe Val Phe Glu Thr Phe Asn Pro		
35 40 45 50		
GGC TCT ATC ACC TAT AAA TAT TTC ACT ATC CAT TCT TCG CTT TTC CAC	248	
Gly Ser Ile Thr Tyr Lys Tyr Phe Thr Ile His Ser Ser Leu Phe His		
55 60 65		
ACA GAC GCT GAT TCT AAG GAT ATT TGG AGT CAA GTG AGG AAG CAA TTT	296	
Thr Asp Ala Asp Ser Lys Asp Ile Trp Ser Gln Val Arg Lys Gln Phe		
70 75 80		
GAT TTC ATT CCA GGA AAA ACC CCT GTG TGT GTT GGC GTG TGC TAT ATC	344	
Asp Phe Ile Pro Gly Lys Thr Pro Val Cys Val Gly Val Cys Tyr Ile		
85 90 95		
GCG CCT TAT AAA AAT CAA GAC CTT ATT GGC TCT AGC GCT TTT GCG TGG	392	
Ala Pro Tyr Lys Asn Gln Asp Leu Ile Gly Ser Ser Ala Phe Ala Trp		
100 105 110		
TCG CTG AAC TTT GGG GCC ACG GTG GTA GGG ACT TTG CTT TTA GGG AGC	440	
Ser Leu Asn Phe Gly Ala Thr Val Val Gly Thr Leu Leu Leu Gly Ser		
115 120 125 130		
GCT CAA GAA AAA GCC AAT AAT AAT GGC GGA TCG ATC TGG TTT GGT AAG	488	
Ala Gln Glu Lys Ala Asn Asn Asn Gly Gly Ser Ile Trp Phe Gly Lys		
135 140 145		

370	375	380
Leu Ala Ile Gly Ile Ile Ile Asp Asp Ala Ile Val Val Ile Glu Asn		
385	390	395
Ile His Lys Lys Leu Glu Met Gly Met Ser Lys Arg Lys Ala Ser Tyr		400
	405	410
Glu Gly Val Arg Glu Ile Gly Phe Ala Leu Val Ala Ile Ser Ala Met		415
	420	425
Leu Leu Ser Val Phe Val Pro Ile Gly Asn Met Lys Gly Ile Ile Gly		430
	435	440
Arg Phe Phe Gln Ser Phe Gly Ile Thr Val Ala Leu Ala Ile Ala Leu		445
	450	455
Ser Tyr Val Val Val Val Thr Ile Ile Pro Met Val Ser Ser Val Val		460
465	470	475
Val Asn Pro Arg His Ser Arg Phe Tyr Val Trp Ser Glu Pro Phe Phe		480
	485	490
Lys Ala Leu Glu Ser Arg Tyr Thr Lys Leu Leu Gln Trp Val Leu Asn		495
	500	505
His Lys Ile Ile Ile Ser Ile Ala Val Val Leu Val Phe Val Gly Ser		510
	515	520
Leu Phe Val Ala Ser Lys Ile Gly Met Glu Phe Met Leu Lys Glu Asp		525
	530	535
Arg Gly Arg Phe Leu Val Trp Leu Lys Ala Lys Pro Gly Val Ser Ile		540
545	550	555
Asp Tyr Met Thr Gln Lys Ser Lys Ile Phe Gln Lys Ala Ile Glu Lys		560
	565	570
His Ala Glu Val Glu Phe Thr Thr Leu Gln Val Gly Tyr Gly Thr Thr		575
	580	585
Gln Asn Pro Phe Lys Ala Lys Ile Phe Val Gln Leu Lys Pro Leu Lys		590
	595	600
Glu Arg Lys Lys Glu His Gln Leu Gly Gln Phe Glu Leu Met Ser Val		605
	610	615
Leu Arg Lys Glu Leu Arg Ser Leu Pro Glu Ala Lys Gly Leu Asp Thr		620
625	630	635
Ile Asn Leu Ser Glu Val Thr Leu Ile Gly Gly Gly Gly Asp Ser Ser		640
	645	650
Pro Phe Gln Thr Phe Val Phe Ser His Ser Gln Glu Ala Val Asp Lys		655
	660	665
Ser Val Glu Asn Leu Lys Lys Phe Leu Leu Glu Ser Pro Glu Leu Lys		670
	675	680
Gly Lys Val Glu Ser Tyr His Thr Ser Thr Ser Glu Ser Gln Pro Gln		685
	690	695
Leu Gln Leu Lys Ile Leu Arg Gln Asn Ala Asn Lys Tyr Gly Val Ser		700
705	710	715
Ala Gln Thr Ile Gly Ser Val Val Ser Ser Ala Phe Ser Gly Thr Ser		720
	725	730
Gln Ala Ser Val Phe Lys Glu Asp Gly Lys Glu Tyr Asp Met Ile Leu		735
	740	745
Glu Cys Leu Met Thr Ser Ala Phe Leu		750
755	760	

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6025 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

```

Met Tyr Lys Thr Ala Ile Asn Arg Pro Ile Thr Thr Leu Met Phe Ala
 1           5           10           15
Leu Ala Ile Val Phe Phe Gly Thr Met Gly Phe Lys Lys Leu Ser Val
      20           25           30
Ala Leu Phe Pro Lys Ile Asp Leu Pro Thr Val Val Val Thr Thr Thr
      35           40           45
Tyr Pro Gly Ala Ser Ala Glu Ile Ile Glu Ser Lys Val Thr Asp Lys
      50           55           60
Ile Glu Glu Ala Val Met Gly Ile Asp Gly Ile Lys Lys Val Thr Ser
      65           70           75           80
Thr Ser Ser Lys Asn Val Ser Ile Val Val Ile Glu Phe Glu Leu Glu
      85           90           95
Lys Pro Asn Glu Glu Ala Leu Asn Asp Val Val Asn Lys Ile Ser Ser
      100          105          110
Val Arg Phe Asp Asp Ser Asn Ile Lys Lys Pro Ser Ile Asn Lys Phe
      115          120          125
Asp Thr Asp Ser Gln Ala Ile Ile Ser Leu Phe Val Ser Ser Ser Ser
      130          135          140
Val Pro Ala Thr Thr Leu Asn Asp Tyr Ala Lys Asn Thr Ile Lys Pro
      145          150          155          160
Met Leu Gln Lys Ile Asn Gly Val Gly Gly Val Gln Leu Asn Gly Phe
      165          170          175
Arg Glu Arg Gln Ile Arg Ile Tyr Ala Asn Pro Thr Leu Met Asn Lys
      180          185          190
Tyr Asn Leu Thr Tyr Ala Asp Leu Phe Ser Thr Leu Lys Ala Glu Asn
      195          200          205
Val Glu Ile Asp Gly Gly Arg Ile Val Asn Ser Gln Arg Glu Phe Ser
      210          215          220
Ile Leu Ile Asn Ala Asn Ser Tyr Ser Val Ala Asp Val Glu Lys Ile
      225          230          235          240
Gln Val Gly Asn His Val Arg Leu Gly Asp Ile Ala Lys Ile Glu Ile
      245          250          255
Gly Leu Glu Glu Asp Asn Thr Phe Ala Ser Phe Lys Asp Lys Pro Gly
      260          265          270
Val Ile Leu Glu Ile Gln Lys Ile Ala Gly Ala Asn Glu Ile Glu Ile
      275          280          285
Val Asp Arg Val Tyr Glu Ala Leu Lys Arg Ile Gln Ala Ile Ser Pro
      290          295          300
Asn Tyr Glu Ile Arg Pro Phe Leu Asp Thr Thr Gly Tyr Ile Arg Thr
      305          310          315          320
Ser Ile Glu Asp Val Lys Phe Asp Leu Val Leu Gly Ala Ile Leu Ala
      325          330          335
Val Leu Val Val Phe Ala Phe Leu Arg Asn Gly Thr Ile Thr Leu Val
      340          345          350
Ser Ala Ile Ser Ile Pro Ile Ser Ile Met Gly Thr Phe Ala Leu Ile
      355          360          365
Gln Trp Met Gly Phe Ser Leu Asn Met Leu Thr Met Val Ala Leu Thr

```

GAA GTG GAA TTC ACC ACC TTG CAA GTG GGT TAT GGC ACC ACA CAA AAC	1832
Glu Val Glu Phe Thr Thr Leu Gln Val Gly Tyr Gly Thr Thr Gln Asn	
580 585 590	
CCT TTT AAG GCT AAG ATT TTT GTG CAA CTC AAG CCT TTA AAA GAG CGT	1880
Pro Phe Lys Ala Lys Ile Phe Val Gln Leu Lys Pro Leu Lys Glu Arg	
595 600 605 610	
AAA AAA GAG CAT CAA TTG GGG CAA TTT GAG TTG ATG AGC GTT TTA AGG	1928
Lys Lys Glu His Gln Leu Gly Gln Phe Glu Leu Met Ser Val Leu Arg	
615 620 625	
AAA GAG TTG AGA AGC TTG CCT GAA GCT AAA GGT TTA GAT ACT ATT AAT	1976
Lys Glu Leu Arg Ser Leu Pro Glu Ala Lys Gly Leu Asp Thr Ile Asn	
630 635 640	
CTT TCT GAA GTT ACT CTT ATA GGG GGC GGT GGG GAT AGT TCG CCC TTC	2024
Leu Ser Glu Val Thr Leu Ile Gly Gly Gly Gly Asp Ser Ser Pro Phe	
645 650 655	
CAA ACC TTT GTG TTT TCC CAT TCT CAA GAA GCG GTG GAT AAA AGC GTG	2072
Gln Thr Phe Val Phe Ser His Ser Gln Glu Ala Val Asp Lys Ser Val	
660 665 670	
GAG AAT TTG AAA AAA TTC TTA TTA GAA AGC CCT GAA TTA AAA GGC AAG	2120
Glu Asn Leu Lys Lys Phe Leu Leu Glu Ser Pro Glu Leu Lys Gly Lys	
675 680 685 690	
GTT GAA AGC TAT CAT ACA AGC ACG AGC GAA TCG CAA CCG CAA TTG CAA	2168
Val Glu Ser Tyr His Thr Ser Thr Ser Glu Ser Gln Pro Gln Leu Gln	
695 700 705	
CTC AAA ATC TTA AGA CAA AAC GCT AAC AAA TAC GGC GTG AGC GCT CAA	2216
Leu Lys Ile Leu Arg Gln Asn Ala Asn Lys Tyr Gly Val Ser Ala Gln	
710 715 720	
ACC ATT GGA TCA GTG GTG AGC TCT GCT TTT TCT GGG ACT TCT CAA GCG	2264
Thr Ile Gly Ser Val Val Ser Ser Ala Phe Ser Gly Thr Ser Gln Ala	
725 730 735	
AGC GTG TTC AAA GAA GAT GGC AAA GAA TAC GAC ATG ATC TTA GAG TGC	2312
Ser Val Phe Lys Glu Asp Gly Lys Glu Tyr Asp Met Ile Leu Glu Cys	
740 745 750	
CTG ATG ACA AGC GCG TTT CTG TAGAAGACAT CAAACGCTTG CAAGTGC GTA ACAA	2367
Leu Met Thr Ser Ala Phe Leu	
755 760	
ATACGATAAA TTGATGTTT	2386

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 761 amino acids

(B) TYPE: amino acid

Ile	Ser	Ile	Pro	Ile	Ser	Ile	Met	Gly	Thr	Phe	Ala	Leu	Ile	Gln	Trp	
355					360					365					370	
ATG	GGC	TTT	TCA	TTA	AAC	ATG	CTC	ACC	ATG	GTG	GCT	TTA	ACG	TTG	GCG	1208
Met	Gly	Phe	Ser	Leu	Asn	Met	Leu	Thr	Met	Val	Ala	Leu	Thr	Leu	Ala	
				375					380					385		
ATA	GGG	ATT	ATC	ATT	GAT	GAT	GCG	ATC	GTG	GTG	ATT	GAA	AAC	ATC	CAT	1256
Ile	Gly	Ile	Ile	Ile	Asp	Asp	Ala	Ile	Val	Val	Ile	Glu	Asn	Ile	His	
			390					395					400			
AAA	AAG	CTA	GAA	ATG	GGC	ATG	AGT	AAA	CGA	AAA	GCG	AGC	TAT	GAG	GGG	1304
Lys	Lys	Leu	Glu	Met	Gly	Met	Ser	Lys	Arg	Lys	Ala	Ser	Tyr	Glu	Gly	
		405					410					415				
GTG	AGA	GAA	ATT	GGC	TTT	GCT	CTA	GTG	GCG	ATT	TCA	GCG	ATG	CTG	CTC	1352
Val	Arg	Glu	Ile	Gly	Phe	Ala	Leu	Val	Ala	Ile	Ser	Ala	Met	Leu	Leu	
	420					425					430					
TCT	GTT	TTT	GTG	CCT	ATA	GGG	AAC	ATG	AAA	GGC	ATT	ATT	GGG	CGT	TTT	1400
Ser	Val	Phe	Val	Pro	Ile	Gly	Asn	Met	Lys	Gly	Ile	Ile	Gly	Arg	Phe	
435					440					445					450	
TTT	CAA	AGT	TTT	GGG	ATC	ACG	GTG	GCT	TTA	GCG	ATC	GCT	CTA	TCG	TAT	1448
Phe	Gln	Ser	Phe	Gly	Ile	Thr	Val	Ala	Leu	Ala	Ile	Ala	Leu	Ser	Tyr	
				455					460					465		
GTG	GTG	GTC	GTT	ACG	ATT	ATC	CCC	ATG	GTA	AGC	TCA	GTC	GTG	GTC	AAT	1496
Val	Val	Val	Val	Thr	Ile	Ile	Pro	Met	Val	Ser	Ser	Val	Val	Val	Asn	
			470					475					480			
CCC	AGG	CAT	TCT	CGT	TTT	TAT	GTG	TGG	AGT	GAG	CCT	TTT	TTT	AAG	GCT	1544
Pro	Arg	His	Ser	Arg	Phe	Tyr	Val	Trp	Ser	Glu	Pro	Phe	Phe	Lys	Ala	
		485					490					495				
TTA	GAG	TCT	CGT	TAT	ACC	AAG	TTG	CTC	CAA	TGG	GTA	TTA	AAC	CAC	AAG	1592
Leu	Glu	Ser	Arg	Tyr	Thr	Lys	Leu	Leu	Gln	Trp	Val	Leu	Asn	His	Lys	
	500					505					510					
ATC	ATT	ATC	TCT	ATA	GCG	GTG	GTT	TTG	GTG	TTT	GTG	GGA	TCG	CTT	TTT	1640
Ile	Ile	Ile	Ser	Ile	Ala	Val	Val	Leu	Val	Phe	Val	Gly	Ser	Leu	Phe	
515					520					525					530	
GTG	GCT	TCT	AAG	ATT	GGT	ATG	GAG	TTC	ATG	CTG	AAA	GAA	GAT	AGG	GGG	1688
Val	Ala	Ser	Lys	Ile	Gly	Met	Glu	Phe	Met	Leu	Lys	Glu	Asp	Arg	Gly	
				535					540					545		
AGG	TTT	TTG	GTG	TGG	CTT	AAG	GCT	AAA	CCG	GGC	GTG	AGC	ATA	GAT	TAC	1736
Arg	Phe	Leu	Val	Trp	Leu	Lys	Ala	Lys	Pro	Gly	Val	Ser	Ile	Asp	Tyr	
			550					555					560			
ATG	ACA	CAA	AAG	AGT	AAG	ATC	TTT	CAA	AAA	GCG	ATT	GAA	AAA	CAT	GCT	1784
Met	Thr	Gln	Lys	Ser	Lys	Ile	Phe	Gln	Lys	Ala	Ile					

135						140						145						
GCT	ACA	ACC	CTT	AAT	GAC	TAC	GCT	AAA	AAC	ACC	ATC	AAA	CCC	ATG	CTC	536		
Ala	Thr	Thr	Leu	Asn	Asp	Tyr	Ala	Lys	Asn	Thr	Ile	Lys	Pro	Met	Leu			
			150					155					160					
CAA	AAA	ATC	AAT	GGG	GTA	GGG	GGC	GTG	CAG	CTC	AAC	GGC	TTT	AGG	GAG	584		
Gln	Lys	Ile	Asn	Gly	Val	Gly	Gly	Val	Gln	Leu	Asn	Gly	Phe	Arg	Glu			
			165					170					175					
CGC	CAG	ATT	AGG	ATT	TAT	GCA	AAT	CCC	ACT	TTG	ATG	AAT	AAA	TAC	AAC	632		
Arg	Gln	Ile	Arg	Ile	Tyr	Ala	Asn	Pro	Thr	Leu	Met	Asn	Lys	Tyr	Asn			
			180					185					190					
CTG	ACT	TAT	GCG	GAT	CTT	TTC	AGC	ACG	CTT	AAA	GCG	GAG	AAT	GTG	GAA	680		
Leu	Thr	Tyr	Ala	Asp	Leu	Phe	Ser	Thr	Leu	Lys	Ala	Glu	Asn	Val	Glu			
195					200					205					210			
ATT	GAT	GGG	GGG	CGC	ATT	GTC	AAT	AGC	CAA	AGG	GAA	TTT	TCT	ATT	TTA	728		
Ile	Asp	Gly	Gly	Arg	Ile	Val	Asn	Ser	Gln	Arg	Glu	Phe	Ser	Ile	Leu			
				215					220					225				
ATC	AAT	GCG	AAT	AGT	TAT	AGC	GTT	GCG	GAT	GTG	GAA	AAG	ATT	CAA	GTG	776		
Ile	Asn	Ala	Asn	Ser	Tyr	Ser	Val	Ala	Asp	Val	Glu	Lys	Ile	Gln	Val			
				230				235					240					
GGT	AAT	CAT	GTG	CGT	CTT	GGC	GAT	ATT	GCA	AAA	ATT	GAA	ATC	GGT	TTG	824		
Gly	Asn	His	Val	Arg	Leu	Gly	Asp	Ile	Ala	Lys	Ile	Glu	Ile	Gly	Leu			
			245					250					255					
GAA	GAA	GAC	AAC	ACT	TTT	GCG	AGC	TTT	AAA	GAC	AAA	CCC	GGT	GTG	ATT	872		
Glu	Glu	Asp	Asn	Thr	Phe	Ala	Ser	Phe	Lys	Asp	Lys	Pro	Gly	Val	Ile			
			260					265					270					
TTA	GAA	ATC	CAA	AAG	ATT	GCC	GGA	GCG	AAT	GAA	ATT	GAA	ATC	GTA	GAT	920		
Leu	Glu	Ile	Gln	Lys	Ile	Ala	Gly	Ala	Asn	Glu	Ile	Glu	Ile	Val	Asp			
275					280					285					290			
AGG	GTG	TAT	GAA	GCT	TTA	AAG	CGC	ATT	CAA	GCC	ATT	AGC	CCT	AAC	TAT	968		
Arg	Val	Tyr	Glu	Ala	Leu	Lys	Arg	Ile	Gln	Ala	Ile	Ser	Pro	Asn	Tyr			
				295					300					305				
GAA	ATC	AGA	CCC	TTT	TTA	GAC	ACC	ACG	GGC	TAT	ATC	CGC	ACC	TCT	ATT	1016		
Glu	Ile	Arg	Pro	Phe	Leu	Asp	Thr	Thr	Gly	Tyr	Ile	Arg	Thr	Ser	Ile			
				310				315					320					
GAA	GAC	GTG	AAA	TTT	GAT	CTA	GTT	TTA	GGG	GCG	ATT	TTA	GCG	GTT	TTA	1064		
Glu	Asp	Val	Lys	Phe	Asp	Leu	Val	Leu	Gly	Ala	Ile	Leu	Ala	Val	Leu			
				325				330					335					
GTG	GTG	TTT	GCG	TTC	TTG	CGT	AAC	GGC	ACG	ATC	ACC	CTC</						

- (A) LENGTH: 2386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...2333
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

TGGGGCTTTT TGGCGATGGG TTTATCCAAA CGAAATAATA GGATATTTTG	ATG TAT	56
	Met Tyr	
	1	
AAA ACA GCG ATT AAT CGT CCT ATT ACG ACC TTA ATG TTT GCT TTG GCG		104
Lys Thr Ala Ile Asn Arg Pro Ile Thr Thr Leu Met Phe Ala Leu Ala		
5 10 15		
ATT GTC TTT TTT GGG ACT ATG GGG TTT AAA AAA TTG AGC GTG GCG CTT		152
Ile Val Phe Phe Gly Thr Met Gly Phe Lys Lys Leu Ser Val Ala Leu		
20 25 30		
TTC CCT AAA ATT GAT TTG CCT ACG GTG GTG GTT ACT ACG ACT TAT CCT		200
Phe Pro Lys Ile Asp Leu Pro Thr Val Val Val Thr Thr Thr Tyr Pro		
35 40 45 50		
GGG GCT AGC GCT GAA ATC ATA GAG AGT AAG GTA ACC GAT AAG ATT GAA		248
Gly Ala Ser Ala Glu Ile Ile Glu Ser Lys Val Thr Asp Lys Ile Glu		
55 60 65		
GAA GCG GTG ATG GGG ATT GAT GGG ATC AAA AAG GTT ACT TCC ACG AGT		296
Glu Ala Val Met Gly Ile Asp Gly Ile Lys Lys Val Thr Ser Thr Ser		
70 75 80		
TCT AAA AAT GTG AGT ATC GTC GTC ATT GAA TTT GAG TTA GAA AAA CCT		344
Ser Lys Asn Val Ser Ile Val Val Ile Glu Phe Glu Leu Glu Lys Pro		
85 90 95		
AAT GAA GAA GCC TTA AAC GAT GTG GTG AAT AAA ATT TCT TCG GTG CGT		392
Asn Glu Glu Ala Leu Asn Asp Val Val Asn Lys Ile Ser Ser Val Arg		
100 105 110		
TTT GAT GAC TCT AAC ATT AAA AAA CCC TCT ATC AAT AAA TTT GAT ACC		440
Phe Asp Asp Ser Asn Ile Lys Lys Pro Ser Ile Asn Lys Phe Asp Thr		
115 120 125 130		
GAC AGC CAA GCC ATT ATT TCA TTG TTT GTG AGC AGT TCA AGC GTG CCG		488
Asp Ser Gln Ala Ile Ile Ser Leu Phe Val Ser Ser Ser Ser Val Pro		

TTT GAT AAG GAC GCT TTG AGC GAA GGG TTG CAT AAA ATG TCC TTA GAC 536
 Phe Asp Lys Asp Ala Leu Ser Glu Gly Leu His Lys Met Ser Leu Asp
 150 155 160

AAT CAA GCG GTG AGT ATC CTT GTG GCT AAA GTG GAA GAA ATC TTT AAA 584
 Asn Gln Ala Val Ser Ile Leu Val Ala Lys Val Glu Glu Ile Phe Lys
 165 170 175

GAT TCT GTC AAT TAC GGA GAT GTT AAA GTC CCT ATA GCC ATG TAGGCTTAG 635
 Asp Ser Val Asn Tyr Gly Asp Val Lys Val Pro Ile Ala Met
 180 185 190

AACAACAAGC GTTCCTCGCT ATCGTCTGTT CTTTGGGGG TGGG 679

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Val	Leu	Glu	Lys	Ser	Phe	Leu	Lys	Ser	Lys	Gln	Leu	Phe	Leu	Cys	Gly
1				5					10					15	
Leu	Gly	Val	Leu	Met	Leu	Gln	Ala	Cys	Thr	Cys	Pro	Asn	Thr	Ser	Gln
			20					25					30		
Arg	Asn	Ser	Phe	Leu	Gln	Asp	Val	Pro	Tyr	Trp	Met	Leu	Gln	Asn	Arg
			35				40					45			
Ser	Glu	Tyr	Ile	Thr	Gln	Gly	Val	Asp	Ser	Ser	His	Ile	Val	Asp	Gly
			50			55					60				
Lys	Lys	Thr	Glu	Glu	Ile	Glu	Lys	Ile	Ala	Thr	Lys	Arg	Ala	Thr	Ile
65					70				75					80	
Arg	Val	Ala	Gln	Asn	Ile	Val	His	Lys	Leu	Lys	Glu	Ala	Tyr	Leu	Ser
				85				90						95	
Lys	Thr	Asn	Arg	Ile	Lys	Gln	Lys	Ile	Thr	Asn	Glu	Met	Phe	Ile	Gln
			100					105					110		
Met	Thr	Gln	Pro	Ile	Tyr	Asp	Ser	Leu	Met	Asn	Val	Asp	Arg	Leu	Gly
			115				120					125			
Ile	Tyr	Ile	Asn	Pro	Asn	Asn	Glu	Glu	Val	Phe	Ala	Leu	Val	Arg	Ala
			130			135					140				
Arg	Gly	Phe	Asp	Lys	Asp	Ala	Leu	Ser	Glu	Gly	Leu	His	Lys	Met	Ser
145				150					155					160	
Leu	Asp	Asn	Gln	Ala	Val	Ser	Ile	Leu	Val	Ala	Lys	Val	Glu	Glu	Ile
				165				170						175	
Phe	Lys	Asp	Ser	Val	Asn	Tyr	Gly	Asp	Val	Lys	Val	Pro	Ile	Ala	Met
			180				185						190		

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...626
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

TCTTAAAGAT TTATGTTACA CTCTGTGAAA TCAAAATCAA AGGGGATAGC	GTG TTA	56
	Val Leu	
	1	
GAA AAA TCT TTT TTA AAA AGC AAG CAA TTA TTT TTA TGC GGA CTG GGT		104
Glu Lys Ser Phe Leu Lys Ser Lys Gln Leu Phe Leu Cys Gly Leu Gly		
5 10 15		
GTT TTG ATG CTG CAG GCT TGC ACT TGC CCA AAC ACT TCA CAA AGG AAT		152
Val Leu Met Leu Gln Ala Cys Thr Cys Pro Asn Thr Ser Gln Arg Asn		
20 25 30		
TCT TTC TTG CAA GAT GTG CCT TAT TGG ATG TTG CAA AAT CGC AGT GAG		200
Ser Phe Leu Gln Asp Val Pro Tyr Trp Met Leu Gln Asn Arg Ser Glu		
35 40 45 50		
TAT ATC ACG CAA GGG GTG GAT AGC TCG CAC ATT GTA GAT GGT AAG AAA		248
Tyr Ile Thr Gln Gly Val Asp Ser Ser His Ile Val Asp Gly Lys Lys		
55 60 65		
ACT GAA GAG ATA GAA AAA ATC GCT ACC AAA AGA GCG ACA ATA AGA GTG		296
Thr Glu Glu Ile Glu Lys Ile Ala Thr Lys Arg Ala Thr Ile Arg Val		
70 75 80		
GCA CAA AAT ATT GTG CAT AAA CTT AAA GAA GCT TAC CTT TCC AAA ACC		344
Ala Gln Asn Ile Val His Lys Leu Lys Glu Ala Tyr Leu Ser Lys Thr		
85 90 95		
AAT CGC ATC AAG CAA AAG ATC ACT AAT GAA ATG TTT ATC CAA ATG ACA		392
Asn Arg Ile Lys Gln Lys Ile Thr Asn Glu Met Phe Ile Gln Met Thr		
100 105 110		
CAG CCC ATT TAT GAC AGC TTG ATG AAT GTG GAT CGT TTA GGG ATT TAT		440
Gln Pro Ile Tyr Asp Ser Leu Met Asn Val Asp Arg Leu Gly Ile Tyr		
115 120 125 130		
ATC AAT CCT AAC AAT GAG GAA GTG TTT GCG TTA GTG CGC GCG CGT GGT		488
Ile Asn Pro Asn Asn Glu Glu Val Phe Ala Leu Val Arg Ala Arg Gly		
135 140 145		

```

Gln Gly Phe Ala Leu Ala Ile Leu Gly Leu His Thr Gln Phe Trp Ala
      100                      105                      110
Leu Phe Val Phe Phe Ser Val Val Val Leu Leu Ala Val Leu Leu Phe
      115                      120                      125
Phe Ala Pro Asn Ala Gln Pro Phe Lys Asp His Ser Leu Asn Ala Leu
      130                      135                      140
Gln Lys Ile Ala Phe Tyr Val Phe Phe Met Val Val Gly Ser Asn Ala
      145                      150                      155                      160
Val Gln Ala Phe Ile Ser Thr Gly Pro Phe Pro Tyr Ile Gly Gln Ser
      165                      170                      175
Asp Pro Val Arg Phe Ser Trp Asn Leu Lys Glu Ser Val Trp Ser Met
      180                      185                      190
Glu Asn Trp Asp His Leu Lys Phe Pro Arg Ser Val Leu Gly Arg Arg
      195                      200                      205
Asp Val Gly Glu Pro Leu Lys Leu Ser Ala Leu Pro Lys Asp Asn Asp
      210                      215                      220
Tyr Glu Arg Ser Pro Leu Glu Ile Thr Lys Thr Leu Lys Ile Gly Lys
      225                      230                      235                      240
Lys Glu Glu Leu Phe Leu Lys Leu Asn Gly Ala Ile Thr Asp Leu Ser
      245                      250                      255
Phe Asn Glu Asp Lys Ala Ile Leu Thr Thr Glu Asn Gln Gly Leu Tyr
      260                      265                      270
Leu Val Ser Asn Asp Leu Lys Thr Ile His Ser His Met Val Leu Asp
      275                      280                      285
Ser Tyr Tyr Ser Ala Thr Val Gly Ser Phe Val Gly Ala Asp Phe Asn
      290                      295                      300
Glu Asp Glu Asn Ile Val Ile Met Gly Asn Asn Lys Thr Ser Val Glu
      305                      310                      315                      320
Ile Thr Pro Asn Lys Asn Ala Asn Met Leu Lys Asn Phe Pro Tyr Phe
      325                      330                      335
Leu Glu Gly Val Asn Ser Phe Asp Glu Val Glu Arg Ser Arg Leu Lys
      340                      345                      350
Thr Ser Arg Ala Lys Asn Tyr Tyr Val Ser Val Ala Arg Arg Gly Ala
      355                      360                      365
Lys Phe Thr Tyr Leu Ile Ser Ala Pro Asn Lys Arg Tyr Lys Asp Leu
      370                      375                      380
Ile Ile Ile Ser Met Arg Asn Ser Asp Lys Gln Val His Gly Glu Phe
      385                      390                      395                      400
Leu Leu Glu Leu Gly Asn Ala Lys Leu Lys Glu Lys Arg Gly Leu Gly
      405                      410                      415
Glu Leu Val Ile Ser Thr Leu Ala Leu Lys Asp Asn Lys Leu Tyr Ala
      420                      425                      430
Phe Ser Lys Glu Phe Asn Thr Leu Leu Val Ile Asp Pro Thr Lys Glu
      435                      440                      445
Glu Ile Leu Glu Val Tyr Gly Leu Pro Lys Glu Ile Lys Asn Ile Ser
      450                      455                      460
Ala Gly Gly Phe Arg Asn Asp Glu Leu Val Leu Val Ser Tyr Glu Asn
      465                      470                      475                      480
Asn Lys Asn Ile Leu Tyr Thr Leu Asn Phe
      485                      490

```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 679 base pairs

```

ATT TCC ATG CGT AAT AGC GAT AAA CAG GTG CAT GGG GAG TTT TTA CTG      1256
Ile Ser Met Arg Asn Ser Asp Lys Gln Val His Gly Glu Phe Leu Leu
              390                      395                      400

GAA TTA GGC AAT GCC AAA CTT AAA GAA AAA AGG GGA TTG GGC GAG TTA      1304
Glu Leu Gly Asn Ala Lys Leu Lys Glu Lys Arg Gly Leu Gly Glu Leu
              405                      410                      415

GTC ATT AGC ACT TTG GCT TTA AAG GAT AAT AAA CTT TAT GCG TTC AGT      1352
Val Ile Ser Thr Leu Ala Leu Lys Asp Asn Lys Leu Tyr Ala Phe Ser
              420                      425                      430

AAG GAA TTT AAC ACG CTT TTA GTC ATA GAC CCT ACA AAA GAA GAG ATT      1400
Lys Glu Phe Asn Thr Leu Leu Val Ile Asp Pro Thr Lys Glu Glu Ile
              435                      440                      445                      450

CTT GAA GTT TAT GGC TTG CCT AAA GAG ATT AAA AAT ATC AGT GCT GGA      1448
Leu Glu Val Tyr Gly Leu Pro Lys Glu Ile Lys Asn Ile Ser Ala Gly
              455                      460                      465

GGG TTT AGA AAC GAT GAG CTT GTC CTT GTG AGC TAT GAG AAT AAT AAA      1496
Gly Phe Arg Asn Asp Glu Leu Val Leu Val Ser Tyr Glu Asn Asn Lys
              470                      475                      480

AAT ATT CTC TAC ACC CTT AAT TTT TAAACTCTTT TAAAGCTACT TTTTCTAAT      1550
Asn Ile Leu Tyr Thr Leu Asn Phe
              485                      490

ATATTAACGC ATTAGAAGAT GGT                                          1573

```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

```

Met Asp Lys Glu Thr Arg Phe Tyr Asn Leu Phe Ser Leu Ala Ile Leu
 1          5          10          15
Gly Ile Leu Ile Phe Pro Val Gly Leu Ala Asn Phe Tyr Phe Gly Tyr
 20          25          30
Val Leu Lys Asp Ser Pro Cys Ile Phe Cys Trp Ala Gln Arg Ile Asn
 35          40          45
Met Ile Leu Ile Gly Ala Val Ala Leu Leu Val Val Arg Phe Gly Phe
 50          55          60
Lys Pro Lys Tyr Ile Ala Leu Leu Leu Leu Met Ala Ser Ser Gly Leu
 65          70          75          80
Tyr Glu Ser Phe Tyr His Thr Gly Ser His Ala Leu Glu Asp Val Gly
 85          90          95

```

GCG TTT ATT TCT ACC GGG CCT TTC CCT TAC ATA GGG CAA AGC GAT CCG	584
Ala Phe Ile Ser Thr Gly Pro Phe Pro Tyr Ile Gly Gln Ser Asp Pro	
165 170 175	
GTG CGT TTT TCG TGG AAT TTG AAA GAA TCG GTC TGG TCT ATG GAG AAT	632
Val Arg Phe Ser Trp Asn Leu Lys Glu Ser Val Trp Ser Met Glu Asn	
180 185 190	
TGG GAT CAT TTG AAA TTC CCA AGA AGC GTT TTG GGC AGA AGG GAT GTG	680
Trp Asp His Leu Lys Phe Pro Arg Ser Val Leu Gly Arg Arg Asp Val	
195 200 205 210	
GGC GAG CCT TTG AAA TTG AGC GCT TTG CCT AAA GAT AAC GAT TAT GAG	728
Gly Glu Pro Leu Lys Leu Ser Ala Leu Pro Lys Asp Asn Asp Tyr Glu	
215 220 225	
CGT TCG CCT TTA GAA ATT ACA AAA ACT CTA AAG ATT GGA AAA AAA GAA	776
Arg Ser Pro Leu Glu Ile Thr Lys Thr Leu Lys Ile Gly Lys Lys Glu	
230 235 240	
GAG CTT TTT TTA AAA TTG AAT GGA GCG ATC ACG GAT TTG AGT TTC AAT	824
Glu Leu Phe Leu Lys Leu Asn Gly Ala Ile Thr Asp Leu Ser Phe Asn	
245 250 255	
GAA GAC AAG GCG ATT CTT ACC ACA GAA AAC CAA GGG CTT TAT CTT GTA	872
Glu Asp Lys Ala Ile Leu Thr Thr Glu Asn Gln Gly Leu Tyr Leu Val	
260 265 270	
AGT AAC GAT TTG AAA ACC ATT CAT AGC CAT ATG GTG TTG GAT AGC TAT	920
Ser Asn Asp Leu Lys Thr Ile His Ser His Met Val Leu Asp Ser Tyr	
275 280 285 290	
TAT AGC GCG ACG GTG GGG TCG TTC GTG GGG GCG GAT TTC AAC GAA GAT	968
Tyr Ser Ala Thr Val Gly Ser Phe Val Gly Ala Asp Phe Asn Glu Asp	
295 300 305	
GAA AAC ATT GTG ATC ATG GGC AAT AAT AAA ACG AGC GTG GAA ATC ACT	1016
Glu Asn Ile Val Ile Met Gly Asn Asn Lys Thr Ser Val Glu Ile Thr	
310 315 320	
CCT AAC AAA AAC GCT AAC ATG CTT AAA AAC TTC CCT TAT TTT TTA GAA	1064
Pro Asn Lys Asn Ala Asn Met Leu Lys Asn Phe Pro Tyr Phe Leu Glu	
325 330 335	
GGG GTC AAC TCT TTT GAC GAA GTG GAA CGC AGC CGC TTG AAA ACT TCT	1112
Gly Val Asn Ser Phe Asp Glu Val Glu Arg Ser Arg Leu Lys Thr Ser	
340 345 350	
AGG GCG AAA AAC TAT TAT GTT AGC GTT GCA AGA AGA GGG GCT AAA TTC	1160
Arg Ala Lys Asn Tyr Tyr Val Ser Val Ala Arg Arg Gly Ala Lys Phe	
355 360 365 370	
ACT TAT TTG ATC AGC GCT CCT AAC AAG CGT TAT AAG GAT TTG ATT ATT	1208
Thr Tyr Leu Ile Ser Ala Pro Asn Lys Arg Tyr Lys Asp Leu Ile Ile	
375 380 385	

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...1520

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

TAGCCACAG	CTCTAGCGTT	TTGCCTAACA	TGAATCTATA	AGGGGGATGC	ATG	GAT	56
					Met	Asp	
					1		
AAA GAA ACC CGA TTT TAC AAC CTT TTT TCT TTG GCA ATT TTA GGG ATT	104						
Lys Glu Thr Arg Phe Tyr Asn Leu Phe Ser Leu Ala Ile Leu Gly Ile							
5 10 15							
TTG ATC TTT CCT GTG GGT TTG GCG AAT TTT TAT TTT GGC TAT GTT TTG	152						
Leu Ile Phe Pro Val Gly Leu Ala Asn Phe Tyr Phe Gly Tyr Val Leu							
20 25 30							
AAA GAT TCG CCT TGT ATT TTT TGC TGG GCG CAA CGC ATC AAC ATG ATT	200						
Lys Asp Ser Pro Cys Ile Phe Cys Trp Ala Gln Arg Ile Asn Met Ile							
35 40 45 50							
TTA ATA GGG GCT GTG GCG CTT TTG GTG GTG CGT TTT GGG TTT AAG CCT	248						
Leu Ile Gly Ala Val Ala Leu Leu Val Val Arg Phe Gly Phe Lys Pro							
55 60 65							
AAA TAC ATT GCC TTG CTG TTG CTT ATG GCT AGT AGC GGG TTA TAT GAG	296						
Lys Tyr Ile Ala Leu Leu Leu Leu Met Ala Ser Ser Gly Leu Tyr Glu							
70 75 80							
AGC TTT TAT CAT ACC GGT AGC CAT GCT TTA GAA GAT GTG GGG CAG GGA	344						
Ser Phe Tyr His Thr Gly Ser His Ala Leu Glu Asp Val Gly Gln Gly							
85 90 95							
TTC GCG CTC GCT ATT TTG GGC TTG CAC ACG CAG TTT TGG GCG CTT TTT	392						
Phe Ala Leu Ala Ile Leu Gly Leu His Thr Gln Phe Trp Ala Leu Phe							
100 105 110							
GTC TTT TTT AGC GTG GTG GTG CTT TTA GCG GTT TTG CTC TTT TTT GCC	440						
Val Phe Phe Ser Val Val Val Leu Leu Ala Val Leu Leu Phe Phe Ala							
115 120 125 130							
CCT AAT GCC CAA CCT TTC AAA GAT CAT TCG TTA AAC GCG CTC CAA AAA	488						
Pro Asn Ala Gln Pro Phe Lys Asp His Ser Leu Asn Ala Leu Gln Lys							
135 140 145							
ATC GCT TTT TAT GTT TTC TTT ATG GTG GTT GGT TCT AAC GCC GTG CAA	536						
Ile Ala Phe Tyr Val Phe Phe Met Val Val Gly Ser Asn Ala Val Gln							
150 155 160							

```

Ala Leu Gln Asp Leu Val Lys Lys Glu His Ala His Met Leu Ser Ala
      325                      330                      335
Phe Ile Glu Ser Ala Pro Arg Thr Val Lys Ser Leu Asp Val Gln Ile
      340                      345                      350
Thr Gly Leu Pro Tyr Ile Asn Asp Asn Asn Leu Val Asn Ser Gly Val
      355                      360                      365
Ile Leu Pro Ser Phe Pro Met Ala Ile Gly Asn Ile Thr Lys Thr Leu
      370                      375                      380
Gly Tyr Lys Asn Asn Phe Tyr Tyr Gly Gly Ser Gly Ile Trp Asn Lys
385                      390                      395                      400
Leu Thr Ser Phe Thr Lys Lys Gln Gly Phe His Ala Leu Tyr Phe Asn
      405                      410                      415
Asn His Leu Leu Glu Phe Ala Gln Asn Lys Pro Tyr Pro Lys Pro Ile
      420                      425                      430
Glu Ser Asn Trp Gly Val His Asp Asn Ile Leu Phe Asp Tyr Ile Leu
      435                      440                      445
Glu Asn Thr Asn Pro His Glu Lys Thr Phe Ser Met Val Met Thr Leu
      450                      455                      460
Ser Asn His Ala Ile Lys Asn Val Asn Leu Lys Ala Phe Gly Val Pro
465                      470                      475                      480
Leu Glu Lys Ile Gln Gln Phe Val Glu Lys Thr Pro Lys Ser Glu Asn
      485                      490                      495
Leu Pro Asp Ala Asn Ser Leu Gly His Ile Tyr Trp Tyr Asp Lys Val
      500                      505                      510
Ile Val Ser Phe Ile Lys Lys Ala Ser Gln Lys Phe Pro Asn Ser Leu
      515                      520                      525
Phe Ile Ile Thr Gly Asp His Phe Asp Arg Ser Tyr Glu Tyr Ala Lys
530                      535                      540
Asn Asp Leu Tyr Ile Ile Lys Ser Val Pro Leu Ile Leu Tyr Ala Pro
545                      550                      555                      560
Thr Leu Lys Pro Lys Lys Ile Ser Gln Val Gly Ser His Leu Asp Ile
      565                      570                      575
Ala Pro Thr Ile Ile Glu Leu Val Ala Pro Lys Gly Phe Gln Phe Val
      580                      585                      590
Ser Phe Gly Lys Pro Leu Phe Ser Asn Asn Thr Thr Asn Pro Pro Ser
      595                      600                      605
His Pro Asn Tyr Ala Leu Gly Tyr Glu Ala Ile Ala Thr Lys Asp Tyr
610                      615                      620
Phe Tyr Asn Pro Ser Leu Gly Leu Arg Tyr Leu Asn Glu Ser Pro Lys
625                      630                      635                      640
Glu Pro Lys Asp Lys Gln Asn Asp Lys Ile Glu Ala Ser Lys Phe Tyr
      645                      650                      655
Gln Gln Leu Glu Ser Leu Lys Ala Leu Ser Tyr Tyr Leu Leu Tyr His
      660                      665                      670
Gly Ala Asn Leu Lys Asp
      675

```

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ATTTTGTGCTA CAATAATAGG ATTTTAATT

2162

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

```

Met Lys Ser Leu Ser Asn Ala Leu Phe Ser Leu Phe Leu Lys Gly Phe
 1           5           10           15
Tyr Phe Thr Phe Phe Met Ser Leu Leu Phe Val Phe Asn Arg Ile Gly
      20           25           30
Phe Ile Leu Tyr Thr Gly Tyr Tyr Lys His Ala Leu Lys Asn Pro Val
      35           40           45
Phe Asp Glu Ile Ile Lys Thr Leu Phe Asn Gly Ala Arg Tyr Asp Asn
      50           55           60
Arg Val Val Ser Ser Leu Ala Ile Leu Phe Ile Ile Ile Gly Leu Leu
      65           70           75           80
Gly Leu Phe Ile Pro Lys His Gln Thr Lys Met Leu Asn Ile Val Ala
      85           90           95
Tyr Phe Ser Ile Ala Ile Ile Leu Phe Leu Asn Ile Ala Asn Ile Val
      100          105          110
Tyr Tyr Gly Ile Tyr Gly Asn Val Phe Asp Glu Asn Leu Leu Glu Phe
      115          120          125
Leu His Glu Asp Thr Leu Thr Ile Leu Lys Met Ser Gly Glu Tyr Pro
      130          135          140
Ile Phe Ser Ser Phe Ser Leu Phe Leu Ile Leu Ser Val Leu Thr Ser
      145          150          155          160
Phe Ile Tyr Phe Lys Leu Gln Asn Asp Leu Phe Lys Pro Lys Asn Ala
      165          170          175
Tyr Gln Ala Ala His Thr Lys Pro Leu Lys Thr Phe Ile Leu Phe Ala
      180          185          190
Leu Phe Ser Leu Thr Gln Met Phe Tyr Ile Asn Ala Gln Leu Ser Phe
      195          200          205
Val Gly Ala Ser Leu Asp Leu Ser Ile Glu Pro Ala Lys Asp Pro Phe
      210          215          220
Leu Met Lys Ile Thr Pro Gly Ala Phe Arg Asn Leu Tyr Leu Leu Ala
      225          230          235          240
Arg Asn Tyr Arg Gln Ser His Asn Leu Lys Phe Ser Asp Phe Ala Lys
      245          250          255
Glu Thr Pro Leu Glu Val Ala Lys Asn Tyr Phe His Leu Lys Glu Asn
      260          265          270
Pro Ser Asn Asn Leu Tyr Glu Leu Leu Thr Gln Thr Ser Arg Asn Asn
      275          280          285
Ser Asn Gln Thr Ile Gln His Val Phe Tyr Ile Val Ser Glu Ser Leu
      290          295          300
Ser Ser Trp His Phe Asp Pro Lys Phe Asp Ala Ile Gly Leu Thr Ser
      305          310          315          320

```

TTA AGC AAC CAT GCG ATC AAA AAC GTG AAT CTC AAA GCC TTT GGC GTG	1502
Leu Ser Asn His Ala Ile Lys Asn Val Asn Leu Lys Ala Phe Gly Val	
465 470 475	
CCT TTA GAA AAA ATC CAA CAA TTT GTG GAA AAA ACC CCC AAA TCA GAA	1550
Pro Leu Glu Lys Ile Gln Gln Phe Val Glu Lys Thr Pro Lys Ser Glu	
480 485 490 495	
AAT TTA CCG GAC GCT AAT TCT TTA GGG CAT ATT TAC TGG TAT GAC AAA	1598
Asn Leu Pro Asp Ala Asn Ser Leu Gly His Ile Tyr Trp Tyr Asp Lys	
500 505 510	
GTA ATC GTC AGT TTC ATC AAA AAA GCC AGC CAA AAA TTC CCT AAC TCG	1646
Val Ile Val Ser Phe Ile Lys Lys Ala Ser Gln Lys Phe Pro Asn Ser	
515 520 525	
CTT TTT ATC ATC ACA GGG GAT CAT TTT GAC AGG AGC TAT GAA TAC GCT	1694
Leu Phe Ile Ile Thr Gly Asp His Phe Asp Arg Ser Tyr Glu Tyr Ala	
530 535 540	
AAA AAC GAT TTG TAT ATC ATT AAA TCC GTG CCG CTT ATT TTA TAT GCC	1742
Lys Asn Asp Leu Tyr Ile Ile Lys Ser Val Pro Leu Ile Leu Tyr Ala	
545 550 555	
CCT ACT TTA AAG CCT AAA AAA ATC AGT CAG GTC GGA TCG CAT TTA GAC	1790
Pro Thr Leu Lys Pro Lys Lys Ile Ser Gln Val Gly Ser His Leu Asp	
560 565 570 575	
ATC GCC CCT ACG ATT ATT GAA TTA GTC GCC CCT AAA GGC TTT CAA TTC	1838
Ile Ala Pro Thr Ile Ile Glu Leu Val Ala Pro Lys Gly Phe Gln Phe	
580 585 590	
GTG AGT TTT GGG AAG CCT TTA TTT TCT AAC AAT ACA ACA AAC CCC CCA	1886
Val Ser Phe Gly Lys Pro Leu Phe Ser Asn Asn Thr Thr Asn Pro Pro	
595 600 605	
AGC CAC CCC AAT TAC GCG CTA GGC TAT GAA GCG ATC GCT ACC AAA GAT	1934
Ser His Pro Asn Tyr Ala Leu Gly Tyr Glu Ala Ile Ala Thr Lys Asp	
610 615 620	
TAT TTT TAT AAC CCA AGT TTG GGG TTA AGG TAT TTG AAC GAA AGC CCT	1982
Tyr Phe Tyr Asn Pro Ser Leu Gly Leu Arg Tyr Leu Asn Glu Ser Pro	
625 630 635	
AAA GAG CCA AAG GAT AAA CAA AAC GAC AAA ATA GAA GCT TCT AAG TTT	2030
Lys Glu Pro Lys Asp Lys Gln Asn Asp Lys Ile Glu Ala Ser Lys Phe	
640 645 650 655	
TAT CAG CAA TTA GAA TCT TTG AAA GCC CTT AGT TAT TAC TTG CTC TAT	2078
Tyr Gln Gln Leu Glu Ser Leu Lys Ala Leu Ser Tyr Tyr Leu Leu Tyr	
660 665 670	
CAT GGG GCT AAT CTT AAA GAT TGACAACTA GGTTTTTATT CCATTAAACG CATG	2133
His Gly Ala Asn Leu Lys Asp	
675	

GCA CGC AAT TAC AGA CAA AGC CAT AAC CTT AAA TTC AGC GAT TTT GCT	830
Ala Arg Asn Tyr Arg Gln Ser His Asn Leu Lys Phe Ser Asp Phe Ala	
240 245 250 255	
AAA GAA ACG CCT TTA GAA GTG GCG AAA AAT TAT TTC CAT CTT AAA GAG	878
Lys Glu Thr Pro Leu Glu Val Ala Lys Asn Tyr Phe His Leu Lys Glu	
260 265 270	
AAC CCT TCA AAC AAC CTC TAT GAG TTG CTA ACT CAG ACA AGC CGC AAC	926
Asn Pro Ser Asn Asn Leu Tyr Glu Leu Leu Thr Gln Thr Ser Arg Asn	
275 280 285	
AAT TCC AAT CAA ACC ATT CAA CAT GTT TTT TAT ATC GTT TCA GAG TCT	974
Asn Ser Asn Gln Thr Ile Gln His Val Phe Tyr Ile Val Ser Glu Ser	
290 295 300	
TTG AGT TCA TGG CAT TTT GAT CCA AAA TTT GAC GCT ATA GGG CTA ACG	1022
Leu Ser Ser Trp His Phe Asp Pro Lys Phe Asp Ala Ile Gly Leu Thr	
305 310 315	
AGC GCT TTA CAA GAC TTG GTT AAA AAA GAG CAT GCC CAC ATG CTT TCT	1070
Ser Ala Leu Gln Asp Leu Val Lys Lys Glu His Ala His Met Leu Ser	
320 325 330 335	
GCT TTT ATT GAA AGC GCC CCA CGG ACC GTT AAA AGC CTA GAT GTC CAA	1118
Ala Phe Ile Glu Ser Ala Pro Arg Thr Val Lys Ser Leu Asp Val Gln	
340 345 350	
ATC ACA GGC TTA CCC TAT ATC AAT GAT AAT AAC TTA GTC AAT TCA GGG	1166
Ile Thr Gly Leu Pro Tyr Ile Asn Asp Asn Asn Leu Val Asn Ser Gly	
355 360 365	
GTG ATC CTC CCT AGC TTT CCT ATG GCG ATT GGC AAT ATC ACA AAA ACT	1214
Val Ile Leu Pro Ser Phe Pro Met Ala Ile Gly Asn Ile Thr Lys Thr	
370 375 380	
CTG GGT TAT AAA AAC AAC TTT TAT TAT GGG GGT AGC GGG ATT TGG AAC	1262
Leu Gly Tyr Lys Asn Asn Phe Tyr Tyr Gly Gly Ser Gly Ile Trp Asn	
385 390 395	
AAA CTC ACT AGT TTC ACC AAA AAA CAA GGT TTT CAC GCC CTT TAT TTC	1310
Lys Leu Thr Ser Phe Thr Lys Lys Gln Gly Phe His Ala Leu Tyr Phe	
400 405 410 415	
AAT AAC CAT CTC TTA GAA TTT GCC CAA AAC AAG CCC TAC CCT AAA CCC	1358
Asn Asn His Leu Leu Glu Phe Ala Gln Asn Lys Pro Tyr Pro Lys Pro	
420 425 430	
ATA GAG AGC AAC TGG GGA GTG CAT GAT AAT ATT TTA TTT GAC TAT ATT	1406
Ile Glu Ser Asn Trp Gly Val His Asp Asn Ile Leu Phe Asp Tyr Ile	
435 440 445	
TTA GAA AAC ACC AAC CCC CAT GAA AAA ACT TTC AGC ATG GTC ATG ACT	1454
Leu Glu Asn Thr Asn Pro His Glu Lys Thr Phe Ser Met Val Met Thr	
450 455 460	

TTT TAT TTC ACC TTT TTT ATG AGC TTG TTG TTT GTG TTT AAT CGT ATC	158
Phe Tyr Phe Thr Phe Phe Met Ser Leu Leu Phe Val Phe Asn Arg Ile	
20 25 30	
GGC TTT ATC CTT TAT ACT GGC TAT TAT AAG CAT GCT TTA AAA AAC CCT	206
Gly Phe Ile Leu Tyr Thr Gly Tyr Tyr Lys His Ala Leu Lys Asn Pro	
35 40 45	
GTT TTT GAT GAA ATC ATC AAA ACC CTA TTC AAT GGA GCC AGA TAT GAT	254
Val Phe Asp Glu Ile Ile Lys Thr Leu Phe Asn Gly Ala Arg Tyr Asp	
50 55 60	
AAT CGT GTG GTC TCA AGC TTA GCG ATT CTT TTT ATC ATC ATC GGG TTA	302
Asn Arg Val Val Ser Ser Leu Ala Ile Leu Phe Ile Ile Ile Gly Leu	
65 70 75	
TTG GGG TTA TTT ATC CCT AAA CAC CAA ACC AAA ATG CTT AAT ATT GTG	350
Leu Gly Leu Phe Ile Pro Lys His Gln Thr Lys Met Leu Asn Ile Val	
80 85 90 95	
GCG TAT TTT TCT ATC GCT ATT ATC CTG TTT TTA AAC ATT GCA AAC ATT	398
Ala Tyr Phe Ser Ile Ala Ile Ile Leu Phe Leu Asn Ile Ala Asn Ile	
100 105 110	
GTT TAT TAT GGT ATT TAT GGG AAT GTG TTT GAT GAA AAT TTA TTG GAA	446
Val Tyr Tyr Gly Ile Tyr Gly Asn Val Phe Asp Glu Asn Leu Leu Glu	
115 120 125	
TTT TTG CAT GAA GAC ACG CTC ACG ATT TTA AAA ATG AGC GGG GAA TAC	494
Phe Leu His Glu Asp Thr Leu Thr Ile Leu Lys Met Ser Gly Glu Tyr	
130 135 140	
CCT ATT TTT TCT AGT TTT TCA CTC TTT TTA ATC CTT AGC GTT TTA ACC	542
Pro Ile Phe Ser Ser Phe Ser Leu Phe Leu Ile Leu Ser Val Leu Thr	
145 150 155	
TCT TTT ATC TAT TTC AAA CTC CAA AAC GAC CTT TTT AAA CCC AAA AAT	590
Ser Phe Ile Tyr Phe Lys Leu Gln Asn Asp Leu Phe Lys Pro Lys Asn	
160 165 170 175	
GCT TAT CAA GCC GCC CAC ACC AAA CCC CTT AAA ACT TTC ATT TTA TTT	638
Ala Tyr Gln Ala Ala His Thr Lys Pro Leu Lys Thr Phe Ile Leu Phe	
180 185 190	
GCG CTT TTT TCC CTC ACA CAA ATG TTT TAC ATT AAC GCG CAA TTG AGT	686
Ala Leu Phe Ser Leu Thr Gln Met Phe Tyr Ile Asn Ala Gln Leu Ser	
195 200 205	
TTT GTG GGC GCG TCT TTA GAT CTC AGC ATA GAG CCA GCC AAA GAT CCT	734
Phe Val Gly Ala Ser Leu Asp Leu Ser Ile Glu Pro Ala Lys Asp Pro	
210 215 220	
TTT TTA ATG AAA ATT ACC CCC GGA GCG TTT CGC AAC CTT TAT CTT TTA	782
Phe Leu Met Lys Ile Thr Pro Gly Ala Phe Arg Asn Leu Tyr Leu Leu	
225 230 235	

65					70					75					80
Glu	Ala	Lys	Leu	Leu	Ser	Leu	Ile	Lys	Asp	Tyr	Asn	Thr	Asp	Gln	Asn
				85					90					95	
Ile	Ser	Gly	Val	Leu	Val	Gln	Leu	Pro	Leu	Pro	Arg	His	Ile	Asp	Thr
			100					105					110		
Lys	Met	Ile	Leu	Glu	Ala	Ile	Asp	Pro	Asn	Lys	Asp	Val	Asp	Gly	Phe
		115					120					125			
His	Pro	Leu	Asn	Ile	Gly	Lys	Leu	Cys	Thr	Gln	Lys	Glu	Ser	Phe	Leu
	130					135					140				
Pro	Ala	Thr	Pro	Met	Gly	Val	Met	Arg	Leu	Leu	Glu	His	Tyr	His	Ile
145					150					155					160
Glu	Ile	Lys	Gly	Lys	Asp	Val	Ala	Ile	Ile	Gly	Ala	Ser	Asn	Ile	Ile
			165					170						175	
Gly	Lys	Pro	Leu	Ser	Met	Leu	Met	Leu	Asn	Ala	Gly	Ala	Ser	Val	Ser
		180					185					190			
Val	Cys	His	Ile	Leu	Thr	Lys	Asp	Ile	Ser	Phe	Tyr	Thr	Gln	Asn	Ala
	195					200					205				
Asp	Ile	Val	Cys	Val	Gly	Val	Gly	Lys	Pro	Asp	Leu	Ile	Lys	Ala	Ser
	210					215				220					
Met	Leu	Lys	Lys	Gly	Ala	Val	Val	Val	Asp	Ile	Gly	Ile	Asn	His	Leu
225					230					235					240
Asn	Asp	Gly	Arg	Ile	Val	Gly	Asp	Val	Asp	Phe	Asn	Asn	Val	Gln	Lys
			245					250						255	
Val	Ala	Gly	Phe	Ile	Thr	Pro	Val	Pro	Lys	Gly	Val	Gly	Pro	Met	Thr
		260					265				270				
Ile	Val	Ser	Leu	Leu	Glu	Asn	Thr	Leu	Ile	Ala	Phe	Glu	Lys	Gln	Gln
		275				280					285				
Arg	Lys	Gly	Phe												
	290														

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...2099
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

CCCTTGCTTC	TTTTTGTCTT	TTTAAAGACT	TTATCTCTTG	TTAAAAAAAG	GTTGTATTAA	60
CGCTT	ATG AAA TCC CTA	TCT AAT GCC CTT	TTT TCG CTC TTT	TTA AAA GGT		110
Met	Lys Ser Leu Ser	Asn Ala Leu Phe	Ser Leu Phe	Leu Lys Gly		
1		5	10	15		

Lys Pro Leu Ser Met Leu Met Leu Asn Ala Gly Ala Ser Val Ser Val
 180 185 190
 TGC CAT ATT TTG ACT AAA GAC ATT AGT TTT TAC ACC CAA AAC GCT GAT 682
 Cys His Ile Leu Thr Lys Asp Ile Ser Phe Tyr Thr Gln Asn Ala Asp
 195 200 205
 ATT GTC TGC GTG GGC GTG GGT AAA CCT GAT TTG ATT AAA GCG AGC ATG 730
 Ile Val Cys Val Gly Val Gly Lys Pro Asp Leu Ile Lys Ala Ser Met
 210 215 220 225
 TTA AAA AAA GGG GCT GTA GTG GTG GAT ATT GGG ATC AAT CAT TTG AAC 778
 Leu Lys Lys Gly Ala Val Val Val Asp Ile Gly Ile Asn His Leu Asn
 230 235 240
 GAT GGG CGT ATC GTG GGC GAT GTG GAT TTT AAC AAC GTG CAA AAA GTC 826
 Asp Gly Arg Ile Val Gly Asp Val Asp Phe Asn Asn Val Gln Lys Val
 245 250 255
 GCC GGT TTT ATC ACC CCT GTG CCT AAA GGC GTG GGG CCT ATG ACG ATT 874
 Ala Gly Phe Ile Thr Pro Val Pro Lys Gly Val Gly Pro Met Thr Ile
 260 265 270
 GTC TCG CTT TTA GAA AAC ACT CTA ATC GCT TTT GAA AAA CAA CAA AGG 922
 Val Ser Leu Leu Glu Asn Thr Leu Ile Ala Phe Glu Lys Gln Gln Arg
 275 280 285
 AAG GGA TTT TAATGAAATT TTTACGCTCT GTTTATGCAT TTTGCTCCAG TTGGGTAGG 980
 Lys Gly Phe
 290
 GACGATTGTT ATTGTGCTGT TGGT 1004

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Met Gly Met Pro Asn Arg Gly Val Val Leu Leu Asp Gly Gln Ala Leu
 1 5 10 15
 Ala Asp Asn Ile Glu Lys Asp Leu Lys His Lys Ile Gln Ile Ile Thr
 20 25 30
 Ala Gln Thr His Lys Arg Pro Lys Leu Ala Val Ile Leu Val Gly Lys
 35 40 45
 Asp Pro Ala Ser Ile Thr Tyr Val Asn Met Lys Ile Lys Ala Cys Glu
 50 55 60
 Arg Val Gly Met Asp Phe Asp Leu Lys Thr Leu Gln Glu Asn Ile Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

CATTAAACGC ATGATTTTGTG CTACAATAAT AGGATTTTAA TTATATAAAG GACAA ATG	58
Met	
1	
GGC ATG CCA AAT AGG GGC GTT GTT TTA TTA GAC GGG CAA GCG CTA GCT	106
Gly Met Pro Asn Arg Gly Val Val Leu Leu Asp Gly Gln Ala Leu Ala	
5 10 15	
GAT AAT ATA GAA AAA GAT TTG AAA CAT AAA ATC CAA ATA ATA ACC GCA	154
Asp Asn Ile Glu Lys Asp Leu Lys His Lys Ile Gln Ile Ile Thr Ala	
20 25 30	
CAA ACG CAT AAA CGC CCC AAA CTA GCC GTG ATT TTA GTG GGG AAA GAT	202
Gln Thr His Lys Arg Pro Lys Leu Ala Val Ile Leu Val Gly Lys Asp	
35 40 45	
CCC GCT AGT ATC ACT TAT GTC AAT ATG AAG ATC AAA GCA TGC GAA AGG	250
Pro Ala Ser Ile Thr Tyr Val Asn Met Lys Ile Lys Ala Cys Glu Arg	
50 55 60 65	
GTG GGC ATG GAT TTT GAC TTA AAA ACC CTC CAA GAA AAT ATT ACT GAA	298
Val Gly Met Asp Phe Asp Leu Lys Thr Leu Gln Glu Asn Ile Thr Glu	
70 75 80	
GCC AAA TTG CTA TCC TTG ATT AAA GAT TAC AAT ACC GAT CAA AAC ATT	346
Ala Lys Leu Leu Ser Leu Ile Lys Asp Tyr Asn Thr Asp Gln Asn Ile	
85 90 95	
TCA GGC GTT TTA GTC CAG CTC CCT TTG CCC AGA CAC ATT GAT ACT AAA	394
Ser Gly Val Leu Val Gln Leu Pro Leu Pro Arg His Ile Asp Thr Lys	
100 105 110	
ATG ATT TTA GAA GCC ATT GAC CCA AAC AAA GAT GTG GAT GGT TTC CAC	442
Met Ile Leu Glu Ala Ile Asp Pro Asn Lys Asp Val Asp Gly Phe His	
115 120 125	
CCC CTT AAT ATC GGT AAG CTC TGC ACT CAA AAA GAA TCG TTT CTG CCA	490
Pro Leu Asn Ile Gly Lys Leu Cys Thr Gln Lys Glu Ser Phe Leu Pro	
130 135 140 145	
GCC ACC CCT ATG GGC GTG ATG CGG CTT TTA GAG CAT TAC CAT ATT GAA	538
Ala Thr Pro Met Gly Val Met Arg Leu Leu Glu His Tyr His Ile Glu	
150 155 160	
ATC AAG GGT AAG GAT GTG GCG ATT ATT GGA GCG AGC AAT ATC ATT GGC	586
Ile Lys Gly Lys Asp Val Ala Ile Ile Gly Ala Ser Asn Ile Ile Gly	
165 170 175	
AAA CCT TTA AGC ATG CTC ATG CTA AAC GCT GGG GCT AGC GTG AGC GTG	634

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

Lys Lys Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys
 1             5             10             15
Asn Leu Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn
      20             25             30
Glu Gln Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val
      35             40             45
Leu Glu Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser
      50             55             60
Arg Leu Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu
      65             70             75             80
Gly Lys Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala
      85             90             95
Ser Ser Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile
      100            105            110
Ser Met Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys
      115            120            125
Thr Ile Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys
      130            135            140
Asp Glu Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp
      145            150            155            160
Ala Leu Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile
      165            170            175
Asp Leu Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe
      180            185            190
Met Lys Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser
      195            200            205
Ser Val Asn Lys Lys
      210

```

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...931
- (D) OTHER INFORMATION:

GAT ATT TTA GAT TTG AAC AAA GCG CAA GCG GTG CAA CAA AAT GAA CAA	152
Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn Glu Gln	
20 25 30	
GAG GTA GAG GAT AAA GAG CGA GAG TCT AAA GAG CCG GTG GTT TTA GAA	200
Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val Leu Glu	
35 40 45 50	
GAT TTG AGC GCT TTA GCG TGG CTT GAA TTA GAA GAG TTT AGC CGC CTT	248
Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser Arg Leu	
55 60 65	
TCA GGG CTT CCT AAA GAA AGG ATT TTG GAA TTA GTG AAT CTT GGT AAA	296
Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu Gly Lys	
70 75 80	
ATC AAG AGC AAA ATA AGC AGC AAC AAG CTT TTA ATT GAT GCG AGC AGC	344
Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala Ser Ser	
85 90 95	
GGG ACA AAC GCT TTA ATC AAA AAG GTA GAA AAT AGT TTG ATT TCT ATG	392
Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile Ser Met	
100 105 110	
GAT ATG AAC GGG CGT TCT TTA GAA CCT GTG TTT GTG GAA AAG ACC ATT	440
Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys Thr Ile	
115 120 125 130	
AAC ACG ATT TTA AAC TTG CAT GAT AAG GTC ATT GGC GCT AAA GAT GAA	488
Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys Asp Glu	
135 140 145	
ACG ATT TCA GCC TTT AAA AAT GAA AAC ATG TTT TTA AAA GAC GCT TTA	536
Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp Ala Leu	
150 155 160	
ATC TCT ATG CAA GAA GTC TAT GAA GAA GAT AAA AAA ACC ATT GAT CTT	584
Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile Asp Leu	
165 170 175	
TTG CGC GAT GAA CTC AAT CAA GCG AGA GAA GAA ATT GAA TTT ATG AAG	632
Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe Met Lys	
180 185 190	
AGG AAA TAC CGC TTG ATG TGG GGG AAA GTC GCT GAC ATG AGC AGC GTG	680
Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser Ser Val	
195 200 205 210	
AAT AAA AAG TAGTTTTAAA TTAACGCCCA TGCTGAGGGC TTATTAGCGG TAATTTTAG	738
Asn Lys Lys	
GTGA	742

(2). INFORMATION FOR SEQ ID NO:370:

```

Asp Asp Asp Lys Pro Lys Pro Leu Thr Ile Asp Lys Asn Asn Glu Lys
 50                               55                               60
Gln Gln Ile Leu Asp Lys Asn Gln Gln Ile Leu Lys Arg Ala Leu Glu
 65                               70                               75                               80
Lys Ser Leu Lys Phe Phe Phe Ile Phe Gly Tyr Asn Tyr Ser Gln Ala
                               85                               90                               95
Thr Phe Ser Thr Ser Asn Gln Thr Leu Thr Phe Val Ala Asn Ser Ile
                               100                               105                               110
Gly Phe Asn Thr Ala Thr Gly Leu Glu His Phe Leu Arg Asn His Pro
                               115                               120                               125
Lys Val Gly Phe Arg Ile Phe Ser Val Tyr Asn Tyr Phe His Ser Val
                               130                               135                               140
Ser Leu Ser Gln Pro Gln Thr Leu Met Val Gln Asn Tyr Gly Gly Ala
 145                               150                               155                               160
Leu Asp Phe Ser Trp Ile Phe Val Asp Lys Asn Ile Tyr Arg Phe Arg
                               165                               170                               175
Ser Tyr Leu Gly Ile Ala Leu Glu Gln Gly Val Leu Leu Val Asp Thr
                               180                               185                               190
Ile Lys Pro Gly Ala Ile Thr Thr Ile Ile Pro Arg Thr Lys Lys Thr
                               195                               200                               205
Phe Phe Gln Ala Pro Leu Arg Phe Gly Phe Ile Val Asp Phe Ile Gly
 210                               215                               220
Tyr Leu Ser Leu Gln Leu Gly Ile Glu Met Pro Leu Val Arg Asn Val
 225                               230                               235                               240
Phe Tyr Thr Tyr Asn Asn His Gln Glu Arg Phe Lys Pro Arg Phe Asn
                               245                               250                               255
Ala Asn Leu Ser Leu Ile Val Ser Phe
                               260                               265

```

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...689
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```

GCACTTCACG CATTCCATAA ACGATATTGA TTATTGCTA GACAGCTTGA AAA AAG      56
                               Lys Lys
                               1

CAG TTA AAA AAT TGC GTT AAG CTA AAA CTA TTT TTA AGG AAA AAT TTG      104
Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys Asn Leu
   5                               10                               15

```

135	140	145	
TCC CAG CCT CAA ACC TTA ATG GTG CAA AAT TAT GGG GGC GCG TTA GAT			536
Ser Gln Pro Gln Thr Leu Met Val Gln Asn Tyr Gly Gly Ala Leu Asp			
150	155	160	
TTT TCT TGG ATT TTT GTA GAT AAA AAT ATT TAT CGC TTT AGG AGT TAT			584
Phe Ser Trp Ile Phe Val Asp Lys Asn Ile Tyr Arg Phe Arg Ser Tyr			
165	170	175	
TTA GGG ATC GCT TTA GAA CAA GGG GTG TTG TTA GTG GAT ACG ATT AAA			632
Leu Gly Ile Ala Leu Glu Gln Gly Val Leu Leu Val Asp Thr Ile Lys			
180	185	190	
CCA GGT GCT ATC ACA ACG ATT ATC CCA AGA ACC AAA AAA ACC TTT TTT			680
Pro Gly Ala Ile Thr Thr Ile Ile Pro Arg Thr Lys Lys Thr Phe Phe			
195	200	205	210
CAA GCC CCT TTG CGT TTT GGT TTT ATC GTG GAT TTT ATC GGC TAT TTG			728
Gln Ala Pro Leu Arg Phe Gly Phe Ile Val Asp Phe Ile Gly Tyr Leu			
215	220	225	
TCT TTG CAA TTA GGG ATT GAA ATG CCT TTA GTG AGG AAT GTT TTT TAC			776
Ser Leu Gln Leu Gly Ile Glu Met Pro Leu Val Arg Asn Val Phe Tyr			
230	235	240	
ACC TAC AAC AAC CAT CAA GAA AGA TTC AAA CCA CGA TTT AAC GCT AAT			824
Thr Tyr Asn Asn His Gln Glu Arg Phe Lys Pro Arg Phe Asn Ala Asn			
245	250	255	
CTT TCT TTA ATC GTT TCG TTT TAGCCCCCCT TTTCCCCTTT TAAATAAGCC CATG			879
Leu Ser Leu Ile Val Ser Phe			
260	265		
ATTTTCCTAG GGTATTTTA			898

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Leu	Gly	Thr	Ile	Ala	Thr	Lys	Ser	Leu	Arg	Leu	Tyr	Leu	Lys	Thr	Leu
1				5				10				15			
Phe	Ser	Ile	Tyr	Leu	Phe	Leu	Ser	Leu	Asn	Pro	Leu	Phe	Leu	Glu	Ala
				20				25				30			
Asn	Glu	Ile	Thr	Trp	Ser	Lys	Phe	Leu	Glu	Asn	Phe	Lys	Asn	Lys	Asn
				35				40				45			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...845
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

GGGGGGTTAT AGTAAAAACA TGCAAGTAAT TTAAAGTTAA TTTAAGATAA  TTA GGC      56
                                   Leu Gly
                                   1

ACA ATA GCC ACA AAA AGT TTA AGG CTG TAT TTG AAA ACT CTA TTT AGT      104
Thr Ile Ala Thr Lys Ser Leu Arg Leu Tyr Leu Lys Thr Leu Phe Ser
      5                      10                      15

ATT TAT CTC TTT TTA TCG TTG AAC CCA CTC TTT TTA GAA GCT AAT GAA      152
Ile Tyr Leu Phe Leu Ser Leu Asn Pro Leu Phe Leu Glu Ala Asn Glu
    20                      25                      30

ATC ACT TGG TCT AAA TTC TTG GAA AAT TTT AAA AAC AAG AAT GAT GAT      200
Ile Thr Trp Ser Lys Phe Leu Glu Asn Phe Lys Asn Lys Asn Asp Asp
    35                      40                      45                      50

GAC AAA CCT AAA CCC CTA ACT ATT GAT AAA AAC AAT GAA AAA CAG CAA      248
Asp Lys Pro Lys Pro Leu Thr Ile Asp Lys Asn Asn Glu Lys Gln Gln
      55                      60                      65

ATC TTA GAC AAA AAC CAG CAA ATC TTA AAA AGG GCT TTG GAA AAA AGC      296
Ile Leu Asp Lys Asn Gln Gln Ile Leu Lys Arg Ala Leu Glu Lys Ser
      70                      75                      80

CTT AAA TTC TTT TTC ATT TTT GGA TAC AAC TAT TCG CAA GCC ACT TTT      344
Leu Lys Phe Phe Phe Ile Phe Gly Tyr Asn Tyr Ser Gln Ala Thr Phe
    85                      90                      95

TCA ACT TCT AAC CAA ACC TTG ACT TTT GTA GCC AAT AGC ATA GGG TTT      392
Ser Thr Ser Asn Gln Thr Leu Thr Phe Val Ala Asn Ser Ile Gly Phe
    100                      105                      110

AAC ACC GCT ACC GGT TTA GAG CAT TTT TTA AGA AAC CAC CCT AAA GTC      440
Asn Thr Ala Thr Gly Leu Glu His Phe Leu Arg Asn His Pro Lys Val
    115                      120                      125                      130

GGT TTT AGA ATC TTT AGC GTC TAT AAC TAT TTC CAT TCT GTT TCC CTC      488
Gly Phe Arg Ile Phe Ser Val Tyr Asn Tyr Phe His Ser Val Ser Leu

```

(A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

Met Leu Val Thr Arg Phe Lys Lys Ala Leu Ile Ser Tyr Ser Leu Gly
 1           5           10           15
Ala Leu Leu Val Ser Ser Leu Leu Gly Val Ala Ser Ala Ser Asn Gln
          20           25           30
Glu Ile Gln Val Lys Asp Tyr Phe Gly Asp Gln Ala Ile Lys Leu Pro
          35           40           45
Val Ser Lys Ile Ile Tyr Leu Gly Ser Phe Ala Glu Val Pro Ala Met
          50           55           60
Phe His Thr Trp Asp Arg Val Val Gly Ile Ser Asp Tyr Ala Phe Lys
65           70           75           80
Ser Asp Ile Val Lys Ala Thr Leu Lys Asp Pro Lys Arg Ile Lys Ser
          85           90           95
Met Ser Ser Asp His Val Ala Ala Leu Asn Val Glu Leu Leu Lys Lys
          100          105          110
Leu Gly Pro Asp Leu Val Val Thr Phe Val Gly Asn Pro Lys Ala Val
          115          120          125
Glu His Ala Lys Lys Phe Gly Ile Leu Phe Leu Ser Phe Gln Glu Lys
          130          135          140
Thr Ile Ala Glu Val Met Glu Asp Ile Asp Ala Gln Ala Lys Ala Leu
145          150          155          160
Glu Ile Asp Ala Ser Lys Lys Leu Ala Lys Met Gln Glu Thr Leu Asp
          165          170          175
Phe Ile Ala Glu Arg Leu Lys Gly Val Lys Lys Lys Gly Val Glu
          180          185          190
Leu Phe His Lys Ala Asn Lys Ile Ser Gly His Gln Ala Leu Asp Ser
          195          200          205
Asp Ile Leu Glu Lys Gly Gly Ile Asp Asn Phe Gly Leu Lys Tyr Val
          210          215          220
Lys Phe Gly Arg Ala Asp Ile Ser Val Glu Lys Ile Val Lys Glu Asn
225          230          235          240
Pro Glu Ile Ile Phe Ile Trp Trp Ile Ser Pro Leu Thr Pro Glu Asp
          245          250          255
Val Leu Asn Asn Pro Lys Phe Ala Thr Ile Lys Ala Ile Lys Asn Lys
          260          265          270
Gln Val Tyr Lys Leu Pro Thr Met Asp Ile Gly Gly Pro Arg Ala Pro
          275          280          285
Leu Ile Ser Leu Phe Ile Ala Leu Lys Ala His Pro Glu Ala Phe Lys
          290          295          300
Gly Val Asp Ile Asn Ala Ile Val Lys Asp Tyr Tyr Lys Val Val Phe
305          310          315          320
Asp Leu Asn Asp Ala Glu Val Glu Pro Phe Leu Trp His
          325          330

```

(2) INFORMATION FOR SEQ ID NO:367:

140	145	150	
ATT GAC GCT CAA GCT AAA GCC TTA GAA ATT GAT GCT TCT AAA AAA CTG			592
Ile Asp Ala Gln Ala Lys Ala Leu Glu Ile Asp Ala Ser Lys Lys Leu			
155	160	165	
GCC AAA ATG CAA GAA ACT TTG GAT TTT ATT GCT GAG CGT TTG AAA GGT			640
Ala Lys Met Gln Glu Thr Leu Asp Phe Ile Ala Glu Arg Leu Lys Gly			
170	175	180	
GTC AAA AAG AAA AAA GGG GTG GAG CTT TTC CAT AAG GCC AAT AAG ATC			688
Val Lys Lys Lys Lys Gly Val Glu Leu Phe His Lys Ala Asn Lys Ile			
185	190	195	200
AGC GGC CAT CAA GCC CTT GAT TCA GAC ATT TTA GAA AAA GGA GGC ATA			736
Ser Gly His Gln Ala Leu Asp Ser Asp Ile Leu Glu Lys Gly Gly Ile			
205	210	215	
GAC AAT TTT GGC TTG AAA TAT GTC AAA TTT GGG CGT GCT GAC ATT AGC			784
Asp Asn Phe Gly Leu Lys Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser			
220	225	230	
GTG GAA AAA ATC GTT AAA GAA AAC CCT GAG ATT ATC TTT ATT TGG TGG			832
Val Glu Lys Ile Val Lys Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp			
235	240	245	
ATA AGC CCA CTC ACG CCT GAA GAT GTG TTA AAC AAC CCC AAA TTT GCT			880
Ile Ser Pro Leu Thr Pro Glu Asp Val Leu Asn Asn Pro Lys Phe Ala			
250	255	260	
ACC ATC AAA GCC ATT AAA AAC AAG CAG GTT TAT AAA CTC CCC ACA ATG			928
Thr Ile Lys Ala Ile Lys Asn Lys Gln Val Tyr Lys Leu Pro Thr Met			
265	270	275	280
GAT ATT GGC GGG CCT AGA GCC CCA CTC ATA AGT CTT TTT ATC GCT CTA			976
Asp Ile Gly Gly Pro Arg Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu			
285	290	295	
AAA GCC CAC CCT GAA GCC TTT AAG GGC GTG GAT ATT AAT GCG ATT GTT			1024
Lys Ala His Pro Glu Ala Phe Lys Gly Val Asp Ile Asn Ala Ile Val			
300	305	310	
AAA GAC TAC TAT AAA GTG GTT TTT GAT TTG AAT GAT GCA GAG GTT GAA			1072
Lys Asp Tyr Tyr Lys Val Val Phe Asp Leu Asn Asp Ala Glu Val Glu			
315	320	325	
CCC TTT TTA TGG CAT TAATTTTAA AAAAGGGCTG ATATTTTATAG CCCTTTGTGT A			1128
Pro Phe Leu Trp His			
330			
TCGCGCTAGG ATTAG			1143

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 89...1087
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

GATTTTGTGA AAAATAGTTT CATTTTACT GCTTGATTTT CCTTAATGGT GTTATAATCG      60
CTCCATAAAT CATACAAAAA GGATCGTT ATG TTA GTT ACT CGC TTT AAA AAA      112
               Met Leu Val Thr Arg Phe Lys Lys
                   1                   5

GCT TTA ATC TCT TAT TCT TTA GGC GCG CTT CTT GTT TCA TCG TTA TTG      160
Ala Leu Ile Ser Tyr Ser Leu Gly Ala Leu Leu Val Ser Ser Leu Leu
   10                   15                   20

GGC GTG GCT AGT GCT TCC AAT CAA GAA ATC CAA GTC AAA GAT TAT TTT      208
Gly Val Ala Ser Ala Ser Asn Gln Glu Ile Gln Val Lys Asp Tyr Phe
   25                   30                   35                   40

GGG GAT CAA GCC ATC AAG CTT CCT GTT TCT AAA ATA ATC TAC TTG GGT      256
Gly Asp Gln Ala Ile Lys Leu Pro Val Ser Lys Ile Ile Tyr Leu Gly
               45                   50                   55

AGC TTT GCA GAA GTG CCT GCT ATG TTC CAT ACT TGG GAT AGG GTC GTG      304
Ser Phe Ala Glu Val Pro Ala Met Phe His Thr Trp Asp Arg Val Val
               60                   65                   70

GGA ATT TCG GAT TAC GCT TTT AAA TCT GAT ATT GTT AAA GCT ACT CTC      352
Gly Ile Ser Asp Tyr Ala Phe Lys Ser Asp Ile Val Lys Ala Thr Leu
   75                   80                   85

AAA GAT CCT AAA CGC ATT AAA TCC ATG AGC AGT GAT CAT GTG GCG GCG      400
Lys Asp Pro Lys Arg Ile Lys Ser Met Ser Ser Asp His Val Ala Ala
   90                   95                   100

TTG AAT GTG GAG CTT TTA AAA AAG CTT GGC CCC GAT CTT GTG GTA ACC      448
Leu Asn Val Glu Leu Leu Lys Lys Leu Gly Pro Asp Leu Val Val Thr
  105                   110                   115                   120

TTT GTG GGC AAC CCT AAA GCG GTA GAG CAT GCG AAA AAA TTT GGT ATA      496
Phe Val Gly Asn Pro Lys Ala Val Glu His Ala Lys Lys Phe Gly Ile
               125                   130                   135

TTA TTT CTT TCT TTC CAA GAA AAA ACC ATT GCA GAA GTC ATG GAA GAT      544
Leu Phe Leu Ser Phe Gln Glu Lys Thr Ile Ala Glu Val Met Glu Asp

```

20	25	30	
TTT TTG AAT GTT ATA GAC AAT TTC ACT ATC TCT TTG ATT TTG TTT ATA			200
Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu Phe Ile			
35	40	45	50
TTT TTT AGC CCC ATA CCA AAG AAA TAT TTG ATA AAA AAT AAG AAA AAT			248
Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys Lys Asn			
	55	60	65
AGC GTA AAA GAA AAA GAA AAT AAA GAA AAA AGA AAG AGA AAA AGA AAG			296
Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys Arg Lys			
	70	75	80
GAT TTT GTT TTG GGT GTA TTG GAA AAT AGA CTC AAA AAT CAA TTG AAA			344
Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln Leu Lys			
	85	90	95
AAC CCC TTT TAGATTAAAA ATAAAAACAA TAAGCGAAAC GACAAAAGCA AGCAGAAAA			402
Asn Pro Phe			
100			
GAAG			406

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Ile Lys Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe			
1	5	10	15
Ile Leu Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile			
	20	25	30
Trp Glu Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu			
	35	40	45
Phe Ile Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys			
	50	55	60
Lys Asn Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys			
	65	70	75
Arg Lys Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln			
	85	90	95
Leu Lys Asn Pro Phe			
100			

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

	595						600				605					
Arg Tyr Gly Asp Asn Lys Glu Pro Val Asn Ala Arg Ser Gln Gly Val 610 615 620	Glu Leu Glu Leu Tyr Tyr Thr Pro Ile Arg Gly Leu Asn Phe His Ala 625 630 635 640	Ala Tyr Thr Phe Ile Asp Ala Asn Ile Thr Ser His Thr Met Val Thr 645 650 655	Asn Pro Ala Asn Pro Lys Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys 660 665 670	Leu Pro Phe Val Ser Pro His Gln Phe Ile Leu Asp Ala Ser Tyr Thr 675 680 685	Tyr Ala Lys Thr Thr Ile Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr 690 695 700	Tyr Ser Asp Val Leu Asn Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr 705 710 715 720	Ile Lys Asn Gly Ala Ile Thr Thr Lys Thr Ala Gly Met Thr Pro Trp 725 730 735	Tyr Trp Val Trp Asn Leu Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys 740 745 750	Lys Gln Ser Val Asn Ala Ser Leu Gln Ile Asn Asn Ile Phe Asn Met 755 760 765	Lys Tyr Trp Phe Ser Gly Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro 770 775 780	Arg Leu Leu Gly Ala Ser Gln Arg Met 785 790					

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...353
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

TCGTCTTTTG	TCGGTTCAAA	AAAATCTCTC	GACTTAAAAA	AACCTATTAA	ATC	AAG	56
					Ile	Lys	
					1		
ATA	ATC	TAT	CAA	ATC	ATC	AAG	104
Ile	Ile	Tyr	Gln	Ile	Ile	Lys	
		5				10	
						15	
TTT	TTT	AGA	ATA	GCA	ACG	ATA	152
Phe	Phe	Arg	Ile	Ala	Thr	Ile	

Asp Val Ile Lys Gly Gly Thr Ser Val Gln Tyr Gly Pro Asn Thr Phe
 165 170 175
 Gly Gly Val Val Asn Ile Ile Thr Lys Glu Ile Pro Lys Glu Trp Glu
 180 185 190
 Asn Gln Ala Ala Glu Arg Ile Thr Phe Trp Gly Arg Ser Ser Asn Gly
 195 200 205
 Asn Phe Val Asp Pro Lys Glu Lys Gly Lys Pro Leu Ala Gln Thr Leu
 210 215 220
 Gly Asn Gln Met Leu Phe Asn Thr Tyr Gly Arg Thr Ala Gly Met Leu
 225 230 235 240
 Gly Lys His Val Gly Ile Ser Ala Gln Gly Asn Trp Ile Asn Gly Gln
 245 250 255
 Gly Phe Arg Gln Asn Ser Pro Thr Lys Val Gln Asn Tyr Leu Leu Asp
 260 265 270
 Ala Val Tyr Lys Ile Asn Ala Thr Asn Thr Phe Lys Ala Tyr Tyr Gln
 275 280 285
 Tyr Tyr Gln Tyr Asn Ser Tyr His Pro Gly Thr Leu Ser Ala Gln Asp
 290 295 300
 Tyr Ala Tyr Asn Arg Phe Ile Asn Glu Arg Pro Asp Asn Gln Asp Gly
 305 310 315 320
 Gly Arg Ala Lys Arg Phe Gly Ile Val Tyr Gln Asn Tyr Phe Gly Asp
 325 330 335
 Pro Asp Arg Lys Val Gly Gly Asp Phe Lys Phe Thr Tyr Phe Thr His
 340 345 350
 Asp Met Ser Arg Asp Phe Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr
 355 360 365
 Met Ser Ser Gln Asn Lys Ile Leu Pro Phe Lys Gly Lys Lys Ile
 370 375 380
 Ser Ala Thr Asn Pro Asn Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn
 385 390 395 400
 Ser Pro Cys Trp Gln Phe Phe Asp Asn Ile Arg Arg Ser Val Val Asn
 405 410 415
 Ala Phe Glu Pro Lys Leu Asn Leu Ile Val Asn Thr Gly Lys Val Lys
 420 425 430
 Gln Thr Phe Asn Met Gly Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg
 435 440 445
 Arg Ser Thr Thr Arg Lys Asn Pro Ser Met Pro Asn Asn Gly Ser Gly
 450 455 460
 Phe Asp Ala Gly Thr Ser Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val
 465 470 475 480
 Tyr Ala Ser Asp Glu Ile Asn Phe Asn Asn Gly Met Leu Thr Ile Thr
 485 490 495
 Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro
 500 505 510
 Pro Phe Lys Ala Gly Gln Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn
 515 520 525
 Gln Trp Asn Pro Ala Val Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu
 530 535 540
 Leu Phe Tyr Phe Asn Tyr Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser
 545 550 555 560
 Asn Ile Gly Ser Phe Val Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe
 565 570 575
 Asn Val Met Glu Gly Gly Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser
 580 585 590
 Phe Asn Ala Asn Tyr Phe Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly

ACT ACC AAA ACA GCG GGC ATG ACG CCA TGG TAT TGG GTG TGG AAT TTG 2683
 Thr Thr Lys Thr Ala Gly Met Thr Pro Trp Tyr Trp Val Trp Asn Leu
 730 735 740

CAA ATT TCT ACC ACT TTT TGG GAA CGC AAA AAG CAA AGC GTT AAT GCG 2731
 Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys Lys Gln Ser Val Asn Ala
 745 750 755

AGC TTG CAA ATC AAT AAC ATT TTT AAC ATG AAA TAT TGG TTT AGC GGG 2779
 Ser Leu Gln Ile Asn Asn Ile Phe Asn Met Lys Tyr Trp Phe Ser Gly
 760 765 770

ATA GGC ACT AGC CTA ACG GGA AAG AAG CCG CGC CTC CTA GGA GCA TCA 2827
 Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro Arg Leu Leu Gly Ala Ser
 775 780 785 790

CAG CGT ATG TGAGCTATCA TTTTAAATTT TAGGGTTGTA ATGTTTGTAG AAGTTGGGC 2885
 Gln Arg Met

GTAAA 2890

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Met Arg Lys Val Ile Thr Met Asn Gly Tyr Leu Arg Val Lys Thr Ser
 1 5 10 15
 Tyr Phe Leu Ala Leu Asn Ala Leu Thr Phe Leu Ser Phe Asn Ser Leu
 20 25 30
 Val Gly Ala Lys Glu Gln His His Thr Leu Gln Lys Val Thr Thr Thr
 35 40 45
 Glu Gln Lys Phe Asn Pro Ser Ala Pro Leu Ser Trp Gln Ser Glu Glu
 50 55 60
 Met Arg Asn Ser Thr Ser Ser Arg Thr Val Ile Ser Asn Lys Glu Leu
 65 70 75 80
 Lys Lys Thr Gly Asn Leu Asn Ile Glu Asn Ala Leu Gln Asn Val Pro
 85 90 95
 Gly Ile Gln Ile Arg Asp Ala Thr Gly Thr Gly Val Leu Pro Lys Ile
 100 105 110
 Ser Val Arg Gly Phe Gly Gly Gly Asn Gly His Ser Asn Thr Asn
 115 120 125
 Met Ile Leu Val Asn Gly Ile Pro Ile Tyr Gly Ala Pro Tyr Ser Asn
 130 135 140
 Ile Glu Leu Ala Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile
 145 150 155 160

TTT	TTA	AAT	TAC	GAA	AAA	AAA	GAC	GCT	CCT	CCT	TTT	AAA	GCA	GGC	CAA	2011
Phe	Leu	Asn	Tyr	Glu	Lys	Lys	Asp	Ala	Pro	Pro	Phe	Lys	Ala	Gly	Gln	
		505					510					515				
ACA	GGA	AAA	ACC	ATT	AAA	GAT	CGT	TAT	AAC	CAA	TGG	AAT	CCA	GCA	GTG	2059
Thr	Gly	Lys	Thr	Ile	Lys	Asp	Arg	Tyr	Asn	Gln	Trp	Asn	Pro	Ala	Val	
	520					525					530					
AAT	GTC	GGC	TAT	AAA	CCC	ATT	AAA	GAA	TTG	TTG	TTT	TAT	TTC	AAT	TAC	2107
Asn	Val	Gly	Tyr	Lys	Pro	Ile	Lys	Glu	Leu	Leu	Phe	Tyr	Phe	Asn	Tyr	
535					540					545					550	
CAA	AGA	AGC	TAC	ATT	CCG	CCT	CAA	TTC	AGC	AAT	ATC	GGT	AGT	TTT	GTA	2155
Gln	Arg	Ser	Tyr	Ile	Pro	Pro	Gln	Phe	Ser	Asn	Ile	Gly	Ser	Phe	Val	
				555					560					565		
GGC	ACA	AGC	ACG	GAT	TAT	TTT	CAA	ATC	TTT	AAT	GTC	ATG	GAA	GGC	GGC	2203
Gly	Thr	Ser	Thr	Asp	Tyr	Phe	Gln	Ile	Phe	Asn	Val	Met	Glu	Gly	Gly	
			570					575					580			
TCA	AGA	TAT	TAT	TTT	AAC	AAC	CAA	GTG	AGT	TTT	AAC	GCG	AAT	TAT	TTT	2251
Ser	Arg	Tyr	Tyr	Phe	Asn	Asn	Gln	Val	Ser	Phe	Asn	Ala	Asn	Tyr	Phe	
		585					590					595				
GTG	ATT	TTT	GCG	AAT	AAC	TAT	TTT	ACC	GGG	CGC	TAT	GGG	GAT	AAT	AAA	2299
Val	Ile	Phe	Ala	Asn	Asn	Tyr	Phe	Thr	Gly	Arg	Tyr	Gly	Asp	Asn	Lys	
	600					605					610					
GAG	CCG	GTC	AAT	GCG	AGA	TCG	CAA	GGC	GTG	GAG	CTA	GAG	TTG	TAT	TAC	2347
Glu	Pro	Val	Asn	Ala	Arg	Ser	Gln	Gly	Val	Glu	Leu	Glu	Leu	Tyr	Tyr	
615					620					625					630	
ACG	CCG	ATT	AGA	GGG	CTT	AAT	TTC	CAT	GCG	GCT	TAC	ACT	TTC	ATA	GAT	2395
Thr	Pro	Ile	Arg	Gly	Leu	Asn	Phe	His	Ala	Ala	Tyr	Thr	Phe	Ile	Asp	
				635					640					645		
GCC	AAT	ATC	ACA	AGC	CAC	ACG	ATG	GTT	ACT	AAC	CCC	GCT	AAT	CCT	AAA	2443
Ala	Asn	Ile	Thr	Ser	His	Thr	Met	Val	Thr	Asn	Pro	Ala	Asn	Pro	Lys	
			650					655					660			
GGG	CCT	AAA	AAA	GAT	ATT	TTT	GGC	AAA	AAG	CTC	CCT	TTT	GTA	AGC	CCG	2491
Gly	Pro	Lys	Lys	Asp	Ile	Phe	Gly	Lys	Lys	Leu	Pro	Phe	Val	Ser	Pro	
		665					670						675			
CAC	CAA	TTC	ATT	TTA	GAC	GCG	AGC	TAC	ACT	TAC	GCT	AAA	ACC	ACG	ATT	2539
His	Gln	Phe	Ile	Leu	Asp	Ala	Ser	Tyr	Thr	Tyr	Ala	Lys	Thr	Thr	Ile	
	680					685					690					
GGG	TTG	AGT	TCT	TTC	TTT	TAT	AGC	CGA	ACT	TAT	AGC	GAT	GTG	TTA	AAC	2587
Gly	Leu	Ser	Ser	Phe	Phe	Tyr	Ser	Arg	Thr	Tyr	Ser	Asp	Val	Leu	Asn	
695					700					705					710	
ACC	GTG	CCT	TTT	ATT	CAA	TAC	GCG	CCC	ACG	ATC	AAA	AAT	GGT	GCT	ATC	2635
Thr	Val	Pro	Phe	Ile	Gln	Tyr	Ala	Pro	Thr	Ile	Lys	Asn	Gly	Ala	Ile	
				715					720					725		

GCG ACC AAT ACT TTT AAA GCT TAT TAC CAA TAT TAT CAA TAC AAC TCT	1339
Ala Thr Asn Thr Phe Lys Ala Tyr Tyr Gln Tyr Tyr Gln Tyr Asn Ser	
280 285 290	
TAC CAT CCA GGC ACT TTG AGT GCA CAA GAT TAT GCT TAT AAC CGC TTC	1387
Tyr His Pro Gly Thr Leu Ser Ala Gln Asp Tyr Ala Tyr Asn Arg Phe	
295 300 305 310	
ATT AAT GAG CGC CCT GAC AAT CAA GAT GGA GGG CGA GCC AAG CGC TTT	1435
Ile Asn Glu Arg Pro Asp Asn Gln Asp Gly Gly Arg Ala Lys Arg Phe	
315 320 325	
GGG ATC GTG TAT CAA AAT TAT TTT GGC GAT CCG GAT AGG AAA GTG GGG	1483
Gly Ile Val Tyr Gln Asn Tyr Phe Gly Asp Pro Asp Arg Lys Val Gly	
330 335 340	
GGA GAT TTT AAA TTC ACT TAT TTC ACG CAT GAC ATG AGT AGG GAT TTT	1531
Gly Asp Phe Lys Phe Thr Tyr Phe Thr His Asp Met Ser Arg Asp Phe	
345 350 355	
GGG TTT TCC AAC CAA TAC CAA AGC GTG TAT ATG AGC AGT CAA AAC AAG	1579
Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr Met Ser Ser Gln Asn Lys	
360 365 370	
ATT TTA CCT TTT AAA GGC AAG GGA AAA ATT AGC GCG ACT AAC CCT AAT	1627
Ile Leu Pro Phe Lys Gly Lys Gly Lys Ile Ser Ala Thr Asn Pro Asn	
375 380 385 390	
TGC GGT TTG TAT TCT TAT AGC GAC ACG AAC AGC CCT TGT TGG CAA TTT	1675
Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn Ser Pro Cys Trp Gln Phe	
395 400 405	
TTT GAC AAT ATC CGC CGA TCC GTG GTG AAT GCC TTT GAG CCA AAA CTC	1723
Phe Asp Asn Ile Arg Arg Ser Val Val Asn Ala Phe Glu Pro Lys Leu	
410 415 420	
AAT CTT ATC GTC AAT ACC GGT AAA GTC AAA CAA ACT TTT AAT ATG GGA	1771
Asn Leu Ile Val Asn Thr Gly Lys Val Lys Gln Thr Phe Asn Met Gly	
425 430 435	
ATG CGC TTT TTA ACT GAA GAT TTA TAC CGC CGA TCC ACC ACC AGG AAA	1819
Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg Arg Ser Thr Thr Arg Lys	
440 445 450	
AAC CCT AGC ATG CCT AAT AAT GGG AGT GGT TTT GAT GCA GGA ACT TCA	1867
Asn Pro Ser Met Pro Asn Asn Gly Ser Gly Phe Asp Ala Gly Thr Ser	
455 460 465 470	
CTC AAT AAT TTC AAC AAT TAT ACC GCT GTG TAT GCC AGC GAT GAG ATC	1915
Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val Tyr Ala Ser Asp Glu Ile	
475 480 485	
AAT TTC AAT AAC GGC ATG CTA ACG ATC ACG CCG GGC TTG AGA TAC ACT	1963
Asn Phe Asn Asn Gly Met Leu Thr Ile Thr Pro Gly Leu Arg Tyr Thr	
490 495 500	

Ser	Ala	Pro	Leu	Ser	Trp	Gln	Ser	Glu	Glu	Met	Arg	Asn	Ser	Thr	Ser	
55					60					65					70	
TCT	CGC	ACG	GTG	ATT	TCC	AAC	AAG	GAA	CTC	AAA	AAA	ACG	GGG	AAT	TTG	715
Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Glu	Leu	Lys	Lys	Thr	Gly	Asn	Leu	
				75					80					85		
AAT	ATT	GAA	AAC	GCC	TTG	CAA	AAC	GTG	CCA	GGG	ATT	CAA	ATC	AGA	GAC	763
Asn	Ile	Glu	Asn	Ala	Leu	Gln	Asn	Val	Pro	Gly	Ile	Gln	Ile	Arg	Asp	
			90					95					100			
GCT	ACA	GGC	ACA	GGC	GTG	CTG	CCT	AAA	ATT	TCG	GTG	CGC	GGT	TTT	GGT	811
Ala	Thr	Gly	Thr	Gly	Val	Leu	Pro	Lys	Ile	Ser	Val	Arg	Gly	Phe	Gly	
		105					110					115				
GGG	GGC	GGT	AAC	GGG	CAT	AGC	AAT	ACC	AAC	ATG	ATT	TTA	GTC	AAT	GGT	859
Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn	Met	Ile	Leu	Val	Asn	Gly	
	120					125				130						
ATC	CCC	ATT	TAT	GGC	GCG	CCG	TAT	TCC	AAT	ATT	GAA	CTG	GCG	ATT	TTC	907
Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn	Ile	Glu	Leu	Ala	Ile	Phe	
135					140					145					150	
CCT	GTA	ACT	TTC	CAG	TCA	GTG	GAT	AGG	ATT	GAT	GTG	ATT	AAA	GGG	GGC	955
Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Asp	Val	Ile	Lys	Gly	Gly	
				155				160					165			
ACG	AGC	GTG	CAA	TAC	GGC	CCT	AAT	ACT	TTT	GGA	GGC	GTG	GTG	AAT	ATC	1003
Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe	Gly	Gly	Val	Val	Asn	Ile	
			170					175					180			
ATC	ACT	AAA	GAA	ATC	CCT	AAA	GAG	TGG	GAA	AAT	CAA	GCG	GCT	GAA	AGG	1051
Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu	Asn	Gln	Ala	Ala	Glu	Arg	
		185					190					195				
ATC	ACT	TTT	TGG	GGG	CGA	TCC	TCT	AAT	GGG	AAT	TTT	GTA	GAT	CCC	AAA	1099
Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly	Asn	Phe	Val	Asp	Pro	Lys	
	200					205					210					
GAA	AAA	GGC	AAG	CCT	TTA	GCC	CAA	ACT	TTA	GGA	AAC	CAA	ATG	CTG	TTT	1147
Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu	Gly	Asn	Gln	Met	Leu	Phe	
215				220						225				230		
AAC	ACT	TAC	GGG	CGA	ACG	GCT	GGA	ATG	TTG	GGT	AAG	CAT	GTA	GGA	ATT	1195
Asn	Thr	Tyr	Gly	Arg	Thr	Ala	Gly	Met	Leu	Gly	Lys	His	Val	Gly	Ile	
				235				240					245			
AGC	GCT	CAA	GGC	AAT	TGG	ATT	AAC	GGG	CAA	GGT	TTC	AGG	CAA	AAC	AGC	1243
Ser	Ala	Gln	Gly	Asn	Trp	Ile	Asn	Gly	Gln	Gly	Phe	Arg	Gln	Asn	Ser	
			250					255					260			
CCC	ACA	AAG	GTG	CAA	AAC	TAC	TTG	CTT	GAT	GCG	GTT	TAT	AAG	ATT	AAT	1291
Pro	Thr	Lys	Val	Gln	Asn	Tyr	Leu	Leu	Asp	Ala	Val	Tyr	Lys	Ile	Asn	
		265					270					275				

```

      1           5           10           15
Gly Phe Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly
      20           25           30
Gly Val Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu
      35           40           45
Gly Ala Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe
      50           55           60
Lys Thr Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu
      65           70           75           80
Gly Lys Lys Ser Ser Leu Cys Ser Asn Lys Lys
      85           90

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 458...2836
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

TCAAAATTTA AGTTAATTTT AATAATTATT TTTATAGTAT GCATCGGTTT GAATTAAATG      60
AGAAAGGTTA TCACAATGAA TGGTTATTTG AGAGTAAAAA CCTCTTATTT TTTAGCGTTG      120
AACGCTTTGA CTTTTTTGTC TTTTAACTCT TTGGTGGGCG CGAAAGAACA GCATCACACT      180
TTGCAAAAAG TGACAACCAC TGAGCAAAAA TTCAATCCAA GCGCGCCGCT TTCATGGCAA      240
AGCGAAGAGA TGCGTAATTC CACAAGCTCT CGCACGGTGA TTTCCAACAA GGAACTCAAA      300
AAAACGGGGA ATTTGAATAT TGAAAACGCC TTGCAAAACG TGCCAGGGAT TCAAATCAGA      360
GACGCTACAG GCACAGGCGT GCTGCCTAAA ATTTGCGTGC TCAAAATTTA AGTTAATTTT      420
AATAATTATT TTTATAGTAT GCATCGGTTT GAATTAA ATG AGA AAG GTT ATC ACA      475
                               Met Arg Lys Val Ile Thr
                               1           5

ATG AAT GGT TAT TTG AGA GTA AAA ACC TCT TAT TTT TTA GCG TTG AAC      523
Met Asn Gly Tyr Leu Arg Val Lys Thr Ser Tyr Phe Leu Ala Leu Asn
      10           15           20

GCT TTG ACT TTT TTG TCT TTT AAC TCT TTG GTG GGC GCG AAA GAA CAG      571
Ala Leu Thr Phe Leu Ser Phe Asn Ser Leu Val Gly Ala Lys Glu Gln
      25           30           35

CAT CAC ACT TTG CAA AAA GTG ACA ACC ACT GAG CAA AAA TTC AAT CCA      619
His His Thr Leu Gln Lys Val Thr Thr Thr Glu Gln Lys Phe Asn Pro
      40           45           50

AGC GCG CCG CTT TCA TGG CAA AGC GAA GAG ATG CGT AAT TCC ACA AGC      667

```

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...323
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

CTTTTTTCTC TTCCACTTTT TCCACTTTT TAAGAGCCTT GTGTTTATGA	TTG GGC	56
	Leu Gly	
	1	
TTT TTG GGT TCA GGT TTG GGT TTT GGT TTA GGC TCA GGC TTA GGC TTT		104
Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu Gly Phe		
5 10 15		
TCT ATA GGT TTT GGC GGG GTT GGC GGG GTT GGC GGA GTT GGG GGT GTG		152
Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly Gly Val		
20 25 30		
GGA GGC GTT GGA GGT TTT TGG GGG CCA GCC AGC GTG GGT TTA GGA GCG		200
Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu Gly Ala		
35 40 45 50		
CCC TGG GTG TTT TTA CTG GGA TCT TGC GAA TGG CCT CTT TTT AAA ACC		248
Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe Lys Thr		
55 60 65		
AAT AAA TTT TCA GGA TTT AAT TTA ACA AGC TTG GGT TTT GAA GGA AAA		296
Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu Gly Lys		
70 75 80		
AAA TCT TCT CTG TGT TCA AAT AAA AAA TAAATCAACC AGTGTAACAA TACAGAC		350
Lys Ser Ser Leu Cys Ser Asn Lys Lys		
85 90		
AGAATGAGAG AAAAGAAAAA ATTCCT		376

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Leu Gly Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu


```

TTT AAA GAA ATT CTA GAG GAC TAC AAA TAT CTA GAA AAA GAA TTT AAA      399
Phe Lys Glu Ile Leu Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys
          95                      100                      105

GAG CTC TCT AAC ACC GCT GAA AAA GAA GGC GAT AAA GTT ACC GTA ACT      447
Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr
          110                      115                      120

TAT GCG GAT GAT CAA TTA GCC AAG TTG CAA AAA TCC ATT TGG ATG CTG      495
Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu
          125                      130                      135

CAA GCC CAT TTG GCT TAAGCGACCA AAAAGAAGCC AGCATGAGAG ATTACAGCGA      550
Gln Ala His Leu Ala
140

```

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```

Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln Ala Asp Ala Ile Val
 1           5           10           15
Leu Phe Met Lys Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp
          20           25           30
Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile Tyr Glu Glu Phe Ala
          35           40           45
Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His
          50           55           60
Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu
65           70           75           80
Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu
          85           90           95
Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr
          100          105          110
Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln
          115          120          125
Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu Gln Ala His Leu Ala
130          135          140

```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```

Asn Thr Glu Ser Ala Val Leu Phe Asp Asn Pro Ser Phe Ala Lys Arg
      355                      360                      365
Val Arg Leu Ser Leu Lys Asp His Ala Gln Gln Ser Trp His Leu Val
      370                      375                      380
Val Tyr Arg His Arg Val Ile Trp Glu Ala Val Glu Glu Gly Ile Leu
      385                      390                      395                      400
Ile His Glu Lys Thr Ser Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile
      405                      410                      415
Lys Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu
      420                      425

```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...510
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```

AACTCTTTTG GTGTAGGATA GCGATCAAGG TTTTATGAA AATAAAAGCC TAAAACAATT      60
TTAAAAAAG GACTTTTG ATG AAA ACA TTT GAA ATT CTA AAA CAT TTG CAA      111
      Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln
              1              5              10

GCG GAT GCG ATC GTG TTA TTT ATG AAA GTG CAT AAC TTC CAT TGG AAT      159
Ala Asp Ala Ile Val Leu Phe Met Lys Val His Asn Phe His Trp Asn
      15              20              25

GTG AAA GGC ACC GAT TTT TTC AAT GTG CAT AAA GCC ACT GAA GAA ATT      207
Val Lys Gly Thr Asp Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile
      30              35              40

TAT GAA GAG TTT GCG GAC ATG TTT GAC GAT CTC GCT GAA AGG ATC GTT      255
Tyr Glu Glu Phe Ala Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val
      45              50              55

CAA TTA GGG CAT CAC CCC TTA GTC ACT TTA TCC GAA GCG ATC AAA CTC      303
Gln Leu Gly His His Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu
      60              65              70              75

ACT CGT GTT AAA GAA GAA ACT AAA ACG AGC TTC CAC TCT AAA GAC ATC      351
Thr Arg Val Lys Glu Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile
      80              85              90

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

```

Met Ser Gln Lys Ser Ile Asp Met Gln Thr Tyr Ile Tyr Lys Asn Asp
 1           5           10           15
Leu Ser Ser Gln Val Ile Ala Lys Glu Leu Leu Asn Ala Ala Asn Arg
      20           25           30
Gly Val Lys Val Arg Ile Leu Leu Asp Asp Asn Gly Leu Asp Ser Asp
      35           40           45
Phe Ser Asp Ile Met Leu Leu Asn Phe His Lys Asn Ile Glu Val Lys
      50           55           60
Ile Phe Asn Pro Tyr Tyr Ile Arg Asn Lys Gly Leu Arg Tyr Phe Glu
      65           70           75           80
Met Leu Ala Asp Tyr Glu Arg Ile Lys Lys Arg Met His Asn Lys Leu
      85           90           95
Phe Ile Val Asp Asn Phe Ala Val Ile Ile Gly Gly Arg Asn Ile Gly
      100          105          110
Asp Asn Tyr Phe Asp Asn Asp Leu Asp Thr Asn Phe Leu Asp Leu Asp
      115          120          125
Ala Leu Phe Phe Gly Gly Val Ala Ser Lys Ala Lys Glu Ser Phe Glu
      130          135          140
Arg Tyr Trp Arg Phe His Arg Ser Ile Pro Val Ser Leu Leu Arg Thr
      145          150          155          160
His Lys Arg Leu Lys Asn Asn Ala Lys Glu Ile Ala Lys Leu His Glu
      165          170          175
Lys Ile Pro Ile Ser Ala Glu Asp Lys Asn Gln Phe Glu Lys Lys Val
      180          185          190
Asn Asp Phe Ile Asp Arg Phe Gln Lys Tyr Gln Tyr Pro Ile Tyr Tyr
      195          200          205
Gly Asn Ala Ile Phe Leu Ala Asp Ser Pro Lys Lys Ile Asp Thr Pro
      210          215          220
Leu Tyr Ser Pro Ile Lys Ile Ala Phe Glu Lys Ala Leu Lys Asn Ala
      225          230          235          240
Lys Asp Ser Val Phe Ile Ala Ser Ser Tyr Phe Ile Pro Gly Lys Lys
      245          250          255
Met Met Lys Ile Phe Lys Asn Gln Ile Ser Lys Gly Ile Glu Leu Asn
      260          265          270
Ile Leu Thr Asn Ser Leu Ser Ser Thr Asp Ala Ile Val Val Tyr Gly
      275          280          285
Ala Trp Glu Arg Tyr Arg Asn Gln Leu Val Arg Met Gly Ala Asn Val
      290          295          300
Tyr Glu Ile Arg Asn Asp Phe Phe Asn Arg Gln Ile Lys Gly Arg Phe
      305          310          315          320
Ser Thr Lys His Ser Leu His Gly Lys Thr Ile Val Phe Asp Asp Asn
      325          330          335
Leu Thr Leu Leu Gly Ser Phe Asn Ile Asp Pro Arg Ser Ala Tyr Ile
      340          345          350

```

Tyr Ser Pro Ile Lys Ile Ala Phe Glu Lys Ala Leu Lys Asn Ala Lys	
230 235 240	
GAC TCC GTT TTT ATC GCT TCA TCG TAT TTT ATT CCA GGC AAA AAG ATG	1064
Asp Ser Val Phe Ile Ala Ser Ser Tyr Phe Ile Pro Gly Lys Lys Met	
245 250 255	
ATG AAA ATC TTT AAA AAT CAA ATT TCT AAG GGG ATT GAA TTG AAC ATC	1112
Met Lys Ile Phe Lys Asn Gln Ile Ser Lys Gly Ile Glu Leu Asn Ile	
260 265 270	
CTT ACC AAT TCC CTT TCA TCT ACT GAT GCG ATA GTG GTC TAT GGG GCA	1160
Leu Thr Asn Ser Leu Ser Ser Thr Asp Ala Ile Val Val Tyr Gly Ala	
275 280 285	
TGG GAA AGG TAT CGC AAC CAA TTA GTG CGA ATG GGC GCG AAT GTC TAT	1208
Trp Glu Arg Tyr Arg Asn Gln Leu Val Arg Met Gly Ala Asn Val Tyr	
290 295 300 305	
GAA ATA CGA AAC GAT TTT TTC AAC CGC CAG ATT AAA GGG CGC TTT AGC	1256
Glu Ile Arg Asn Asp Phe Phe Asn Arg Gln Ile Lys Gly Arg Phe Ser	
310 315 320	
ACC AAA CAT TCC TTG CAT GGC AAG ACG ATT GTT TTT GAT GAC AAT TTA	1304
Thr Lys His Ser Leu His Gly Lys Thr Ile Val Phe Asp Asp Asn Leu	
325 330 335	
ACG CTT CTA GGG AGT TTC AAT ATT GAT CCG CGC TCT GCA TAC ATC AAC	1352
Thr Leu Leu Gly Ser Phe Asn Ile Asp Pro Arg Ser Ala Tyr Ile Asn	
340 345 350	
ACT GAA AGC GCG GTT TTG TTT GAC AAC CCG TCT TTT GCT AAA AGG GTG	1400
Thr Glu Ser Ala Val Leu Phe Asp Asn Pro Ser Phe Ala Lys Arg Val	
355 360 365	
CGT TTG TCG CTT AAA GAT CAT GCC CAA CAA TCA TGG CAT TTG GTG GTG	1448
Arg Leu Ser Leu Lys Asp His Ala Gln Gln Ser Trp His Leu Val Val	
370 375 380 385	
TAT CGG CAT AGA GTG ATT TGG GAA GCG GTG GAA GAA GGC ATT TTA ATC	1496
Tyr Arg His Arg Val Ile Trp Glu Ala Val Glu Glu Gly Ile Leu Ile	
390 395 400	
CAT GAA AAA ACT TCG CCT GAC ACT TCC TTC TTT TTG CGC TTG ATT AAA	1544
His Glu Lys Thr Ser Pro Asp Thr Ser Phe Phe Leu Arg Leu Ile Lys	
405 410 415	
GAA TGG TCT AAA GTC CTT CCT GAA AGA GAG CTT TAAACTTTT AATGCGCTTT	1597
Glu Trp Ser Lys Val Leu Pro Glu Arg Glu Leu	
420 425	
ATTTTGCGAA AAAGCGATGT TATTGGTAAC GGC	1630

(2) INFORMATION FOR SEQ ID NO:356:

5					10					15						
TCT	TCT	CAA	GTG	ATT	GCT	AAA	GAA	CTT	TTA	AAT	GCG	GCC	AAT	CGT	GGG	392
Ser	Ser	Gln	Val	Ile	Ala	Lys	Glu	Leu	Leu	Asn	Ala	Ala	Asn	Arg	Gly	
20					25					30						
GTA	AAA	GTG	CGC	ATC	CTT	TTA	GAC	GAT	AAC	GGA	TTG	GAT	TCG	GAT	TTT	440
Val	Lys	Val	Arg	Ile	Leu	Leu	Asp	Asp	Asn	Gly	Leu	Asp	Ser	Asp	Phe	
35					40					45						
TCA	GAT	ATT	ATG	CTC	TTA	AAT	TTC	CAT	AAA	AAC	ATT	GAG	GTG	AAA	ATT	488
Ser	Asp	Ile	Met	Leu	Leu	Asn	Phe	His	Lys	Asn	Ile	Glu	Val	Lys	Ile	
50					55					60					65	
TTT	AAC	CCC	TAC	TAT	ATC	CGC	AAT	AAA	GGC	TTG	CGT	TAT	TTT	GAA	ATG	536
Phe	Asn	Pro	Tyr	Tyr	Ile	Arg	Asn	Lys	Gly	Leu	Arg	Tyr	Phe	Glu	Met	
70					75					80						
CTT	GCG	GAT	TAT	GAG	CGC	ATT	AAA	AAA	CGC	ATG	CAC	AAC	AAG	CTT	TTC	584
Leu	Ala	Asp	Tyr	Glu	Arg	Ile	Lys	Lys	Arg	Met	His	Asn	Lys	Leu	Phe	
85					90					95						
ATC	GTG	GAT	AAT	TTC	GCT	GTC	ATT	ATA	GGG	GGG	CGC	AAT	ATT	GGG	GAC	632
Ile	Val	Asp	Asn	Phe	Ala	Val	Ile	Ile	Gly	Gly	Arg	Asn	Ile	Gly	Asp	
100					105					110						
AAT	TAT	TTT	GAT	AAC	GAT	TTA	GAC	ACG	AAT	TTT	TTA	GAT	TTA	GAC	GCT	680
Asn	Tyr	Phe	Asp	Asn	Asp	Leu	Asp	Thr	Asn	Phe	Leu	Asp	Leu	Asp	Ala	
115					120					125						
TTG	TTT	TTT	GGG	GGG	GTT	GCT	TCA	AAA	GCC	AAA	GAA	AGC	TTT	GAA	CGC	728
Leu	Phe	Phe	Gly	Gly	Val	Ala	Ser	Lys	Ala	Lys	Glu	Ser	Phe	Glu	Arg	
130					135					140					145	
TAT	TGG	AGA	TTC	CAC	CGC	TCT	ATC	CCT	GTT	TCA	TTA	CTA	AGA	ACC	CAT	776
Tyr	Trp	Arg	Phe	His	Arg	Ser	Ile	Pro	Val	Ser	Leu	Leu	Arg	Thr	His	
150					155					160						
AAA	AGA	CTC	AAA	AAC	AAC	GCT	AAA	GAA	ATC	GCT	AAA	CTC	CAT	GAA	AAA	824
Lys	Arg	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Ala	Lys	Leu	His	Glu	Lys	
165					170					175						
ATC	CCT	ATC	AGC	GCT	GAA	GAC	AAA	AAC	CAG	TTT	GAA	AAA	AAA	GTC	AAT	872
Ile	Pro	Ile	Ser	Ala	Glu	Asp	Lys	Asn	Gln	Phe	Glu	Lys	Lys	Val	Asn	
180					185					190						
GAT	TTT	ATA	GAT	CGT	TTC	CAA	AAA	TAC	CAA	TAC	CCC	ATT	TAT	TAT	GGG	920
Asp	Phe	Ile	Asp	Arg	Phe	Gln	Lys	Tyr	Gln	Tyr	Pro	Ile	Tyr	Tyr	Gly	
195					200					205						
AAT	GCC	ATT	TTT	TTA	GCC	GAT	TCA	CCC	AAA	AAA	ATT	GAC	ACG	CCC	TTG	968
Asn	Ala	Ile	Phe	Leu	Ala	Asp	Ser	Pro	Lys	Lys	Ile	Asp	Thr	Pro	Leu	
210					215					220					225	
TAT	TCG	CCT	ATC	AAA	ATC	GCT	TTT	GAG	AAA	GCC	CTT	AAA	AAC	GCT	AAG	1016

```

Leu Ala Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly
305                      310                      315                      320
Thr Cys Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala
                      325                      330                      335
Tyr Leu Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln
                      340                      345                      350
Leu Phe Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu
                      355                      360                      365
Cys Gly Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu
                      370                      375                      380
Leu Ile Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val
385                      390                      395                      400
Ile Lys Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser
                      405                      410                      415
Met Lys Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe
                      420                      425                      430
Gln Leu Lys Met Ala Gln Phe Phe Ser Pro Leu Gly Lys Leu Leu Ala
                      435                      440                      445
Pro Ile Leu Pro Leu Val Lys Glu Trp Ala Ser Val Arg Thr Leu Pro
                      450                      455                      460
Asn Met Asp Thr Ser Leu His Ala Lys Val Gln His Leu Glu Gly Val
465                      470                      475                      480
Ile Tyr Glu

```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 294...1577
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```

GTATCGCCAC TTTGCGTAAC AGGATGTTGA AAGTGGGTAA AAGCCGCTAA TTTCTTTTTA      60
GTGGGTCGTT TTTGAAAATC TTTTATAGTCT TTTTAAGCGT CTTTTTTTTT AATGGGTGTT      120
TTGGGTTAGT CTATAAGACT CCCATTTCAA GCTCTCCTAT CTCTTATGAT CCCTACACTA      180
CCCCCATTTG GAGCTTGTAT GCTGAAAAAT TAAAAGAAAA CCCTAACCAT AGCGCGGCCA      240
TTCTTTTAGA AGATGGCTTT GACGCTCTGT TGCATAGAGT GGGACTTATT AGA ATG      296
                                     Met
                                     1

AGC CAA AAA AGC ATT GAC ATG CAA ACT TAT ATC TAT AAA AAC GAC CTT      344
Ser Gln-Lys Ser Ile Asp Met Gln Thr Tyr Ile Tyr Lys Asn Asp Leu

```

GAG TAAAGAGCTT ATTTTAAAGC GCATTAAAGA AGCCAGAGCC AAGCATGCCA TTCAGG 1555
Glu

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met	Ile	Met	Glu	Lys	Tyr	His	Ser	Asp	Gln	Glu	Tyr	Glu	Glu	Ile	Ile	1	5	10	15
Thr	Asp	Gln	Leu	Gly	Asp	Met	Gln	Leu	Arg	Glu	Asn	Leu	Arg	Ser	Ala	20	25	30	
Met	Asp	Thr	Leu	Arg	Ala	Asn	Arg	Lys	Asn	Leu	Leu	Lys	Asn	Arg	Tyr	35	40	45	
Ser	Glu	Trp	Glu	Asn	Leu	Arg	Glu	Leu	Gly	Lys	Glu	Val	Lys	Leu	Lys	50	55	60	
Ile	Leu	Ser	Arg	Leu	Asp	Glu	Tyr	Leu	Glu	Leu	Phe	Glu	Lys	Asn	Ala	65	70	75	80
Thr	Gln	Asn	Gly	Phe	Lys	Ile	His	Tyr	Ala	Lys	Asp	Gly	Asp	Glu	Ala	85	90	95	
Asn	Glu	Ile	Ile	Tyr	Asn	Leu	Ala	Lys	Glu	Lys	Asn	Ile	Lys	Arg	Ile	100	105	110	
Leu	Lys	Gln	Lys	Ser	Met	Ala	Ser	Glu	Glu	Ile	Gly	Leu	Asn	His	Tyr	115	120	125	
Leu	Lys	Glu	Lys	Gly	Ile	Gln	Ala	Gln	Glu	Thr	Asp	Leu	Gly	Glu	Leu	130	135	140	
Ile	Ile	Gln	Leu	Ile	Asn	Glu	His	Pro	Val	His	Ile	Val	Val	Pro	Ala	145	150	155	160
Ile	His	Lys	Asn	Arg	Lys	Gln	Ile	Gly	Lys	Ile	Phe	Glu	Glu	Lys	Leu	165	170	175	
Asn	Ala	Ala	Tyr	Glu	Glu	Glu	Pro	Glu	Lys	Leu	Asn	Ala	Ile	Ala	Arg	180	185	190	
Lys	His	Met	Arg	Lys	Glu	Phe	Glu	Ser	Phe	Lys	Met	Gly	Ile	Ser	Gly	195	200	205	
Val	Asn	Phe	Ala	Ile	Ala	Asn	Glu	Gly	Ala	Ile	Trp	Leu	Val	Glu	Asn	210	215	220	
Glu	Gly	Asn	Gly	Arg	Met	Ser	Thr	Thr	Ala	Cys	Asp	Val	His	Val	Ala	225	230	235	240
Ile	Cys	Gly	Ile	Glu	Lys	Leu	Val	Glu	Ser	Phe	Asp	Asp	Ala	Ala	Ile	245	250	255	
Leu	Asn	Asn	Leu	Leu	Ala	Pro	Ser	Ala	Val	Gly	Val	Pro	Ile	Thr	Cys	260	265	270	
Tyr	Gln	Asn	Ile	Ile	Thr	Gly	Pro	Arg	Lys	Glu	Gly	Asp	Leu	Asp	Gly	275	280	285	
Pro	Lys	Glu	Ala	His	Ile	Ile	Leu	Leu	Asp	Asn	Asn	Arg	Ser	Asn	Ile	290	295	300	

AAT	TTG	CTC	GCC	CCA	AGC	GCT	GTG	GGT	GTG	CCT	ATC	ACT	TGC	TAT	CAA	872
Asn	Leu	Leu	Ala	Pro	Ser	Ala	Val	Gly	Val	Pro	Ile	Thr	Cys	Tyr	Gln	
260						265					270					
AAC	ATT	ATC	ACA	GGC	CCT	AGA	AAA	GAG	GGC	GAT	TTA	GAC	GGC	CCT	AAA	920
Asn	Ile	Ile	Thr	Gly	Pro	Arg	Lys	Glu	Gly	Asp	Leu	Asp	Gly	Pro	Lys	
275					280					285					290	
GAA	GCC	CAC	ATC	ATT	TTA	TTA	GAC	AAC	AAC	CGC	TCT	AAT	ATT	TTG	GCT	968
Glu	Ala	His	Ile	Ile	Leu	Leu	Asp	Asn	Asn	Arg	Ser	Asn	Ile	Leu	Ala	
				295					300					305		
GAT	GAA	AAG	TAT	TAT	CGC	GCT	CTT	TCA	TGC	ATC	CGT	TGC	GGG	ACT	TGT	1016
Asp	Glu	Lys	Tyr	Tyr	Arg	Ala	Leu	Ser	Cys	Ile	Arg	Cys	Gly	Thr	Cys	
			310					315					320			
TTG	AAC	CAC	TGC	CCT	GTG	TAT	GAT	AAA	ATC	GGT	GGG	CAT	GCC	TAT	CTT	1064
Leu	Asn	His	Cys	Pro	Val	Tyr	Asp	Lys	Ile	Gly	Gly	His	Ala	Tyr	Leu	
		325					330					335				
TCT	ACT	TAT	CCT	GGC	CCT	ATA	GGC	GTG	GTG	GTA	TCC	CCC	CAA	CTC	TTT	1112
Ser	Thr	Tyr	Pro	Gly	Pro	Ile	Gly	Val	Val	Val	Ser	Pro	Gln	Leu	Phe	
		340				345					350					
GGC	TTG	AAT	AAT	TAC	GGG	CAT	ATC	CCT	AAT	TTG	TGC	AGT	CTT	TGC	GGG	1160
Gly	Leu	Asn	Asn	Tyr	Gly	His	Ile	Pro	Asn	Leu	Cys	Ser	Leu	Cys	Gly	
355					360				365					370		
CGT	TGC	ACT	GAA	GTA	TGC	CCC	GTA	GAA	ATC	CCT	TTA	GCC	GAA	CTC	ATT	1208
Arg	Cys	Thr	Glu	Val	Cys	Pro	Val	Glu	Ile	Pro	Leu	Ala	Glu	Leu	Ile	
			375					380						385		
AGG	GAT	TTA	CGA	TCC	GAT	AAA	GTG	GGC	GAG	GGC	AGG	GGT	GTA	ATT	AAG	1256
Arg	Asp	Leu	Arg	Ser	Asp	Lys	Val	Gly	Glu	Gly	Arg	Gly	Val	Ile	Lys	
		390						395					400			
GGG	GCT	AAA	AGC	ACC	CAA	CAC	AGC	GGG	ATG	GAA	AAA	TTC	TCT	ATG	AAA	1304
Gly	Ala	Lys	Ser	Thr	Gln	His	Ser	Gly	Met	Glu	Lys	Phe	Ser	Met	Lys	
		405					410					415				
ATG	TTT	GCC	AAA	ATG	GCA	AGC	GAT	GGG	GCT	AAG	TGG	CGT	TTC	CAA	TTG	1352
Met	Phe	Ala	Lys	Met	Ala	Ser	Asp	Gly	Ala	Lys	Trp	Arg	Phe	Gln	Leu	
		420				425					430					
AAA	ATG	GCT	CAA	TTT	TTC	TCG	CCT	TTA	GGC	AAG	CTT	TTA	GCT	CCC	ATA	1400
Lys	Met	Ala	Gln	Phe	Phe	Ser	Pro	Leu	Gly	Lys	Leu	Leu	Ala	Pro	Ile	
435					440				445					450		
CTG	CCT	TTA	GTC	AAA	GAG	TGG	GCG	AGC	GTT	AGG	ACC	TTA	CCC	AAT	ATG	1448
Leu	Pro	Leu	Val	Lys	Glu	Trp	Ala	Ser	Val	Arg	Thr	Leu	Pro	Asn	Met	
			455					460						465		
GAC	ACG	AGC	TTG	CAT	GCA	AAA	GTC	CAG	CAC	TTA	GAA	GGG	GTG	ATT	TAT	1496
Asp	Thr	Ser	Leu	His	Ala	Lys	Val	Gln	His	Leu	Glu	Gly	Val	Ile	Tyr	
			470					475					480			

Thr	Leu	Arg	Ala	Asn	Arg	Lys	Asn	Leu	Leu	Lys	Asn	Arg	Tyr	Ser	Glu	
35					40					45					50	
TGG	GAA	AAT	TTA	AGG	GAA	TTA	GGC	AAA	GAA	GTC	AAG	CTT	AAA	ATC	TTA	248
Trp	Glu	Asn	Leu	Arg	Glu	Leu	Gly	Lys	Glu	Val	Lys	Leu	Lys	Ile	Leu	
				55					60					65		
TCC	AGG	CTT	GAT	GAA	TAT	TTG	GAA	TTG	TTT	GAA	AAA	AAC	GCC	ACT	CAA	296
Ser	Arg	Leu	Asp	Glu	Tyr	Leu	Glu	Leu	Phe	Glu	Lys	Asn	Ala	Thr	Gln	
				70				75					80			
AAC	GGC	TTT	AAA	ATC	CAT	TAC	GCT	AAA	GAC	GGC	GAT	GAA	GCT	AAT	GAA	344
Asn	Gly	Phe	Lys	Ile	His	Tyr	Ala	Lys	Asp	Gly	Asp	Glu	Ala	Asn	Glu	
			85				90					95				
ATC	ATT	TAC	AAC	CTC	GCT	AAA	GAA	AAG	AAT	ATC	AAG	CGC	ATT	TTA	AAG	392
Ile	Ile	Tyr	Asn	Leu	Ala	Lys	Glu	Lys	Asn	Ile	Lys	Arg	Ile	Leu	Lys	
	100					105					110					
CAA	AAA	TCC	ATG	GCG	AGC	GAA	GAA	ATT	GGC	TTG	AAC	CAT	TAC	TTG	AAA	440
Gln	Lys	Ser	Met	Ala	Ser	Glu	Glu	Ile	Gly	Leu	Asn	His	Tyr	Leu	Lys	
115					120					125					130	
GAA	AAG	GGC	ATT	CAA	GCA	CAA	GAA	ACG	GAT	TTG	GGC	GAA	TTG	ATT	ATC	488
Glu	Lys	Gly	Ile	Gln	Ala	Gln	Glu	Thr	Asp	Leu	Gly	Glu	Leu	Ile	Ile	
				135					140					145		
CAA	CTC	ATC	AAT	GAA	CAC	CCT	GTG	CAT	ATT	GTC	GTG	CCA	GCT	ATC	CAT	536
Gln	Leu	Ile	Asn	Glu	His	Pro	Val	His	Ile	Val	Val	Pro	Ala	Ile	His	
			150					155					160			
AAA	AAC	CGC	AAG	CAA	ATC	GGT	AAG	ATT	TTT	GAA	GAA	AAA	CTC	AAC	GCC	584
Lys	Asn	Arg	Lys	Gln	Ile	Gly	Lys	Ile	Phe	Glu	Glu	Lys	Leu	Asn	Ala	
		165					170					175				
GCT	TAT	GAA	GAA	GAG	CCT	GAA	AAG	CTT	AAT	GCG	ATC	GCC	AGA	AAA	CAC	632
Ala	Tyr	Glu	Glu	Glu	Pro	Glu	Lys	Leu	Asn	Ala	Ile	Ala	Arg	Lys	His	
	180					185					190					
ATG	CGC	AAA	GAA	TTT	GAA	AGC	TTT	AAA	ATG	GGG	ATT	AGT	GGG	GTT	AAT	680
Met	Arg	Lys	Glu	Phe	Glu	Ser	Phe	Lys	Met	Gly	Ile	Ser	Gly	Val	Asn	
195					200					205					210	
TTT	GCT	ATC	GCT	AAC	GAA	GGA	GCG	ATC	TGG	TTA	GTG	GAA	AAT	GAA	GGC	728
Phe	Ala	Ile	Ala	Asn	Glu	Gly	Ala	Ile	Trp	Leu	Val	Glu	Asn	Glu	Gly	
				215					220					225		
AAT	GGC	AGA	ATG	AGC	ACC	ACT	GCA	TGC	GAT	GTG	CAT	GTC	GCA	ATT	TGT	776
Asn	Gly	Arg	Met	Ser	Thr	Thr	Ala	Cys	Asp	Val	His	Val	Ala	Ile	Cys	
			230					235					240			
GGG	ATT	GAA	AAA	TTA	GTA	GAA	AGC	TTT	GAT	GAT	GCG	GCG	ATT	TTA	AAC	824
Gly	Ile	Glu	Lys	Leu	Val	Glu	Ser	Phe	Asp	Asp	Ala	Ala	Ile	Leu	Asn	
		245					250					255				

115	120	125
Ser Leu Pro Leu Phe Asn Trp	Leu Tyr Lys Gly Ser Asp Phe Gly Ala	
130	135	140
Leu His Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu		
145	150	155
Ile Ser Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp		
165	170	175
Ala Ile Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys		
180	185	190
Ala Ala Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp		
195	200	205
Ser Pro Glu Phe Ile Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn		
210	215	220
Ser Asp Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala		
225	230	235
Ser Lys Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys		
245	250	255
Lys Arg Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln		
260	265	270
Glu Phe Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys		
275	280	285

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1499
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CTTTT	TAGCC	TCAAGACTTG	GGCTTTAACA	TTAAAGAATT	ATTTTAAGGA	ATG ATC	56
						Met Ile	
						1	
ATG GAA AAA TAC CAT AGC GAC CAA GAA TAC GAA GAA ATC ATC ACC GAC						104	
Met Glu Lys Tyr His Ser Asp Gln Glu Tyr Glu Glu Ile Ile Thr Asp							
5		10		15			
CAA TTA GGC GAT ATG CAA TTA AGG GAA AAT TTG CGT TCT GCA ATG GAT						152	
Gln Leu Gly Asp Met Gln Leu Arg Glu Asn Leu Arg Ser Ala Met Asp							
20		25		30			
ACC TTA AGG GCT AAT CGT AAG AAT CTC CTT AAA AAT CGT TAC AGC GAA						200	

```

TTT CAA AAG AGG AGC AGT GGG GAG CTT GAA AGC CAT ACT GAT AGC CCT      680
Phe Gln Lys Arg Ser Ser Gly Glu Leu Glu Ser His Thr Asp Ser Pro
195                      200                      205                      210

GAA TTT ATA AGC TCT TCT AAG AGG ACA CAG AAC GCT TCT AAT TCG GAT      728
Glu Phe Ile Ser Ser Ser Lys Arg Thr Gln Asn Ala Ser Asn Ser Asp
                215                      220                      225

CTC AAT TCT ATG ACC AAT GCT AAC GCG CTC AAA GAA ACA GCT TCA AAA      776
Leu Asn Ser Met Thr Asn Ala Asn Ala Leu Lys Glu Thr Ala Ser Lys
                230                      235                      240

GAG CCA GAG GCT TCT TCA AAA AAA GAG AAA AAG TCT AAG AAA AAA CGT      824
Glu Pro Glu Ala Ser Ser Lys Lys Glu Lys Lys Ser Lys Lys Lys Arg
                245                      250                      255

CGC CTT TCA AAG AAA GAA AAA CAA CAA CAA GCC TTG CAA CAA GAG TTT      872
Arg Leu Ser Lys Lys Glu Lys Gln Gln Gln Ala Leu Gln Gln Glu Phe
                260                      265                      270

GAA AAA CAA ATT AGC GAC TCT AGT AAG TCT GAA AAA TAGTAATAAT AGTTAA      924
Glu Lys Gln Ile Ser Asp Ser Ser Lys Ser Glu Lys
275                      280                      285

GCTTACCTTT TTAGGGGGCT TTCAATAAAT CTCTTAA      961

```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```

Val Lys Arg Ile Leu Phe Phe Leu Val Ala Thr Thr Phe Leu Leu Arg
 1                      5                      10                      15
Ala Glu Thr Asp Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val
                20                      25                      30
Met Phe Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg
                35                      40                      45
Val Leu Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe
 50                      55                      60
Asn Arg Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe
65                      70                      75                      80
Gly Ala Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile
                85                      90                      95
Cys Tyr Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp
                100                      105                      110
Arg Glu Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

AGAACAGTAT CTATTTTGT TCGGTTGTA TATTTAATTA GGAGTTTGGT GTG AAA	56
Val Lys	
1	
CGG ATT TTA TTT TTT TTA GTA GCT ACG ACT TTT TTG TTG AGA GCA GAA	104
Arg Ile Leu Phe Phe Leu Val Ala Thr Thr Phe Leu Leu Arg Ala Glu	
5 10 15	
ACG GAT TCT GCC ACT ATT AAC ACT ACA GTT GAT CCC AAT GTT ATG TTT	152
Thr Asp Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val Met Phe	
20 25 30	
TCT GAA AGC TCC ACA GGG AAT GTG AAA AAA GAC CGC AAG AGG GTT TTA	200
Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg Val Leu	
35 40 45 50	
AAG AGC ATG GTT AAT TTG GAA AAA GAG CGC GTG AAG AAT TTT AAC CGG	248
Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe Asn Arg	
55 60 65	
TAT TCT GAA ACC AAG ATG AGT AAG GGC GAC TTA TCC GCT TTT GGA GCT	296
Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe Gly Ala	
70 75 80	
TTC TTT AAG GGG AGT TTG GAA AGT TGT GTG GAT CAA AAG ATT TGT TAT	344
Phe Phe Lys Gly Ser Leu Glu Ser Cys Val Asp Gln Lys Ile Cys Tyr	
85 90 95	
TAT GAG CAT AAA GAT GGC AAG GTT TCT TTT GTG GTG AAT GAC AGG GAG	392
Tyr Glu His Lys Asp Gly Lys Val Ser Phe Val Val Asn Asp Arg Glu	
100 105 110	
AAG TTT TAT AAA CAT GTG CTT AAA GAC TTA GGG ACA GAG CTT TCG CTC	440
Lys Phe Tyr Lys His Val Leu Lys Asp Leu Gly Thr Glu Leu Ser Leu	
115 120 125 130	
CCT TTG TTT AAC TGG CTT TAC AAA GGC TCG GAT TTT GGG GCT TTG CAT	488
Pro Leu Phe Asn Trp Leu Tyr Lys Gly Ser Asp Phe Gly Ala Leu His	
135 140 145	
GAG CAG TTT GGG GAT ATG TAT GAT GGG TAT ATC AAA TAC TTG ATC AGT	536
Glu Gln Phe Gly Asp Met Tyr Asp Gly Tyr Ile Lys Tyr Leu Ile Ser	
150 155 160	
ATG GTT AGA ATA AGC CAA AAA GAA AAG GCT AGA AAA GTG GAT GCA ATC	584
Met Val Arg Ile Ser Gln Lys Glu Lys Ala Arg Lys Val Asp Ala Ile	
165 170 175	
GTT CTT AAG AAA ATG GAA GAA CAA GCT GAG AAA GAC ACT AAG GCA GCG	632
Val Leu Lys Lys Met Glu Glu Gln Ala Glu Lys Asp Thr Lys Ala Ala	
180 185 190	

```

Ala Gly Gly Ala Lys Arg Trp Ile Arg Leu Gly Phe Phe Ser Leu Ala
      100                      105                      110
Pro Leu Glu Phe Leu Lys Ile Gly Phe Thr Phe Phe Leu Ala Trp Ser
      115                      120                      125
Leu Ser Arg Thr Phe Val Ala Lys Glu Lys Ala Asn Val Lys Glu Glu
      130                      135                      140
Leu Ile Thr Phe Val Pro Tyr Ser Val Val Phe Val Ala Leu Ala Ile
      145                      150                      155                      160
Gly Val Gly Val Leu Gln Asn Asp Leu Gly Gln Ile Val Leu Leu Gly
      165                      170                      175
Ala Val Leu Ala Val Leu Leu Val Phe Ser Gly Gly Ser Val His Leu
      180                      185                      190
Phe Gly Leu Ile Ile Ser Gly Ala Phe Ala Ile Ser Val Leu Ala Ile
      195                      200                      205
Val Thr Ser Glu His Arg Ile Leu Arg Leu Lys Leu Trp Trp Ser Asn
      210                      215                      220
Leu Gln Asn Ser Leu Phe Thr Leu Leu Pro Asp Arg Leu Ala Asn Ala
      225                      230                      235                      240
Leu Arg Ile Ser Asp Leu Pro Glu Ser Tyr Gln Val Phe His Ala Gly
      245                      250                      255
Asn Ala Met His Asn Gly Gly Leu Phe Gly Gln Gly Leu Gly Leu Gly
      260                      265                      270
Gln Ile Lys Leu Gly Phe Leu Ser Glu Val His Thr Asp Met Val Leu
      275                      280                      285
Ala Gly Ile Ala Glu Glu Trp Gly Phe Leu Gly Leu Cys Val Cys Phe
      290                      295                      300
Ile Leu Phe Ser Val Leu Ile Val Leu Ile Phe Arg Ile Ala Asn Arg
      305                      310                      315                      320
Leu Lys Glu Pro Lys Tyr Ser Leu Phe Cys Val Gly Val Val Leu Leu
      325                      330                      335
Ile Ser Phe Ser Leu Val Ile Asn Ala Phe Gly Val Gly Gly Ile Leu
      340                      345                      350
Pro Val Lys Gly Leu Ala Val Pro Phe Leu Ser Tyr Gly Gly Ser Ser
      355                      360                      365
Leu Leu Ala Asn Cys Ile Ala Ile Gly Leu Val Leu Ser Leu Ala Arg
      370                      375                      380
Tyr Thr Lys Gly
      385

```

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...908
- (D) OTHER INFORMATION:

```

GCT GGG ATC GCC GAA GAA TGG GGG TTT TTG GGG CTA TGC GTT TGT TTT      972
Ala Gly Ile Ala Glu Glu Trp Gly Phe Leu Gly Leu Cys Val Cys Phe
    290                      295                      300

ATT TTG TTT TCT GTT TTG ATT GTT TTG ATT TTT AGG ATC GCT AAC CGC      1020
Ile Leu Phe Ser Val Leu Ile Val Leu Ile Phe Arg Ile Ala Asn Arg
    305                      310                      315                      320

TTG AAA GAG CCA AAA TAT TCG CTA TTT TGC GTG GGC GTG GTG CTG CTT      1068
Leu Lys Glu Pro Lys Tyr Ser Leu Phe Cys Val Gly Val Val Leu Leu
    325                      330                      335

ATT AGT TTT TCT TTG GTG ATC AAC GCC TTT GGG GTG GGC GGG ATT CTT      1116
Ile Ser Phe Ser Leu Val Ile Asn Ala Phe Gly Val Gly Gly Ile Leu
    340                      345                      350

CCG GTT AAA GGT CTA GCG GTG CCG TTT TTG AGC TAT GGA GGG AGT TCG      1164
Pro Val Lys Gly Leu Ala Val Pro Phe Leu Ser Tyr Gly Gly Ser Ser
    355                      360                      365

CTT CTA GCG AAT TGT ATC GCT ATA GGG CTT GTT CTA AGC CTA GCG CGA      1212
Leu Leu Ala Asn Cys Ile Ala Ile Gly Leu Val Leu Ser Leu Ala Arg
    370                      375                      380

TAC ACG AAA GGC TAAAAACATC AACCCCTTTT TAAAAATTAA TGCCATAAAA AGGGC      1269
Tyr Thr Lys Gly
    385

TCAACCTC                                                                1277

```

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

Met Thr Thr Asp Arg Asn Leu Phe Phe Cys Ala Ser Leu Leu Ile Phe
 1          5          10          15
Leu Gly Val Leu Met Ser Tyr Ser Leu Ser Thr Tyr Thr Thr Val Val
    20          25          30
Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser
    35          40          45
Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro
    50          55          60
Ser Lys Trp Phe Ser Arg Leu Gly Phe Phe Leu Leu Phe Val Pro Pro
    65          70          75          80
Leu Leu Ile Ile Gly Met Phe Phe Leu Pro Glu Ser Leu Ser Ser Ser
    85          90          95

```

AGC	AAG	TGG	TTT	AGC	CGT	TTG	GGG	TTT	TTT	CTT	CTT	TTT	GTC	CCA	CCA	300
Ser	Lys	Trp	Phe	Ser	Arg	Leu	Gly	Phe	Phe	Leu	Leu	Phe	Val	Pro	Pro	
65					70					75					80	
TTA	CTC	ATT	ATT	GGC	ATG	TTT	TTT	TTG	CCA	GAA	AGC	CTT	TCT	AGC	AGT	348
Leu	Leu	Ile	Ile	Gly	Met	Phe	Phe	Leu	Pro	Glu	Ser	Leu	Ser	Ser	Ser	
				85					90						95	
GCT	GGG	GGG	GCG	AAG	CGA	TGG	ATT	CGT	TTG	GGG	TTT	TTT	TCT	CTA	GCG	396
Ala	Gly	Gly	Ala	Lys	Arg	Trp	Ile	Arg	Leu	Gly	Phe	Phe	Ser	Leu	Ala	
			100					105						110		
CCT	TTG	GAG	TTT	TTG	AAG	ATT	GGT	TTC	ACC	TTT	TTT	CTT	GCG	TGG	AGT	444
Pro	Leu	Glu	Phe	Leu	Lys	Ile	Gly	Phe	Thr	Phe	Phe	Leu	Ala	Trp	Ser	
		115					120					125				
TTG	TCT	CGC	ACT	TTT	GTG	GCA	AAA	GAA	AAG	GCT	AAT	GTT	AAA	GAA	GAA	492
Leu	Ser	Arg	Thr	Phe	Val	Ala	Lys	Glu	Lys	Ala	Asn	Val	Lys	Glu	Glu	
	130					135					140					
CTC	ATC	ACT	TTT	GTG	CCT	TAT	TCA	GTG	GTG	TTT	GTA	GCC	TTA	GCG	ATT	540
Leu	Ile	Thr	Phe	Val	Pro	Tyr	Ser	Val	Val	Phe	Val	Ala	Leu	Ala	Ile	
145					150					155					160	
GGG	GTG	GGG	GTT	TTG	CAA	AAC	GAT	TTG	GGG	CAG	ATT	GTT	CTT	TTG	GGG	588
Gly	Val	Gly	Val	Leu	Gln	Asn	Asp	Leu	Gly	Gln	Ile	Val	Leu	Leu	Gly	
				165					170					175		
GCG	GTT	TTA	GCG	GTG	TTG	TTG	GTT	TTT	TCT	GGG	GGG	AGC	GTG	CAT	TTG	636
Ala	Val	Leu	Ala	Val	Leu	Leu	Val	Phe	Ser	Gly	Gly	Ser	Val	His	Leu	
			180					185					190			
TTT	GGC	TTG	ATT	ATT	TCA	GGG	GCG	TTT	GCG	ATC	AGC	GTT	TTA	GCG	ATT	684
Phe	Gly	Leu	Ile	Ile	Ser	Gly	Ala	Phe	Ala	Ile	Ser	Val	Leu	Ala	Ile	
		195					200					205				
GTT	ACA	AGC	GAG	CAT	AGG	ATT	TTG	CGC	CTG	AAA	TTG	TGG	TGG	TCT	AAT	732
Val	Thr	Ser	Glu	His	Arg	Ile	Leu	Arg	Leu	Lys	Leu	Trp	Trp	Ser	Asn	
	210					215					220					
TTG	CAA	AAT	TCG	CTT	TTC	ACG	CTC	TTG	CCG	GAT	AGA	TTA	GCG	AAC	GCT	780
Leu	Gln	Asn	Ser	Leu	Phe	Thr	Leu	Leu	Pro	Asp	Arg	Leu	Ala	Asn	Ala	
225					230					235					240	
CTT	AGA	ATA	AGC	GAC	TTG	CCC	GAA	TCC	TAT	CAG	GTC	TTT	CAT	GCA	GGC	828
Leu	Arg	Ile	Ser	Asp	Leu	Pro	Glu	Ser	Tyr	Gln	Val	Phe	His	Ala	Gly	
				245					250					255		
AAT	GCC	ATG	CAT	AAT	GGG	GGG	TTG	TTT	GGG	CAA	GGG	CTT	GGG	CTT	GGG	876
Asn	Ala	Met	His	Asn	Gly	Gly	Leu	Phe	Gly	Gln	Gly	Leu	Gly	Leu	Gly	
			260					265					270			
CAA	ATC	AAG	CTT	GGG	TTT	TTG	AGC	GAA	GTG	CAT	ACG	GAC	ATG	GTC	TTA	924
Gln	Ile	Lys	Leu	Gly	Phe	Leu	Ser	Glu	Val	His	Thr	Asp	Met	Val	Leu	
		275					280						285			

```

      35              40              45
Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser
      50              55              60
Arg Leu Ala Ser Glu Lys Asp Ala Asp Ser Ile Ile Ile Ile Glu Ile
      65              70              75              80
Thr Asn Val Thr Asp Thr Ser Ile Thr Gln Asn Lys Glu Gly Phe Thr
      85              90              95
Thr Phe Tyr Arg Ala Thr Val Ser Val Asn Tyr Thr Tyr Asp Asn Lys
      100             105             110
Arg Gly Thr Gln Lys Thr Phe Gln Asp Ser Gly Tyr Tyr Asn Tyr Ala
      115             120             125
Val Asn Leu Gln Asp Pro Leu Asn Thr Tyr Gln Asn Arg Tyr Tyr Ala
      130             135             140
Ile Asn Gln Ala Val Glu Gln Thr Leu Thr Lys Phe Val Ala Gln Ile
      145             150             155             160
Ala Tyr Glu Gly Lys Phe Asn Asn Glu Lys
      165             170

```

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 61...1224
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

AATACCCATA AAATACCTTA AGAGAACGCC TATTCAAAAA CAAAAAATAA GGAAATCCTA      60
ATG ACT ACA GAC AGA AAT TTG TTT TTT TGC GCT TCG CTA TTG ATT TTT      108
Met Thr Thr Asp Arg Asn Leu Phe Phe Cys Ala Ser Leu Leu Ile Phe
  1              5              10              15

TTG GGG GTA TTG ATG AGC TAT TCG CTC TCA ACT TAC ACC ACA GTG GTG      156
Leu Gly Val Leu Met Ser Tyr Ser Leu Ser Thr Tyr Thr Thr Val Val
      20              25              30

CTG TAT CAT TAT GGG GAG TTC CAT TTT TTC ATA CGC CAG CTT GTG AGC      204
Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser
      35              40              45

GCG ATC ATA GGG ATT GTT ATC ATG TGG GGG TTG TCT AGG GTT GAT CCT      252
Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro
      50              55              60

```


Val	Tyr	Val	Lys	Leu	Ile	Val	Asn	Leu	Pro	Asn	Pro	Glu	Asn	Ser	Val	
	35						40					45				
GAG	TTT	AAG	GAT	TTG	ATG	AAT	CGT	TTA	GTC	GTG	CAA	CGC	TTC	CAA	AGC	253
Glu	Phe	Lys	Asp	Leu	Met	Asn	Arg	Leu	Val	Val	Gln	Arg	Phe	Gln	Ser	
	50					55					60					
CGC	TTA	GCG	AGT	GAA	AAG	GAT	GCG	GAT	TCT	ATC	ATT	ATT	ATA	GAA	ATC	301
Arg	Leu	Ala	Ser	Glu	Lys	Asp	Ala	Asp	Ser	Ile	Ile	Ile	Ile	Glu	Ile	
65					70					75					80	
ACG	AAT	GTA	ACC	GAT	ACG	AGT	ATC	ACG	CAA	AAT	AAA	GAA	GGC	TTC	ACG	349
Thr	Asn	Val	Thr	Asp	Thr	Ser	Ile	Thr	Gln	Asn	Lys	Glu	Gly	Phe	Thr	
			85						90					95		
ACT	TTC	TAT	CGC	GCA	ACC	GTG	TCT	GTG	AAT	TAC	ACC	TAC	GAT	AAT	AAA	397
Thr	Phe	Tyr	Arg	Ala	Thr	Val	Ser	Val	Asn	Tyr	Thr	Tyr	Asp	Asn	Lys	
			100					105					110			
AGA	GGC	ACA	CAA	AAG	ACT	TTT	CAA	GAT	AGC	GGG	TAT	TAC	AAT	TAC	GCT	445
Arg	Gly	Thr	Gln	Lys	Thr	Phe	Gln	Asp	Ser	Gly	Tyr	Tyr	Asn	Tyr	Ala	
		115					120					125				
GTG	AAT	TTG	CAA	GAC	CCC	CTT	AAT	ACC	TAC	CAG	AAC	CGC	TAT	TAT	GCT	493
Val	Asn	Leu	Gln	Asp	Pro	Leu	Asn	Thr	Tyr	Gln	Asn	Arg	Tyr	Tyr	Ala	
	130					135					140					
ATC	AAT	CAG	GCT	GTG	GAA	CAG	ACT	TTG	ACT	AAA	TTT	GTG	GCT	CAA	ATC	541
Ile	Asn	Gln	Ala	Val	Glu	Gln	Thr	Leu	Thr	Lys	Phe	Val	Ala	Gln	Ile	
145					150					155					160	
GCT	TAT	GAG	GGG	AAA	TTC	AAT	AAT	GAA	AAA	TAGCCCTTTG	AATGGATTGA	ATG				594
Ala	Tyr	Glu	Gly	Lys	Phe	Asn	Asn	Glu	Lys							
				165					170							
GACTAAAGGC	GT	TTTTTAGAA	ACAA													618

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Met	Arg	Ala	Leu	Leu	Phe	Phe	Ile	Leu	Leu	Leu	Trp	Phe	Lys	Gly	Cys	
1				5				10						15		
Gly	Tyr	Lys	Pro	Ile	Ala	Ala	Tyr	Ala	Gln	Asn	Ala	Leu	Gly	Asp	Ser	
			20					25					30			
Val	Tyr	Val	Lys	Leu	Ile	Val	Asn	Leu	Pro	Asn	Pro	Glu	Asn	Ser	Val	

```

Val Val Thr Phe Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile
65          70          75          80
Asn Met Glu Glu His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe
          85          90          95
Glu Ser Phe Tyr Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala
          100         105         110
Leu Ser Arg Leu Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys
          115         120         125
Phe Leu Lys Ala Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp
          130         135         140
Leu Asn Val Ala His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn
145          150          155          160
Arg Lys Asn Ala Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu
          165         170         175
Leu Leu Asn Ala Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn
          180         185         190
Lys Glu Lys Ala Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp
          195         200         205
Lys Asn Ile Gly Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu
          210         215         220
Lys Thr Arg Leu Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser
225          230          235          240
Asp His Cys Pro Val Gly Leu Glu Leu Val
          245          250

```

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...571
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```

AGAATGCGAG CGTTAAAAAA GAAATTTATG TGCCTAATAA GCTTGTTAAT TTTGTTATCG      60
C ATG AGG GCT TTA CTT TTT TTT ATT TTG TTA CTT TGG TTC AAG GGT TGT      109
  Met Arg Ala Leu Leu Phe Phe Ile Leu Leu Trp Phe Lys Gly Cys
    1          5          10          15

GGG TAT AAG CCT ATT GCA GCT TAC GCT CAA AAC GCT TTA GGC GAT AGC      157
Gly Tyr Lys Pro Ile Ala Ala Tyr Ala Gln Asn Ala Leu Gly Asp Ser
    20          25          30

GTA TAC GTG AAA CTC ATT GTG AAT TTG CCT AAC CCT GAA AAC TCT GTA      205

```

TTA GAG TTG AAA AAA CCG GTC ATT GTG TGT GGG GAT TTG AAT GTG GCT	489
Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp Leu Asn Val Ala	
135 140 145	
CAC AAT GAA ATT GAT TTA GAA AAC CCC AAA ACC AAC CGA AAA AAT GCC	537
His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn Arg Lys Asn Ala	
150 155 160	
GGC TTT AGC GAT GAA GAG AGA GAA AAA TTC AGC GAG CTT TTG AAC GCC	585
Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu Leu Leu Asn Ala	
165 170 175 180	
GGT TTT ATT GAC ACT TTC CGT TAT TTT TAC CCT AAC AAA GAA AAG GCT	633
Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn Lys Glu Lys Ala	
185 190 195	
TAC ACC TGG TGG AGT TAC ATG CAA CAA GCA AGG GAT AAA AAC ATT GGT	681
Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp Lys Asn Ile Gly	
200 205 210	
TGG CGC ATT GAT TAT TTT TTA TGC TCT AAC CCT TTA AAA ACG CGC TTA	729
Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu Lys Thr Arg Leu	
215 220 225	
AAA GAC GCT TTA ATC TAT AAA GAT ATT TTA GGG AGC GAT CAT TGC CCG	777
Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser Asp His Cys Pro	
230 235 240	
GTA GGG TTG GAA TTA GTT TAAAGGTAGA AAGTGTGCGA AATAAAGACA GAAAAAAG	833
Val Gly Leu Glu Leu Val	
245 250	
CCTTACAA	841

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met Lys Leu Ile Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr	
1 5 10 15	
Lys Gly Phe Met Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys	
20 25 30	
Ile Gln Glu Ser Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys	
35 40 45	
Gly Tyr Phe Asp Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly	
50 55 60	

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...795
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

ATGACTAAAA AGATATAATT CATTCAAAAT TAAACAAGGA TTACA ATG AAA CTG ATT      57
                                   Met Lys Leu Ile
                                   1

TCA TGG AAT GTG AAC GGG TTA AGG GCT TGC ATG ACT AAG GGC TTT ATG      105
Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr Lys Gly Phe Met
  5                10                15                20

GAT TTT TTC AAT AGC GTT GAT GCG GAT GTT TTT TGC ATT CAA GAA TCT      153
Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys Ile Gln Glu Ser
          25                30                35

AAA ATG CAG CAA GAA CAA AAC ACC TTT GAA TTT AAA GGG TAT TTT GAT      201
Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys Gly Tyr Phe Asp
          40                45                50

TTT TGG AAT TGC GCG ATT AAA AAG GGC TAT TCT GGG GTG GTA ACT TTC      249
Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly Val Val Thr Phe
          55                60                65

ACT AAA AAA GAG CCT TTA AGC GTG AGC TAT GGT ATT AAT ATG GAA GAG      297
Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile Asn Met Glu Glu
          70                75                80

CAT GAC AAA GAA GGG CGC GTA ATA ACT TGC GAA TTT GAG TCG TTT TAT      345
His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe Glu Ser Phe Tyr
          85                90                95                100

TTG GTG AAT GTT TAT ACC CCT AAT TCC CAA CAA GCC CTA TCC AGG CTT      393
Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala Leu Ser Arg Leu
          105                110                115

AGT TAT CGC ATG AGT TGG GAA GTG GAG TTT AAG AAA TTT TTA AAA GCT      441
Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys Phe Leu Lys Ala
          120                125                130

```

```

ATCGCTCAAA TTTCAACGAC CATGCTTGTT AAAAAAACT AAAGGAATGT T ATG CAA      57
                                     Met Gln
                                     1

GAT GAA TTA TTT GAA ACC GAA AAA ATC CCC CCA AAA AAC ACT AAA AAT      105
Asp Glu Leu Phe Glu Thr Glu Lys Ile Pro Pro Lys Asn Thr Lys Asn
      5                      10                      15

ACT AAA AAC GCC CCT AAA AAA AGT TTT GAA GAG CAT GTT CAT TCC CTA      153
Thr Lys Asn Ala Pro Lys Lys Ser Phe Glu Glu His Val His Ser Leu
      20                      25                      30

GAG CGA GCC ATA GAT CGC TTG AAT GAT CCC AAT TTA TCC TTA AAA GAC      201
Glu Arg Ala Ile Asp Arg Leu Asn Asp Pro Asn Leu Ser Leu Lys Asp
      35                      40                      45                      50

GGG ATG GAT TTG TAT AAA ACG GCC ATG CAA GAG TTG TTT TTG GCT CAA      249
Gly Met Asp Leu Tyr Lys Thr Ala Met Gln Glu Leu Phe Leu Ala Gln
      55                      60                      65

AAG CTT TTA GAA AAC GCT TAT TTA GAG CAT GAA AAA CTC CAA ACG CCA      297
Lys Leu Leu Glu Asn Ala Tyr Leu Glu His Glu Lys Leu Gln Thr Pro
      70                      75                      80

GAC CAA AAG GCT TAAAGCATGC GAGTGTGTTGC TTTGCAATTA GAATCTTTTA AAGAA      354
Asp Gln Lys Ala
      85

AATCTC                                                                    360

```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Met Gln Asp Glu Leu Phe Glu Thr Glu Lys Ile Pro Pro Lys Asn Thr
 1                      5                      10                      15
Lys Asn Thr Lys Asn Ala Pro Lys Lys Ser Phe Glu Glu His Val His
      20                      25                      30
Ser Leu Glu Arg Ala Ile Asp Arg Leu Asn Asp Pro Asn Leu Ser Leu
      35                      40                      45
Lys Asp Gly Met Asp Leu Tyr Lys Thr Ala Met Gln Glu Leu Phe Leu
      50                      55                      60
Ala Gln Lys Leu Leu Glu Asn Ala Tyr Leu Glu His Glu Lys Leu Gln
      65                      70                      75                      80
Thr Pro Asp Gln Lys Ala
      85

```

```

                35                40                45
ATT GCT TTA GGC GAT AGG GTT AAG CTA GAG CTT ACG CCC TAT AGC TTA      255
Ile Ala Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu
                50                55                60

GAC AAA GGT CGG ATA ACT TTT AGA TAT AAA TGAATTTAAG GGTTATTTCA ATG    308
Asp Lys Gly Arg Ile Thr Phe Arg Tyr Lys
                65                70

AAAATATGTT AATATAA                                                    325

```

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```

Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile Glu Ala
 1              5              10              15
Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His Val Val
                20              25              30
Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg Ile Ala
                35              40              45
Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu Asp Lys
                50              55              60
Gly Arg Ile Thr Phe Arg Tyr Lys
65              70

```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...309
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

50		55		60	
Thr	Tyr	Asp	Ile	Leu	Phe
65		70		75	
Lys	Cys	Glu	Ile	Ala	Leu
		85		90	
Glu	Ser	Leu	Ile	Asn	Ser
		100		105	
Glu	Ala	Lys	Arg	Ala	Tyr
		115		120	
Tyr	Arg	Lys	Gly	Asn	Ala
		130		135	
Ile	Val	Asp	Arg	Gly	Ile
145		150		155	
Gln	Thr	Cys	Leu	Lys	Lys
		165		170	
Ile	Val	Ala	Gln	Asn	Val
		180		185	
Val	Ile	Ser	Val	Tyr	Arg
		195		200	
Tyr	Lys	Glu	Leu	Lys	Arg
		210		215	
Gly	Ala	Asn	Asn	Met	Pro
225		230		235	

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...285
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

TAACACAAGC	CACCATGAGC	ATACTATCGC	CATAGTTGGC	AATAAAGCAG	TGATTCTTAC	60
GGAGCGTTA	ATG GCA AGA GAT GAT GTT ATA GAA GTG GAT GGG AAA GTG ATT	111				
	Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile					
	1 5 10					
GAG GCG TTG CCT AAC GCT ACT TTT AAG GTG GAG TTA GAC AAT AAG CAT	159					
Glu Ala Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His						
15 20 25 30						
GTG GTG TTG TGC CGT ATT TCT GGA AAG ATG CGC ATG CAC TAT ATT AGG	207					
Val Val Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg						

GCC AAG CGA GCT TAT GAA GAA GAC ATT TTG TCT CAC ATC TAT CAG TAT	444
Ala Lys Arg Ala Tyr Glu Glu Asp Ile Leu Ser His Ile Tyr Gln Tyr	
115 120 125	
CGC AAA GGC AAT GCG ATC AAA AGC TTA AAA GAT AAA AAT ATT TTT ATC	492
Arg Lys Gly Asn Ala Ile Lys Ser Leu Lys Asp Lys Asn Ile Phe Ile	
130 135 140 145	
GTA GAT AGG GGG ATT GAA ACC GGG TTT AGA GCA GGG TTA GGC GTG CAA	540
Val Asp Arg Gly Ile Glu Thr Gly Phe Arg Ala Gly Leu Gly Val Gln	
150 155 160	
ACT TGC TTG AAA AAA GAA TGC CAA GAC ATT TAT ATT TTA ACC CCC ATT	588
Thr Cys Leu Lys Lys Glu Cys Gln Asp Ile Tyr Ile Leu Thr Pro Ile	
165 170 175	
GTC GCG CAA AAT GTC GCT CAA GGC TTA GAA AGT TTG TGC GAT GGG GTG	636
Val Ala Gln Asn Val Ala Gln Gly Leu Glu Ser Leu Cys Asp Gly Val	
180 185 190	
ATT AGT GTG TAT CGC CCT GAA TGT TTT GTC TCT GTG GAG CAT CAT TAT	684
Ile Ser Val Tyr Arg Pro Glu Cys Phe Val Ser Val Glu His His Tyr	
195 200 205	
AAA GAA CTC AAG CGA TTA AGC AAT GAA GAA GTT GAA AAA TAC TTG GGC	732
Lys Glu Leu Lys Arg Leu Ser Asn Glu Glu Val Glu Lys Tyr Leu Gly	
210 215 220 225	
GCT AAC AAC ATG CCT AAT TTA AAA AAG GAA CAT TAAATATGGA TTTTATCACC	785
Ala Asn Asn Met Pro Asn Leu Lys Lys Glu His	
230 235	
ATCAATTCTA GTAACAAAAC CGAA	809

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Met His Leu Asn Thr Asp Phe Ser His Ile Thr Asp Ile Glu Gly Met	
1 5 10 15	
Arg Phe Ile Asn Glu Glu Asp Ala Leu Asn Lys Leu Ile Asn Glu Ile	
20 25 30	
His Thr Arg His Ile Asp Leu Lys Asp Ser Ile Met Leu Ala Leu Ser	
35 40 45	
Phe Asn Ala Leu Tyr Leu Ala His Ala Leu Ala Gln Lys Phe Gly Ala	

Tyr Lys Gln Glu Glu Asn Ser
130 135

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...765
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

ACCGATCACT AAAACCAATG TAACTTACCG CTCTTTACAG CGTAAGTGAG AAAAGGA ATG	60
Met	
1	
CAT TTG AAT ACG GAT TTT AGC CAT ATC ACC GAT ATA GAG GGC ATG CGT	108
His Leu Asn Thr Asp Phe Ser His Ile Thr Asp Ile Glu Gly Met Arg	
5 10 15	
TTT ATC AAT GAA GAA GAC GCT TTG AAC AAA TTG ATT AAT GAA ATC CAC	156
Phe Ile Asn Glu Glu Asp Ala Leu Asn Lys Leu Ile Asn Glu Ile His	
20 25 30	
ACG CGC CAC ATT GAT TTA AAA GAT TCC ATC ATG CTC GCT TTG AGT TTT	204
Thr Arg His Ile Asp Leu Lys Asp Ser Ile Met Leu Ala Leu Ser Phe	
35 40 45	
AAC GCT CTG TAT TTA GCT CAC GCT TTA GCG CAA AAA TTT GGA GCG ACT	252
Asn Ala Leu Tyr Leu Ala His Ala Leu Ala Gln Lys Phe Gly Ala Thr	
50 55 60 65	
TAT GAT ATA CTT TTT TTA GAA CCT ATC CTA GCC CCT TTA AAC TCA AAA	300
Tyr Asp Ile Leu Phe Leu Glu Pro Ile Leu Ala Pro Leu Asn Ser Lys	
70 75 80	
TGC GAG ATC GCT TTA GTG AGT GAG AGC ATG GAT ATA GTG ATG AAT GAA	348
Cys Glu Ile Ala Leu Val Ser Glu Ser Met Asp Ile Val Met Asn Glu	
85 90 95	
AGT TTG ATC AAT TCC TTT GAC ATC ACT TTA GAC TAT GTT TAT GGG GAA	396
Ser Leu Ile Asn Ser Phe Asp Ile Thr Leu Asp Tyr Val Tyr Gly Glu	
100 105 110	

```

TCT ATC ATG TTC CCT ACC ATC TTT TCT TTG GCT ACG CTC AAT TTA GGG      426
Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala Thr Leu Asn Leu Gly
      55                      60                      65

CAT CTC ACT TCT AAA GCT TCT GGG GTG ATT AGC ATG GCG ATT GTG GGA      474
His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser Met Ala Ile Val Gly
      70                      75                      80                      85

GGG GCG TTA ATC CCC CCC ATT CAA GGT GCG GTT ACA GAC ATG CTA ACA      522
Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val Thr Asp Met Leu Thr
                      90                      95                      100

GCA ACC GAA TCA AAT TTG CTC TAC GCT TAT GGT GTG CCG TTG TTG TGC      570
Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly Val Pro Leu Leu Cys
                      105                      110                      115

TAT TTT TAT ATT CTC TTC TTT GCG CTT AAA GGG TAT AAG CAA GAA GAA      618
Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly Tyr Lys Gln Glu Glu
                      120                      125                      130

AAC TCC TAAAAAAGG GGGGGTTTCT TTCTTCTTTC CTTTCTTTTA TCTTGTTTAA AA      676
Asn Ser
      135

AATCAGTAA                                                                685

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Met Val Gly Arg Phe Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro
 1           5           10           15
Asn Lys Tyr Leu Ala Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala
      20           25           30
Leu Ala Ile Ile Ile Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe
      35           40           45
Val Gly Phe Phe Asn Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala
      50           55           60
Thr Leu Asn Leu Gly His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser
      65           70           75           80
Met Ala Ile Val Gly Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val
      85           90           95
Thr Asp Met Leu Thr Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly
      100          105          110
Val Pro Leu Leu Cys Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly
      115          120          125

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```

Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val
 1           5           10           15
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala
          20           25           30
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro
          35           40           45
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg
          50           55           60
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro
65           70           75           80
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys
          85           90           95
Asp Gln Leu Phe Lys Lys Asn
          100

```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 220...624
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

TCTTTTGAAA TTGCCTGATG TGGAAAAAGA AATGCCCAAA GAGACGACTC AAAAAAGCTT      60
GTTTTTCGCAC AAACACTTTG TTTTGGGGC TTGGGGATCT TTTTTTATGT GGGGGGAGAA      120
NTGGCGATTG GCTCATTCTT GGTGCTAAGC TTTGAAAAGC TTTTGAATTT AGACTCTCAA      180
TCAAGCGCGC ATTACTTGGT GTATTATTGG GGAGGCGCG ATG GTG GGC CGT TTC      234
                               Met Val Gly Arg Phe
                               1           5

TTA GGC AGT GTG TTG ATG AAT AAA ATT GCC CCT AAT AAA TAC TTG GCT      282
Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro Asn Lys Tyr Leu Ala
          10           15           20

TTC AAC GCC TTA AGC TCT ATT GTT CTC ATC GCT TTA GCC ATT ATC ATT      330
Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala Leu Ala Ile Ile Ile
          25           30           35

GGA GGC AAG ATC GCT TTA TTC GCT CTG ACT TTT GTG GGC TTT TTC AAC      378
Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe Val Gly Phe Phe Asn
          40           45           50

```

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 120...428
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```

GTCGGTCGGG TAATGTTCAA ATTCACAAAT GAGTCTGAAG ACAAAGAAGT CTTGATCTAG      60
AAGCCGAAAT TCTCATACCG CACTTAGAAT TCGCTCAAAA ACAAATTGAT GCGCTGTTG      119

GTG CAC GAT ATT ACC AAG CTA TGT TAC ACC AAA CCA CTA GGG TGT GTT      167
Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val
  1             5             10             15

GTG CTG TTC AGC AAG GAT ACT GAT CTT GTG CCT GTG TTA GAA TCC GCT      215
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala
             20             25             30

TGG GAG AAA GGC TTT GAA GTC TTC ATT GCT AAC ATT CAA GAA TGC CCC      263
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro
             35             40             45

AAT TCT GTC CCT TCA GAC TTG AAG AAG TCT TGC AAT GTG AGG GAA CGC      311
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg
             50             55             60

AGT GTC GCT GAA ATT GTA GAT AAC TTG CCC AAA AAT CAG CAC ACT CCC      359
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro
        65             70             75             80

AAG AAA AAG AAC TTT TCC ACC AAC GAG CCT TTT AAC AAC CCA TTT AAA      407
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys
             85             90             95

GAC CAA CTC TTT AAG AAG AAC TAACACGATC CCCACACCAA GGGGACAAAA AAGCA      463
Asp Gln Leu Phe Lys Lys Asn
             100

CCCATTTTTAA AAGG      477

```

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

BNSDOCID: <WO_9843478A1_1_>

```

Met Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro
 1           5           10           15
Leu Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val
          20           25           30
Thr Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val
          35           40           45
Thr Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu
          50           55           60
Phe Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly
65           70           75           80
Gln Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr
          85           90           95
Val Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn
          100          105          110
Thr Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly
          115          120          125
Ala Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys
          130          135          140
Met Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr
145          150          155          160
Ala Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu
          165          170          175
Thr Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr
          180          185          190
Tyr Thr His Gln Asn Ile Phe Tyr Tyr Arg Ser Gly Ala Thr Ala Met
          195          200          205
Lys Asn Leu Phe Asn Pro Thr Gln Ala Asp Lys Glu Pro Gly Thr Pro
          210          215          220
Ser Glu Gln Asn Asn Ala Leu Ile Lys Met Asn Gly Tyr Leu Ser Asp
225          230          235          240
Arg Asp Thr Leu Thr Phe Ser Trp Asn Met Thr Arg Asp Asn Ala Thr
          245          250          255
Arg Pro Leu Arg Ser Asn Ala Ile Gly Leu Ala Tyr Pro Cys Glu Ala
          260          265          270
Pro Phe Ser Pro Asp Ser Ser Gln Gly Cys Pro Asn Val Leu Asp Ser
          275          280          285
Phe Thr Arg Tyr Met Tyr His Ser Ile Asn Ser Ala Asn Asn Leu Ser
          290          295          300
Leu Gln Tyr Lys Arg Glu Ala Gly Asn Ser Phe Gly Asp Pro Arg Leu
305          310          315          320
Asp Phe Thr Leu Tyr Thr Ser Ile Arg Asn Ala Gln Phe Asp Pro Leu
          325          330          335
Phe Asp Pro Asn Gly Val Tyr Ala Lys Phe Pro Thr Ser Leu Ala Ser
          340          345          350
Ala Trp Glu Lys Glu Asn Tyr Pro Cys Val Glu Gly Ala Tyr Cys Thr
          355          360          365
Pro Ser Phe Ser Asp Val Asp Lys Pro Ser Ser Gln Pro Arg Asn Leu
          370          375          380
Phe Leu Asn Asn Thr Gly Leu Asn Leu Lys Val Ala His Val Ile Asp
385          390          395          400
Glu Ala Thr Asp Ser Leu Phe Glu Tyr Gly Phe Asn Tyr Gln Asn Leu
          405          410          415
Ser Val Phe Asp Ala Arg Ile Pro Lys Ser Glu Leu Tyr Arg Pro Asn
          420          425          430
Gln Val Tyr Thr Asp Asp Lys Gly Gln Lys Gln Ile Ala Cys Ser Leu

```

AGC TAT GAG CTT GCC GCA AGC ACC GGT AAT GTT TTT ATC ATC AAA TTG	2028
Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys Leu	
645 650 655	
GAT TAC ACC ATC CCC AAA ACA GGG ATC AAT CTT GCA TGG CTT AGC CGC	2076
Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser Arg	
660 665 670	
TTT GTT ACC GGT TTA GAT TAT TGC GGG TTT GAT ATT TAC TTG CCT GAT	2124
Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro Asp	
675 680 685	
TAT GGG ACG GCT GAG AAA CCC AAA ACC CCT ACC GAT TTA GCC AAA TGC	2172
Tyr Gly Thr Ala Glu Lys Pro Lys Thr Pro Thr Asp Leu Ala Lys Cys	
690 695 700 705	
GGA TCT CAA TTA GGG TTA GTG CAT ATG CAT AAA CCG GGC TAT GGC GTG	2220
Gly Ser Gln Leu Gly Leu Val His Met His Lys Pro Gly Tyr Gly Val	
710 715 720	
AGT AAT TTT TAT ATC AAT TGG AGT CCT AAA ACC AAA AGC CGC TGG AAG	2268
Ser Asn Phe Tyr Ile Asn Trp Ser Pro Lys Thr Lys Ser Arg Trp Lys	
725 730 735	
GGT TTG TTG CTT TCA GCC GTG TTT AAT AAT GTT TTC AAC AAA TTC TAT	2316
Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe Tyr	
740 745 750	
GTG GAT CAA ACA AGC CCT TAT GTC ATG AGC CCG GAT ATG CCA GGC ACT	2364
Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly Thr	
755 760 765	
GAC GCT GTT AAA AGA GCG ATC GCT GAG CCT GGG TTT AAC GCG CGT TTT	2412
Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg Phe	
770 775 780 785	
GAA GTG GCT TAC AAA TGG TAGTTAATGG AGCTTTAAGC GTTGCGCATG CGTGATAG	2468
Glu Val Ala Tyr Lys Trp	
790	
CAACGGCTAT CGC	2481

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GTT TTT GAC GCT CGC ATC CCT AAA TCA GAA TTA TAC AGG CCT AAT CAA	1356
Val Phe Asp Ala Arg Ile Pro Lys Ser Glu Leu Tyr Arg Pro Asn Gln	
420 425 430	
GTT TAT ACT GAT GAT AAA GGA CAA AAA CAA ATC GCT TGC TCT CTT GTG	1404
Val Tyr Thr Asp Asp Lys Gly Gln Lys Gln Ile Ala Cys Ser Leu Val	
435 440 445	
AAT AAT AAC CCC AAT GAC CCC ACT CTG TGC CAA AGA GGG AAA GCG AAC	1452
Asn Asn Asn Pro Asn Asp Pro Thr Leu Cys Gln Arg Gly Lys Ala Asn	
450 455 460 465	
GGG AAT ATT TAT GGA GGC TAC GTG CAA GCG AAT TAC TCG CCT CAT AAA	1500
Gly Asn Ile Tyr Gly Gly Tyr Val Gln Ala Asn Tyr Ser Pro His Lys	
470 475 480	
ATC ATC ACT TTT GGA GCC GGG GTA AGG TGG GAC GCT TAC ACG CTT TAT	1548
Ile Ile Thr Phe Gly Ala Gly Val Arg Trp Asp Ala Tyr Thr Leu Tyr	
485 490 495	
GAT AAA GAC TGG AAC CAC CGC TAC ACT CAA GGC TTT AGC CCT AGC GCG	1596
Asp Lys Asp Trp Asn His Arg Tyr Thr Gln Gly Phe Ser Pro Ser Ala	
500 505 510	
GCT CTT GTG CTA AGC CCC ATT GAG CCT TTA TCT TTA AAA ATC ACT TAT	1644
Ala Leu Val Leu Ser Pro Ile Glu Pro Leu Ser Leu Lys Ile Thr Tyr	
515 520 525	
TCT CAA GTT ACA AGA GGG GTG ATG CCA GGA GAT GGC GTG TAC ATG CGT	1692
Ser Gln Val Thr Arg Gly Val Met Pro Gly Asp Gly Val Tyr Met Arg	
530 535 540 545	
CAA AAC GAT TTA CGA TAC GCC AAA AAC ATC AAG CCT GAA GTG GGC TCT	1740
Gln Asn Asp Leu Arg Tyr Ala Lys Asn Ile Lys Pro Glu Val Gly Ser	
550 555 560	
AAC GCT GAA TTT AAT ATT GAT TAT TCA AGC CAG TAT TTT AGC GGG AGG	1788
Asn Ala Glu Phe Asn Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly Arg	
565 570 575	
GCT GCG GCG TTT TAT CAG GCT TTG GAT AAT TTC ATC TCA CAA TAC GCA	1836
Ala Ala Ala Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Gln Tyr Ala	
580 585 590	
CAA AAT TTG ATT GTA ACC AAT TTG AGT CAA GCG ATT CGT ATT TAT GGC	1884
Gln Asn Leu Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr Gly	
595 600 605	
TAT GAA GTG GGT GGG ACT TTC AGA TAC AAG GGC GTG AGT TTG AAT GTA	1932
Tyr Glu Val Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn Val	
610 615 620 625	
GGG GTC TCG CGC ACC TGG CCC ACC ACT AGG GGG TAT TTA ATG GCG GAT	1980
Gly Val Ser Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala Asp	
630 635 640	

Thr	His	Gln	Asn	Ile	Phe	Tyr	Tyr	Arg	Ser	Gly	Ala	Thr	Ala	Met	Lys	
195						200					205					
AAC	CTT	TTC	AAT	CCC	ACA	CAA	GCC	GAT	AAA	GAG	CCA	GGA	ACT	CCT	AGC	732
Asn	Leu	Phe	Asn	Pro	Thr	Gln	Ala	Asp	Lys	Glu	Pro	Gly	Thr	Pro	Ser	
210					215					220					225	
GAG	CAA	AAC	AAC	GCT	TTG	ATT	AAA	ATG	AAT	GGT	TAT	TTG	AGC	GAC	AGA	780
Glu	Gln	Asn	Asn	Ala	Leu	Ile	Lys	Met	Asn	Gly	Tyr	Leu	Ser	Asp	Arg	
				230					235						240	
GAC	ACG	CTC	ACT	TTC	AGC	TGG	AAC	ATG	ACA	CGA	GAT	AAC	GCT	ACA	CGC	828
Asp	Thr	Leu	Thr	Phe	Ser	Trp	Asn	Met	Thr	Arg	Asp	Asn	Ala	Thr	Arg	
			245					250					255			
CCT	TTA	AGG	AGT	AAC	GCT	ATA	GGG	TTA	GCC	TAT	CCT	TGT	GAA	GCC	CCC	876
Pro	Leu	Arg	Ser	Asn	Ala	Ile	Gly	Leu	Ala	Tyr	Pro	Cys	Glu	Ala	Pro	
	260						265					270				
TTT	AGT	CCT	GAT	AGT	TCT	CAA	GGG	TGT	CCT	AAT	GTG	TTA	GAT	AGT	TTC	924
Phe	Ser	Pro	Asp	Ser	Ser	Gln	Gly	Cys	Pro	Asn	Val	Leu	Asp	Ser	Phe	
	275					280					285					
ACA	AGA	TAC	ATG	TAT	CAC	TCT	ATT	AAT	AGT	GCC	AAC	AAT	CTT	TCC	TTA	972
Thr	Arg	Tyr	Met	Tyr	His	Ser	Ile	Asn	Ser	Ala	Asn	Asn	Leu	Ser	Leu	
290					295					300					305	
CAA	TAC	AAA	AGG	GAA	GCG	GGA	AAT	TCT	TTT	GGC	GAC	CCA	CGA	TTA	GAT	1020
Gln	Tyr	Lys	Arg	Glu	Ala	Gly	Asn	Ser	Phe	Gly	Asp	Pro	Arg	Leu	Asp	
				310					315						320	
TTT	ACC	CTT	TAT	ACA	AGC	ATC	AGG	AAC	GCT	CAG	TTT	GAT	CCC	CTA	TTT	1068
Phe	Thr	Leu	Tyr	Thr	Ser	Ile	Arg	Asn	Ala	Gln	Phe	Asp	Pro	Leu	Phe	
			325					330					335			
GAT	CCT	AAT	GGC	GTT	TAT	GCT	AAA	TTC	CCC	ACT	TCT	TTA	GCG	AGC	GCA	1116
Asp	Pro	Asn	Gly	Val	Tyr	Ala	Lys	Phe	Pro	Thr	Ser	Leu	Ala	Ser	Ala	
		340					345					350				
TGG	GAA	AAA	GAA	AAT	TAC	CCA	TGC	GTT	GAA	GGC	GCT	TAT	TGC	ACC	CCA	1164
Trp	Glu	Lys	Glu	Asn	Tyr	Pro	Cys	Val	Glu	Gly	Ala	Tyr	Cys	Thr	Pro	
	355					360					365					
AGC	TTT	TCA	GAT	GTG	GAT	AAA	CCA	AGC	TCA	CAG	CCT	AGG	AAT	TTG	TTT	1212
Ser	Phe	Ser	Asp	Val	Asp	Lys	Pro	Ser	Ser	Gln	Pro	Arg	Asn	Leu	Phe	
370					375					380					385	
TTA	AAC	AAC	ACC	GGC	TTA	AAC	CTT	AAA	GTC	GCG	CAT	GTG	ATT	GAT	GAA	1260
Leu	Asn	Asn	Thr	Gly	Leu	Asn	Leu	Lys	Val	Ala	His	Val	Ile	Asp	Glu	
				390					395					400		
GCC	ACA	GAC	AGC	CTT	TTT	GAA	TAC	GGA	TTC	AAC	TAC	CAA	AAT	TTG	AGC	1308
Ala	Thr	Asp	Ser	Leu	Phe	Glu	Tyr	Gly	Phe	Asn	Tyr	Gln	Asn	Leu	Ser	
			405					410					415			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

```

TTTTTTTTTT TTTTIGATTT TTATTTTSTA AATTTTSTA TTAAGGAGAG TTGTTGG ATG      60
                                         Met
                                         1

TTT TTA AGA GTA TAC CCA AAG CTT AGA TAC GCT TTA TGT TTC CCC CTA      108
Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro Leu
                    5                      10                      15

CTC GCT GAG ACT TGC TAT AGC GAA GAG CGG ACT TTA AAT AAG GTT ACC      156
Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val Thr
                20                      25                      30

ACC CAA GCT AAA AGG ATT TTC ACT TAC AAC AAT GAG TTT AAA GTA ACT      204
Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val Thr
                35                      40                      45

TCT AAA GAA CTA GAT CAA CGC CAA AGC AAT GAA GTC AAG GAC TTG TTT      252
Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu Phe
                50                      55                      60                      65

AGG ACT AAC CCT GAT GTG AAT GTG GGC GGA GGG AGC GTG ATG GGG CAG      300
Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly Gln
                    70                      75                      80

AAA ATC TAT GTG AGA GGC GTT GAA GAC AGG CTT TTA AGG GTT ACA GTG      348
Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr Val
                    85                      90                      95

GAT GGG GCT GCA CAA AAT GGC AAT ATC TAC CAC CAC CAA GGC AAC ACC      396
Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn Thr
                100                      105                      110

GTG ATT GAC CCT GGC ATG CTC AAA AGC GTG GAA GTT ACC AAA GGC GCG      444
Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly Ala
                115                      120                      125

GCG AAT GCG AGC GCG GGG CCA GGA GCG ATT GCG GGA GTG ATT AAA ATG      492
Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys Met
                130                      135                      140                      145

GAG ACT AAA GGA GCG GCT GAT TTT ATC CCT AGG GGG AAA AAT TAT GCT      540
Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr Ala
                    150                      155                      160

GCC AGT GGG GCG GTG AGT TTT TAT ACC AAT TTT GGC GAT CGA GAG ACT      588
Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu Thr
                    165                      170                      175

TTC AGA TCG GCT TAT CAA AAC GCG CAT TTT GAT ATT ATC GCT TAC TAC      636
Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr Tyr
                180                      185                      190

ACG CAC CAA AAC ATC TTC TAT TAT AGA AGC GGC GCT ACA GCG ATG AAA      684

```

Glu Met Gly Trp Leu Ala Phe Leu Ala Leu Ala His Arg Met Asn Leu
 30 35 40

GGC ATT AAA AAA AGC GTG AGA AAA AAA GCT ATG AAA AAC CCT AAC CCT 256
 Gly Ile Lys Lys Ser Val Arg Lys Lys Ala Met Lys Asn Pro Asn Pro
 45 50 55

GCT CTA AAA GTC AAA TAC TGG AAA AGA TTG ATA TTG AAA TAGCCATATA GT 307
 Ala Leu Lys Val Lys Tyr Trp Lys Arg Leu Ile Leu Lys
 60 65 70

AAAGAATAGA GCATAAAATC CCCTAAAATC GCCA 341

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met Val Ala Lys Thr Asn Thr Ile Pro Pro Ile Val Gly Val Ser Phe
 1 5 10 15

Leu Phe Trp Trp Leu Gly Thr Lys Leu Glu Met Gly Trp Leu Ala Phe
 20 25 30

Leu Ala Leu Ala His Arg Met Asn Leu Gly Ile Lys Lys Ser Val Arg
 35 40 45

Lys Lys Ala Met Lys Asn Pro Asn Pro Ala Leu Lys Val Lys Tyr Trp
 50 55 60

Lys Arg Leu Ile Leu Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...2430
- (D) OTHER INFORMATION:

```

Met Arg Phe Lys Gly Val Val Ala Phe Ile Ser Leu Ala Val Ala Leu
 1      5      10      15
Gly Val Leu Ala Tyr Leu Phe Leu Ser Val Lys Lys Glu Met Pro Ala
      20      25      30
Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn Glu
      35      40      45
Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu Glu
      50      55      60
Asn Ser Pro Thr Glu Thr Ser His Asn Glu Lys Ala Ser His Asn Glu
      65      70      75      80
Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu Ser
      85      90      95
Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu Glu
      100      105      110
Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp Tyr
      115      120      125
Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp Tyr
      130      135      140
Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu Asp
      145      150      155      160
Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys Ile
      165      170      175
Arg Tyr His Ala Val Phe
      180

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 86...295
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

ACCCACAAAA CTAAAACCCA CTAACACAAT TAACCCTAAC AACACATAAA GATTGCCCAA      60
AGACGCGCAC AACACGCTCG CAACA ATG GTT GCA AAA ACA AAC ACA ATC CCC      112
                Met Val Ala Lys Thr Asn Thr Ile Pro
                1                5

CCC ATC GTA GGG GTA TCT TTT TTA TTC TGG TGG CTT GGC ACG AAG CTA      160
Pro Ile Val Gly Val Ser Phe Leu Phe Trp Trp Leu Gly Thr Lys Leu
10                15                20                25

GAA ATG GGC TGG TTA GCC TTT TTA GCC TTG GCC CAT AGA ATG AAT TTA      208

```

GCT ACT TCT CAT GCG ATC TCT CAA ACA CAT GCG ATC TCT CAA ACC AAT	206
Ala Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn	
35 40 45	
GAA GGC CTC TCT CAA ACA GAT GCA AAA AGC CAT GAC ATC GAT CTA GAA	254
Glu Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu	
50 55 60	
GAA AAT AGC CCC ACT GAA ACC TCT CAT AAT GAA AAA GCC TCC CAT AAC	302
Glu Asn Ser Pro Thr Glu Thr Ser His Asn Glu Lys Ala Ser His Asn	
65 70 75	
GAA GAA GAT CAC AAT AAC GCC CTT TCT CAA AAT CTT GAT GCG CAA GAA	350
Glu Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu	
80 85 90 95	
TCT ATC AAT TAC CCC GTT GTG GAA CAT TAT TCT GAA ATC CCT TTT GAA	398
Ser Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu	
100 105 110	
GAA AAA AAA AGG GAA TAT TCA AAG CTT ATC ATT AAG GAT TTA AAG GAC	446
Glu Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp	
115 120 125	
TAT CAA TGG TGG TGC TTA AAA GAA ATC CTC AAA AAA GAA CAG ATT GAT	494
Tyr Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp	
130 135 140	
TAC GCT TAC GAT AAC ACC AAA AAC CAA CCT AAC CTC ATC ATC TAT TTA	542
Tyr Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu	
145 150 155	
GAT GAA AAT AAA AAA GAA CGC TTG CTG GCT GAT TTA GAC TAT TAT AAA	590
Asp Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys	
160 165 170 175	
ATA CGC TAT CAT GCT GTT TTT TAAATTCAAA GGATAAAAAT GTATCAAGTA GCCA	645
Ile Arg Tyr His Ala Val Phe	
180	
TTTGCGACCC CATCCATGCT AAAGGC	671

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Pro Leu Met Trp Ser Tyr Gln
50 55

TACAACTAAA ACG

269

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Met	Leu	Ser	Lys	Leu	Pro	Phe	Thr	Gly	Val	Leu	Ala	Leu	Val	Leu	Lys
1				5				10					15		
Ala	Val	His	Val	Ser	Leu	Ala	Glu	Asp	Lys	Ser	Lys	Phe	Thr	Ala	Cys
			20				25					30			
Lys	Asn	Pro	Ala	Ser	Lys	Thr	Asp	Thr	Lys	Thr	Ile	Phe	Phe	Ile	His
	35					40					45				
Tyr	Pro	Leu	Met	Trp	Ser	Tyr	Gln								
50					55										

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...611
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

AATGACTTTA	GGGGATATTC	TTAAAGAAAA	ACTCTAAAGA	GTGATTTTAA	AAGCATGAGA	60
ATGGC	ATG	AGA	TTT	AAG	GGT	110
	Met	Arg	Phe	Lys	Gly	
1			5		10	15
CTT	GGC	GTT	TTA	GCC	TAT	
Leu	Gly	Val	Leu	Ala	Tyr	
	20			25		30

1		5		10		15									
Ala	Phe	Gly	Leu	Asp	Tyr	Gly	Ile	Asp	Lys	Thr	Leu	Glu	Leu	Lys	Lys
		20						25					30		
Asp	Glu	Val	Phe	Lys	Ala	Ile	Ile	Lys	Asp	Thr	Ser	Asn	Glu	Gln	Thr
		35					40					45			
Lys	Glu	Ile	Thr	Leu	Tyr	Trp	Thr	Leu	Tyr	Ala	Asn	Lys	Gly	Leu	Val
	50					55					60				
Ile	Asn	Met	Arg	Phe	Asn	His	Phe	Pro	Tyr	Gln	Phe	Ile	Leu	Tyr	Thr
65					70					75				80	
Asp	His	Ala	Arg	Asn	Thr	Tyr	Asn	Leu	Lys	Val	Phe	Glu	Glu	Lys	Phe
			85						90				95		
Ser	Ser	Asn	Ser	Thr	Leu	Ser	Leu	Val	Phe	Lys	Asp	Phe	Lys	Glu	Asp
		100						105					110		
Lys	Ala	Ala	Leu	Arg	Leu	Leu	Ala	Leu	Met	Pro	Leu	Val	Phe	Ser	Pro
		115					120					125			
Lys	Glu	Pro													
		130													

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...222
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GCTCCCTCTA AAAGGGTTTT TAACTATCT TGAGATTTAC CCAATTTATA GGTG ATG	57
Met	
1	
CTT TCA AAA CTC CCA TTT ACT GGT GTT TTA GCC TTA GTT TTA AAG GCT	105
Leu Ser Lys Leu Pro Phe Thr Gly Val Leu Ala Leu Val Leu Lys Ala	
5 10 15	
GTC CAT GTT AGC TTA GCC GAA GAT AAA TCC AAA TTC ACC GCT TGC AAA	153
Val His Val Ser Leu Ala Glu Asp Lys Ser Lys Phe Thr Ala Cys Lys	
20 25 30	
AAC CCT GCT AGT AAA ACC GAT ACC AAA ACC ATT TTT TTC ATT CAT TAT	201
Asn Pro Ala Ser Lys Thr Asp Thr Lys Thr Ile Phe Phe Ile His Tyr	
35 40 45	
CCT TTA-ATG TGG TCT TAT CAA TAACGCTTAT TATTTTAGTG TAAATAAGCA CGCT	256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

GTTGCAACAA AAAATAGAGA GCAGGAAAAC AGACATTGTG ATCCAATCCA TGGCGAATAT      60
TCTCAGCGGG A ATG AAT GAG CTT ATC CGC TAT GGC TTG ATA TTT CTC TTT      110
      Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe
              1              5              10

TTT TTA AAG GCG TTT GGG CTT GAT TAT GGG ATA GAT AAA ACG CTA GAA      158
Phe Leu Lys Ala Phe Gly Leu Asp Tyr Gly Ile Asp Lys Thr Leu Glu
      15              20              25

TTA AAA AAA GAT GAA GTG TTT AAA GCG ATC ATC AAA GAC ACT TCA AAT      206
Leu Lys Lys Asp Glu Val Phe Lys Ala Ile Ile Lys Asp Thr Ser Asn
      30              35              40              45

GAA CAA ACC AAA GAA ATC ACG CTC TAT TGG ACG CTA TAT GCA AAT AAA      254
Glu Gln Thr Lys Glu Ile Thr Leu Tyr Trp Thr Leu Tyr Ala Asn Lys
              50              55              60

GGT TTA GTC ATC AAC ATG CGT TTT AAC CAT TTC CCT TAC CAG TTT ATT      302
Gly Leu Val Ile Asn Met Arg Phe Asn His Phe Pro Tyr Gln Phe Ile
              65              70              75

TTA TAC ACC GAT CAT GCG AGA AAC ACC TAT AAT CTC AAA GTT TTT GAA      350
Leu Tyr Thr Asp His Ala Arg Asn Thr Tyr Asn Leu Lys Val Phe Glu
              80              85              90

GAA AAA TTT TCT TCT AAC AGC ACT CTG TCG CTT GTG TTT AAA GAT TTT      398
Glu Lys Phe Ser Ser Asn Ser Thr Leu Ser Leu Val Phe Lys Asp Phe
              95              100              105

AAA GAA GAT AAA GCC GCT TTA AGG CTT TTA GCC CTT ATG CCC CTT GTT      446
Lys Glu Asp Lys Ala Ala Leu Arg Leu Leu Ala Leu Met Pro Leu Val
      110              115              120              125

TTT TCT CCT AAA GAG CCT TAAGGAATTT GCATGCAAGA AAAACAACTT AAAACCAT      502
Phe Ser Pro Lys Glu Pro
              130

TCAAAATAAG ATCGCTTCC      521

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe Phe Leu Lys

95 100 105
 ATC TCT TTA GAG CAT AAA GAA GAG CGT AAG GAT TCT CCT AAG CCT TAATC 450
 Ile Ser Leu Glu His Lys Glu Glu Arg Lys Asp Ser Pro Lys Pro
 110 115 120
 AAAGCGCTTG ATTTATGCTA AAATGGAGCG TTGCATTTTT GTTTTG 496

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp Trp Leu Ser Leu
 1 5 10 15
 Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu Tyr Gly Met Ala
 20 25 30
 Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys Cys His Gly Ile
 35 40 45
 Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu Lys Gly Glu Lys
 50 55 60
 Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp Phe Lys Thr Phe
 65 70 75 80
 Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro Lys Tyr Asn Leu
 85 90 95
 Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile Ile Ser Leu Glu
 100 105 110
 His Lys Glu Glu Arg Lys Asp Ser Pro Lys Pro
 115 120

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 72...464
- (D) OTHER INFORMATION:

```

        660              665              670
Tyr Lys Ala Arg Asn Met Arg Leu Glu Asp Glu Glu Val Arg Ala Arg
        675              680              685
Gly Glu His Leu Tyr Ser Phe Asn Val His Glu Leu Leu Asp Gln His
        690              695              700
Asn Ala Asn Leu Lys Gly Glu His His Glu
705              710

```

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 77...445
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

ATTTAGTTCA AGAGCTTTTA GAAGAATTTT TGCAAAGCGG GGCTAAAGAG ATTTTAGAAA      60
AGGCGCAGTT GTTTTA ATG CGT TTG TTT ATC GCG CTA GTT TTG TTT TGG TGG      112
      Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp
              1              5              10

TGG TTA AGC TTG AAC GCT AAA GAA GCG GAT TTT ATC TCT GAT TTA GAA      160
Trp Leu Ser Leu Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu
      15              20              25

TAC GGG ATG GCT CTT TAT AAA AAC CCT AGG GGT GTT GCG TGC GCG AAA      208
Tyr Gly Met Ala Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys
      30              35              40

TGC CAT GGC ATT AAA GGC GAA CAA CAA GAA ATC ACC TTT TAT TAT GAA      256
Cys His Gly Ile Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu
      45              50              55              60

AAA GGC GAG AAA AAA ATC CTC TAC GCC CCT AAA ATC AAC CAT TTG GAT      304
Lys Gly Glu Lys Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp
              65              70              75

TTT AAA ACC TTT AAA GAC GCC TTG AGT TTA GGC AAA GGC ATG ATG CCT      352
Phe Lys Thr Phe Lys Asp Ala Leu Ser Leu Gly Lys Gly Met Met Pro
      80              85              90

AAA TAC AAT CTC AAT TTA GAA GAA ATC CAA GCG ATT TAT CTT TAT ATC      400
Lys Tyr Asn Leu Asn Leu Glu Glu Ile Gln Ala Ile Tyr Leu Tyr Ile

```

His Thr Thr Asn Ala Val Ile Cys Asp Gly Ala Gly Ala Ala Ser Ala
 225 230 235 240
 Leu Glu Thr Gly Val Ala Lys Leu Gly Asn Met Glu Ala Val Gln Phe
 245 250 255
 His Pro Thr Ala Leu Val Pro Ser Gly Ile Leu Met Thr Glu Gly Cys
 260 265 270
 Arg Gly Asp Gly Gly Val Leu Arg Asp Lys Phe Gly Arg Arg Phe Met
 275 280 285
 Pro Ala Tyr Glu Pro Glu Lys Lys Glu Leu Ala Ser Arg Asp Val Val
 290 295 300
 Ser Arg Arg Ile Leu Glu His Ile Gln Lys Gly Tyr Gly Ala Lys Ser
 305 310 315 320
 Pro Tyr Gly Asp His Val Trp Leu Asp Ile Ala Ile Leu Gly Arg Asn
 325 330 335
 His Val Glu Lys Asn Leu Arg Asp Val Arg Asp Ile Ala Met Thr Phe
 340 345 350
 Ala Gly Ile Asp Pro Ala Asp Ser Lys Glu Gln Thr Lys Asp Asn Met
 355 360 365
 Gln Gly Val Pro Ala Asn Glu Pro Glu Tyr Gly Gln Ala Met Ala Lys
 370 375 380
 Gln Lys Gly Trp Ile Pro Ile Lys Pro Met Gln His Tyr Ser Met Gly
 385 390 395 400
 Gly Val Arg Thr Asn Pro Lys Gly Glu Thr His Leu Lys Gly Leu Phe
 405 410 415
 Cys Ala Gly Glu Ala Ala Cys Trp Asp Leu His Gly Phe Asn Arg Leu
 420 425 430
 Gly Gly Asn Ser Val Ser Glu Ala Val Val Ala Gly Met Ile Ile Gly
 435 440 445
 Asp Tyr Phe Ala Ser His Cys Leu Glu Ala Gln Ile Glu Ile Asn Thr
 450 455 460
 Gln Lys Val Glu Ala Phe Ile Lys Glu Ser Gln Asp Tyr Met His Phe
 465 470 475 480
 Leu Leu His Asn Glu Gly Lys Glu Asp Val Tyr Glu Ile Arg Glu Arg
 485 490 495
 Met Lys Glu Val Met Asp Glu Lys Val Gly Val Phe Arg Glu Gly Lys
 500 505 510
 Arg Leu Glu Glu Ala Leu Lys Glu Leu Gln Glu Leu Tyr Ala Arg Ser
 515 520 525
 Lys Asn Ile Cys Val Lys Asn Lys Val Leu His Asn Asn Pro Glu Leu
 530 535 540
 Glu Asp Ala Tyr Arg Thr Lys Lys Met Leu Lys Leu Ala Leu Cys Ile
 545 550 555 560
 Thr Gln Gly Ala Leu Leu Arg Thr Glu Ser Arg Gly Ala His Thr Arg
 565 570 575
 Ile Asp Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu
 580 585 590
 Ala Ser Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu
 595 600 605
 Glu Leu Asp Val Met Lys Met Glu Ile Ser Pro Asp Phe Arg Gly Tyr
 610 615 620
 Gly Lys Lys Gly Asn Phe Ile Pro His Pro Lys Lys Glu Glu Arg Asp
 625 630 635 640
 Ala Glu Ile Leu Lys Thr Ile Leu Glu Leu Glu Lys Leu Gly Lys Asp
 645 650 655
 Arg Ile Glu Val Gln His Ala Leu Met Pro Phe Glu Leu Gln Glu Lys

GCT AGG AAT ATG CGT TTA GAA GAT GAG GAA GTC AGG GCT AGG GGG GAA 2121
 Ala Arg Asn Met Arg Leu Glu Asp Glu Glu Val Arg Ala Arg Gly Glu
 675 680 685 690

CAT TTG TAT TCT TTC AAT GTC CAT GAG TTA TTG GAC CAA CAC AAC GCT 2169
 His Leu Tyr Ser Phe Asn Val His Glu Leu Leu Asp Gln His Asn Ala
 695 700 705

AAC CTA AAA GGA GAA CAC CAT GAG TGATAATGAA CGAACGATTG TAGTTAGAGT 2223
 Asn Leu Lys Gly Glu His His Glu
 710

GCTAAAATTT GACCCTCA 2241

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met	Lys	Ile	Thr	Tyr	Cys	Asp	Ala	Leu	Ile	Ile	Gly	Gly	Gly	Leu	Ala
1			5					10						15	
Gly	Leu	Arg	Ala	Ser	Ile	Ala	Cys	Lys	Gln	Lys	Gly	Leu	Asn	Thr	Ile
		20						25					30		
Val	Leu	Ser	Leu	Val	Pro	Val	Arg	Arg	Ser	His	Ser	Ala	Ala	Ala	Gln
		35					40					45			
Gly	Gly	Met	Gln	Ala	Ser	Leu	Ala	Asn	Ala	Lys	Lys	Ser	Glu	Gly	Asp
	50					55				60					
Asn	Glu	Asp	Leu	His	Phe	Leu	Asp	Thr	Val	Lys	Gly	Ser	Asp	Trp	Gly
65				70				75						80	
Cys	Asp	Gln	Gln	Val	Ala	Arg	Met	Phe	Val	Thr	Thr	Ala	Pro	Lys	Ala
				85				90						95	
Ile	Arg	Glu	Leu	Ala	Ser	Trp	Gly	Val	Pro	Trp	Thr	Arg	Ile	Lys	Lys
			100					105					110		
Gly	Asp	Arg	Pro	Ala	Val	Val	Asn	Gly	Glu	His	Val	Thr	Ile	Thr	Glu
		115					120					125			
Arg	Asp	Asp	Arg	His	Gly	Tyr	Ile	Leu	Ser	Arg	Asp	Phe	Gly	Gly	Thr
	130					135					140				
Lys	Lys	Trp	Arg	Thr	Cys	Phe	Thr	Ala	Asp	Ala	Thr	Gly	His	Thr	Met
145					150					155				160	
Leu	Tyr	Ala	Val	Ala	Asn	Glu	Ala	Leu	His	Lys	Val	Asp	Ile	Gln	
			165					170					175		
Asp	Arg	Lys	Asp	Met	Leu	Ala	Phe	Ile	His	His	Asp	Asn	Lys	Cys	Tyr
			180					185				190			
Gly	Ala	Val	Val	Arg	Asp	Leu	Ile	Thr	Gly	Glu	Ile	Ser	Ala	Tyr	Val
		195				200						205			
Ser	Lys	Gly	Thr	Leu	Leu	Ala	Thr	Gly	Gly	Tyr	Gly	Arg	Val	Tyr	Lys
	210					215					220				

TTT GCC TCG CAT TGT TTA GAA GCG CAA ATT GAA ATC AAC ACG CAA AAA	1449
Phe Ala Ser His Cys Leu Glu Ala Gln Ile Glu Ile Asn Thr Gln Lys	
455 460 465	
GTT GAA GCT TTC ATT AAA GAA AGC CAA GAC TAT ATG CAT TTT TTA TTG	1497
Val Glu Ala Phe Ile Lys Glu Ser Gln Asp Tyr Met His Phe Leu Leu	
470 475 480	
CAT AAT GAA GGC AAA GAA GAT GTG TAT GAA ATT AGA GAG CGC ATG AAA	1545
His Asn Glu Gly Lys Glu Asp Val Tyr Glu Ile Arg Glu Arg Met Lys	
485 490 495	
GAA GTC ATG GAT GAA AAA GTG GGC GTT TTT AGA GAA GGC AAA AGG CTA	1593
Glu Val Met Asp Glu Lys Val Gly Val Phe Arg Glu Gly Lys Arg Leu	
500 505 510	
GAA GAA GCC CTT AAA GAA TTG CAA GAG CTT TAT GCA CGC TCC AAA AAC	1641
Glu Glu Ala Leu Lys Glu Leu Gln Glu Leu Tyr Ala Arg Ser Lys Asn	
515 520 525 530	
ATT TGC GTG AAA AAC AAG GTT TTA CAC AAT AAC CCT GAA TTA GAA GAC	1689
Ile Cys Val Lys Asn Lys Val Leu His Asn Asn Pro Glu Leu Glu Asp	
535 540 545	
GCT TAC CGC ACC AAA AAA ATG CTC AAA CTC GCG CTT TGT ATC ACT CAA	1737
Ala Tyr Arg Thr Lys Lys Met Leu Lys Leu Ala Leu Cys Ile Thr Gln	
550 555 560	
GGA GCG TTA CTG CGC ACT GAA AGC AGA GGG GCT CAC ACA AGG ATT GAC	1785
Gly Ala Leu Leu Arg Thr Glu Ser Arg Gly Ala His Thr Arg Ile Asp	
565 570 575	
TAC CCT AAA AGA GAC GAT GAA AAA TGG CTT AAT CGG ACT CTA GCG AGC	1833
Tyr Pro Lys Arg Asp Asp Glu Lys Trp Leu Asn Arg Thr Leu Ala Ser	
580 585 590	
TGG CCT AGC GCT GAG CAA GAC ATG CCC ACG ATT GAA TAC GAA GAA TTA	1881
Trp Pro Ser Ala Glu Gln Asp Met Pro Thr Ile Glu Tyr Glu Glu Leu	
595 600 605 610	
GAT GTG ATG AAA ATG GAA ATC AGC CCT GAT TTT AGG GGC TAT GGC AAA	1929
Asp Val Met Lys Met Glu Ile Ser Pro Asp Phe Arg Gly Tyr Gly Lys	
615 620 625	
AAG GGT AAT TTC ATC CCC CAC CCC AAA AAA GAA GAG CGC GAC GCT GAG	1977
Lys Gly Asn Phe Ile Pro His Pro Lys Lys Glu Glu Arg Asp Ala Glu	
630 635 640	
ATT TTG AAA ACG ATT TTA GAA CTA GAA AAG CTT GGA AAA GAC AGA ATA	2025
Ile Leu Lys Thr Ile Leu Glu Leu Glu Lys Leu Gly Lys Asp Arg Ile	
645 650 655	
GAA GTC CAA CAT GCG CTC ATG CCT TTT GAA TTG CAA GAA AAA TAC AAG	2073
Glu Val Gln His Ala Leu Met Pro Phe Glu Leu Gln Glu Lys Tyr Lys	
660 665 670	

Thr	Asn	Ala	Val	Ile	Cys	Asp	Gly	Ala	Gly	Ala	Ala	Ser	Ala	Leu	Glu		
			230					235					240				
ACC	GGC	GTG	GCT	AAA	TTG	GGC	AAC	ATG	GAA	GCG	GTG	CAA	TTC	CAC	CCT	825	
Thr	Gly	Val	Ala	Lys	Leu	Gly	Asn	Met	Glu	Ala	Val	Gln	Phe	His	Pro		
		245					250					255					
ACC	GCT	TTA	GTG	CCA	AGC	GGG	ATT	TTA	ATG	ACC	GAA	GGT	TGC	AGG	GGC	873	
Thr	Ala	Leu	Val	Pro	Ser	Gly	Ile	Leu	Met	Thr	Glu	Gly	Cys	Arg	Gly		
	260					265					270						
GAT	GGC	GGT	GTT	TTA	AGA	GAC	AAG	TTT	GGC	AGA	CGC	TTC	ATG	CCC	GCT	921	
Asp	Gly	Gly	Val	Leu	Arg	Asp	Lys	Phe	Gly	Arg	Arg	Phe	Met	Pro	Ala		
275					280				285						290		
TAT	GAG	CCG	GAG	AAA	AAA	GAG	CTT	GCA	AGC	AGA	GAT	GTG	GTC	TCA	AGG	969	
Tyr	Glu	Pro	Glu	Lys	Lys	Glu	Leu	Ala	Ser	Arg	Asp	Val	Val	Ser	Arg		
				295				300						305			
CGG	ATT	TTA	GAG	CAT	ATC	CAA	AAA	GGC	TAT	GGA	GCC	AAA	TCG	CCT	TAT	1017	
Arg	Ile	Leu	Glu	His	Ile	Gln	Lys	Gly	Tyr	Gly	Ala	Lys	Ser	Pro	Tyr		
			310					315					320				
GGG	GAT	CAT	GTG	TGG	CTG	GAT	ATT	GCT	ATT	TTA	GGG	CGT	AAC	CAT	GTG	1065	
Gly	Asp	His	Val	Trp	Leu	Asp	Ile	Ala	Ile	Leu	Gly	Arg	Asn	His	Val		
		325					330					335					
GAA	AAA	AAC	TTA	AGG	GAT	GTG	CGC	GAT	ATA	GCC	ATG	ACT	TTT	GCG	GGC	1113	
Glu	Lys	Asn	Leu	Arg	Asp	Val	Arg	Asp	Ile	Ala	Met	Thr	Phe	Ala	Gly		
	340					345					350						
ATT	GAT	CCG	GCT	GAT	AGC	AAG	GAA	CAA	ACC	AAA	GAC	AAC	ATG	CAA	GGA	1161	
Ile	Asp	Pro	Ala	Asp	Ser	Lys	Glu	Gln	Thr	Lys	Asp	Asn	Met	Gln	Gly		
355					360					365					370		
GTG	CCC	GCA	AAT	GAG	CCT	GAA	TAC	GGG	CAA	GCG	ATG	GCC	AAG	CAA	AAA	1209	
Val	Pro	Ala	Asn	Glu	Pro	Glu	Tyr	Gly	Gln	Ala	Met	Ala	Lys	Gln	Lys		
				375				380						385			
GGC	TGG	ATC	CCC	ATA	AAA	CCC	ATG	CAA	CAC	TAT	TCT	ATG	GGT	GGG	GTT	1257	
Gly	Trp	Ile	Pro	Ile	Lys	Pro	Met	Gln	His	Tyr	Ser	Met	Gly	Gly	Val		
			390					395					400				
AGG	ACA	AAC	CCT	AAA	GGC	GAA	ACC	CAT	TTA	AAA	GGC	TTG	TTT	TGC	GCG	1305	
Arg	Thr	Asn	Pro	Lys	Gly	Glu	Thr	His	Leu	Lys	Gly	Leu	Phe	Cys	Ala		
		405					410					415					
GGT	GAA	GCG	GCA	TGC	TGG	GAT	TTG	CAT	GGG	TTT	AAC	CGC	TTG	GGG	GGT	1353	
Gly	Glu	Ala	Ala	Cys	Trp	Asp	Leu	His	Gly	Phe	Asn	Arg	Leu	Gly	Gly		
	420					425					430						
AAT	TCT	GTG	AGT	GAA	GCG	GTG	GTC	GCT	GGC	ATG	ATC	ATT	GGG	GAT	TAT	1401	
Asn	Ser	Val	Ser	Glu	Ala	Val	Val	Ala	Gly	Met	Ile	Ile	Gly	Asp	Tyr		
435					440				445						450		

5	10	15	
AGG GCT AGT ATC GCA TGC AAA CAA AAG GGT TTA AAC ACC ATC GTT TTA			153
Arg Ala Ser Ile Ala Cys Lys Gln Lys Gly Leu Asn Thr Ile Val Leu			
20	25	30	
AGC CTA GTG CCT GTC AGG CGT TCG CAC TCT GCA GCC GCT CAA GGG GGC			201
Ser Leu Val Pro Val Arg Arg Ser His Ser Ala Ala Ala Gln Gly Gly			
35	40	45	50
ATG CAA GCG AGC CTT GCG AAC GCT AAA AAA AGC GAG GGC GAT AAT GAA			249
Met Gln Ala Ser Leu Ala Asn Ala Lys Lys Ser Glu Gly Asp Asn Glu			
55	60	65	
GAT TTA CAC TTT TTA GAC ACG GTT AAG GGG AGC GAT TGG GGG TGC GAT			297
Asp Leu His Phe Leu Asp Thr Val Lys Gly Ser Asp Trp Gly Cys Asp			
70	75	80	
CAG CAA GTG GCT AGG ATG TTT GTA ACC ACT GCT CCT AAA GCC ATT AGG			345
Gln Gln Val Ala Arg Met Phe Val Thr Thr Ala Pro Lys Ala Ile Arg			
85	90	95	
GAA TTG GCC AGT TGG GGG GTG CCT TGG ACT AGG ATT AAA AAG GGC GAT			393
Glu Leu Ala Ser Trp Gly Val Pro Trp Thr Arg Ile Lys Lys Gly Asp			
100	105	110	
AGG CCT GCG GTC GTC AAT GGT GAG CAT GTA ACT ATC ACT GAA AGA GAC			441
Arg Pro Ala Val Val Asn Gly Glu His Val Thr Ile Thr Glu Arg Asp			
115	120	125	130
GAC AGG CAT GGT TAT ATC TTA AGC CGT GAT TTT GGC GGC ACT AAA AAA			489
Asp Arg His Gly Tyr Ile Leu Ser Arg Asp Phe Gly Gly Thr Lys Lys			
135	140	145	
TGG CGC ACA TGC TTT ACG GCT GAT GCC ACA GGG CAT ACC ATG CTT TAT			537
Trp Arg Thr Cys Phe Thr Ala Asp Ala Thr Gly His Thr Met Leu Tyr			
150	155	160	
GCG GTC GCT AAT GAA GCC TTA CAC CAC AAA GTG GAT ATT CAA GAC AGA			585
Ala Val Ala Asn Glu Ala Leu His His Lys Val Asp Ile Gln Asp Arg			
165	170	175	
AAG GAC ATG CTC GCT TTC ATT CAT CAT GAT AAT AAA TGC TAT GGG GCG			633
Lys Asp Met Leu Ala Phe Ile His His Asp Asn Lys Cys Tyr Gly Ala			
180	185	190	
GTG GTA AGG GAT TTG ATC ACA GGC GAA ATT TCA GCG TAT GTT TCT AAA			681
Val Val Arg Asp Leu Ile Thr Gly Glu Ile Ser Ala Tyr Val Ser Lys			
195	200	205	210
GGC ACG CTT TTA GCT ACC GGA GGT TAT GGG CGC GTG TAT AAA CAC ACC			729
Gly Thr Leu Leu Ala Thr Gly Gly Tyr Gly Arg Val Tyr Lys His Thr			
215	220	225	
ACT AAC GCT GTG ATT TGC GAT GGA GCC GGG GCT GCA AGC GCC TTA GAA			777

[illegible]

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...2193
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

CAAGAAGCCA TAGAAGCTGA TGGGAAATTC CACAAAGAAT AAGGGTAGAA A ATG AAA 57
Met Lys
1

ATA ACA TAT TGT GAT GCG CTA ATT ATT GGA GGC GGA CTA GCT GGG TTA 105
Ile Thr Tyr Cys Asp Ala Leu Ile Ile Gly Gly Gly Leu Ala Gly Leu

TTT TCA TAT TCT AAA GAA TGG CAT GAG ACT CTT TTA AAA ACC CCT TTT 1024
 Phe Ser Tyr Ser Lys Glu Trp His Glu Thr Leu Leu Lys Thr Pro Phe
 300 305 310

TAT GCT GAA TAT TCC GTG AAA TTC CTT AAA CAA ATG ACA GAA TGT TTA 1072
 Tyr Ala Glu Tyr Ser Val Lys Phe Leu Lys Gln Met Thr Glu Cys Leu
 315 320 325

AGC CTT AAA GAC AAA CAA AAA ACC TTT GAA TTT CTT GCC CCC CTA CTC 1120
 Ser Leu Lys Asp Lys Gln Lys Thr Phe Glu Phe Leu Ala Pro Leu Leu
 330 335 340 345

AAT AAA AAA ACC CTT TTA GAA TAC GTC TTT TTT AGA TTG AAT AGG ATT 1168
 Asn Lys Lys Thr Leu Leu Glu Tyr Val Phe Phe Arg Leu Asn Arg Ile
 350 355 360

TTC AAA CGC TTA AAA GAA AAA TTT TTT AAC TCT TAGCGTTCTC GTTTGGGCAA 1221
 Phe Lys Arg Leu Lys Glu Lys Phe Phe Asn Ser
 365 370

CACGCTATAG GCGAATTTGA CATAAATCGC 1251

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met Ser Ile Ile Ile Pro Ile Val Ile Ala Phe Asp Asn His Tyr Ala
 1 5 10 15
 Met Pro Ala Gly Val Ser Leu Tyr Ser Met Leu Ala Cys Ala Lys Thr
 20 25 30
 Glu His Pro Gln Ser Gln Asn Asp Ser Glu Lys Leu Phe Tyr Lys Ile
 35 40 45
 His Cys Leu Val Asp Asn Leu Ser Leu Glu Asn Gln Ser Lys Leu Lys
 50 55 60
 Glu Thr Leu Ala Pro Phe Ser Ala Phe Ser Ser Leu Glu Phe Leu Asp
 65 70 75 80
 Ile Ser Thr Pro Asn Leu His Ala Thr Pro Ile Glu Pro Ser Ala Ile
 85 90 95
 Asp Lys Ile Asn Glu Ala Phe Leu Gln Leu Asn Ile Tyr Ala Lys Thr
 100 105 110
 Arg Phe Ser Lys Met Val Met Cys Arg Leu Phe Leu Ala Ser Leu Phe
 115 120 125
 Pro Gln Tyr Asp Lys Ile Ile Met Phe Asp Ala Asp Thr Leu Phe Leu
 130 135 140
 Asn Asp Val Ser Glu Ser Phe Phe Ile Pro Leu Asp Gly Tyr Tyr Phe
 145 150 155 160

TCG	AGC	CTA	GAA	TTT	TTA	GAC	ATT	TCA	ACC	CCC	AAT	CTT	CAC	GCC	ACT	352
Ser	Ser	Leu	Glu	Phe	Leu	Asp	Ile	Ser	Thr	Pro	Asn	Leu	His	Ala	Thr	
75						80					85					
CCA	ATA	GAA	CCC	TCT	GCG	ATT	GAT	AAA	ATC	AAT	GAA	GCT	TTT	TTG	CAA	400
Pro	Ile	Glu	Pro	Ser	Ala	Ile	Asp	Lys	Ile	Asn	Glu	Ala	Phe	Leu	Gln	
90					95					100					105	
CTC	AAT	ATT	TAC	GCT	AAG	ACT	CGC	TTT	TCT	AAA	ATG	GTC	ATG	TGC	CGC	448
Leu	Asn	Ile	Tyr	Ala	Lys	Thr	Arg	Phe	Ser	Lys	Met	Val	Met	Cys	Arg	
				110					115					120		
TTG	TTT	TTG	GCT	TCT	TTA	TTC	CCA	CAA	TAC	GAC	AAA	ATC	ATC	ATG	TTT	496
Leu	Phe	Leu	Ala	Ser	Leu	Phe	Pro	Gln	Tyr	Asp	Lys	Ile	Ile	Met	Phe	
			125					130					135			
GAT	GCA	GAC	ACT	TTG	TTT	TTA	AAC	GAT	GTG	AGC	GAG	AGC	TTT	TTC	ATC	544
Asp	Ala	Asp	Thr	Leu	Phe	Leu	Asn	Asp	Val	Ser	Glu	Ser	Phe	Phe	Ile	
		140					145					150				
CCA	CTA	GAT	GGC	TAT	TAT	TTT	GGA	GCG	GCT	AAA	GAT	TTT	GCT	TCC	GAT	592
Pro	Leu	Asp	Gly	Tyr	Tyr	Phe	Gly	Ala	Ala	Lys	Asp	Phe	Ala	Ser	Asp	
	155					160					165					
AAA	AGC	CCT	AAA	CAT	TTT	CAA	ATA	GTG	CGA	GAA	AAA	GAC	CCT	CGT	CAA	640
Lys	Ser	Pro	Lys	His	Phe	Gln	Ile	Val	Arg	Glu	Lys	Asp	Pro	Arg	Gln	
170					175					180					185	
GCC	TTT	TCC	CTT	TAT	GAG	CAT	TAC	CTT	AAT	GAA	AGC	GAT	ATG	CAA	ATC	688
Ala	Phe	Ser	Leu	Tyr	Glu	His	Tyr	Leu	Asn	Glu	Ser	Asp	Met	Gln	Ile	
				190					195					200		
ATC	TAT	GAA	AGC	AAT	TAT	AAC	GCC	GGG	TTT	TTA	GTC	GTG	AAT	TTA	AAG	736
Ile	Tyr	Glu	Ser	Asn	Tyr	Asn	Ala	Gly	Phe	Leu	Val	Val	Asn	Leu	Lys	
			205					210					215			
CTG	TGG	CGT	GCT	GAT	CAT	TTA	GAA	GAG	CGC	TTA	CTC	AAT	TTA	ACC	CAT	784
Leu	Trp	Arg	Ala	Asp	His	Leu	Glu	Glu	Arg	Leu	Leu	Asn	Leu	Thr	His	
		220					225					230				
CAA	AAA	GGC	CAG	TGC	GTG	TTT	TAC	CCT	GAA	CAG	GAC	CTT	TTA	ACG	CTC	832
Gln	Lys	Gly	Gln	Cys	Val	Phe	Tyr	Pro	Glu	Gln	Asp	Leu	Leu	Thr	Leu	
	235					240					245					
GCA	TGC	TAT	CAA	AAA	GTT	TTA	ATC	TTG	CCT	TAT	ATT	TAT	AAC	ACC	CAC	880
Ala	Cys	Tyr	Gln	Lys	Val	Leu	Ile	Leu	Pro	Tyr	Ile	Tyr	Asn	Thr	His	
250					255					260				265		
CCT	TTC	ATG	GCC	AAT	CAA	AAA	CGC	TTC	ATC	CCT	GAC	AAA	AAA	GAA	ATC	928
Pro	Phe	Met	Ala	Asn	Gln	Lys	Arg	Phe	Ile	Pro	Asp	Lys	Lys	Glu	Ile	
				270					275					280		
GTC	ATG	CTG	CAT	TTT	TAT	TTT	GTA	GGA	AAA	CCT	TGG	GTT	TTA	CCT	ACT	976
Val	Met	Leu	His	Phe	Tyr	Phe	Val	Gly	Lys	Pro	Trp	Val	Leu	Pro	Thr	
			285					290					295			

```

Leu Glu Leu Phe Pro Ile Asp Leu Pro Tyr Ala Ser Ala Lys Glu Ile
  50                      55                      60
Ala Ile Ala Lys Met Gln His Leu Pro Lys Leu Val Arg Asp Ala Leu
  65                      70                      75                      80
Lys Cys Met Gly Phe Asp Arg Val Ser Gln Glu Ile Val Phe Glu Tyr
                      85                      90                      95
Glu Pro Lys Leu Leu Lys Pro Ser Arg Leu Thr Tyr Phe Phe Gly Tyr
          100                      105                      110
Phe Gln Asp Pro Arg Tyr Phe Asp Ala Ile Ser Pro Leu Ile Lys Gln
          115                      120                      125
Thr Phe Thr Leu Pro Pro Pro Pro Lys Ile Ile Arg Ile Ile Ile
          130                      135                      140
Lys Lys Arg Lys Asn Ile Ser Ala Ser Phe Leu
145                      150                      155

```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 86...1201
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

GGTTATTATA GTATAATATT GTCAAAAAAT AAATTCAACT TTGGATTAAA TTGATTAAAA      60
ACCTATTTTA GGGAAACCGC TTAAA ATG AGT ATT ATT ATT CCT ATT GTC ATC      112
                Met Ser Ile Ile Ile Pro Ile Val Ile
                1                      5

GCT TTT GAT AAT CAC TAT GCC ATG CCG GCT GGC GTG AGC TTG TAT TCC      160
Ala Phe Asp Asn His Tyr Ala Met Pro Ala Gly Val Ser Leu Tyr Ser
10                      15                      20                      25

ATG CTA GCT TGC GCT AAA ACA GAA CAC CCC CAA TCA CAA AAT GAT AGT      208
Met Leu Ala Cys Ala Lys Thr Glu His Pro Gln Ser Gln Asn Asp Ser
                30                      35                      40

GAA AAA CTT TTT TAT AAG ATC CAC TGC CTG GTG GAT AAC TTA AGC CTT      256
Glu Lys Leu Phe Tyr Lys Ile His Cys Leu Val Asp Asn Leu Ser Leu
                45                      50                      55

GAA AAC CAG AGC AAA CTA AAA GAG ACT CTA GCC CCC TTT AGC GCT TTT      304
Glu Asn Gln Ser Lys Leu Lys Glu Thr Leu Ala Pro Phe Ser Ala Phe
        60                      65                      70

```

25										30					35					
ATC	ACT	TCT	TTT	GAT	TGG	AGC	GAT	AGG	AAA	ATG	CAA	TTA	GAA	CTT	TTC	201				
Ile	Thr	Ser	Phe	Asp	Trp	Ser	Asp	Arg	Lys	Met	Gln	Leu	Glu	Leu	Phe					
40				45				50												
CCT	ATT	GAT	TTG	CCC	TAT	GCG	AGC	GCG	AAA	GAA	ATC	GCT	ATA	GCT	AAA	249				
Pro	Ile	Asp	Leu	Pro	Tyr	Ala	Ser	Ala	Lys	Glu	Ile	Ala	Ile	Ala	Lys					
55				60				65												
ATG	CAA	CAC	CTC	CCC	AAG	CTA	GTA	AGA	GAC	GCG	CTC	AAA	TGC	ATG	GGA	297				
Met	Gln	His	Leu	Pro	Lys	Leu	Val	Arg	Asp	Ala	Leu	Lys	Cys	Met	Gly					
70				75				80												
TTT	GAT	AGG	GTG	AGT	CAA	GAA	ATC	GTT	TTT	GAA	TAC	GAG	CCT	AAA	TTG	345				
Phe	Asp	Arg	Val	Ser	Gln	Glu	Ile	Val	Phe	Glu	Tyr	Glu	Pro	Lys	Leu					
85				90				95				100								
CTA	AAG	CCA	AGC	CGC	TTG	ACT	TAT	TTT	TTT	GGC	TAT	TTC	CAA	GAT	CCA	393				
Leu	Lys	Pro	Ser	Arg	Leu	Thr	Tyr	Phe	Phe	Gly	Tyr	Phe	Gln	Asp	Pro					
105				110				115												
CGA	TAC	TTT	GAT	GCT	ATA	TCC	CCT	TTA	ATC	AAG	CAA	ACC	TTC	ACT	CTA	441				
Arg	Tyr	Phe	Asp	Ala	Ile	Ser	Pro	Leu	Ile	Lys	Gln	Thr	Phe	Thr	Leu					
120				125				130												
CCC	CCC	CCC	CCC	CCG	AAA	ATA	ATA	AGA	ATA	ATA	ATA	AAA	AAG	AGG	AAG	489				
Pro	Pro	Pro	Pro	Pro	Lys	Ile	Ile	Arg	Ile	Ile	Ile	Lys	Lys	Arg	Lys					
135				140				145												
AAT	ATC	AGT	GCA	AGC	TTT	CTT	TGATTTTAGC	CGCTAAAAAC	AGCGTGTGTTG	TGCA	544									
Asn	Ile	Ser	Ala	Ser	Phe	Leu														
150				155																
TATAAGAAGA GGGGATT															561					

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met	Ala	Phe	Lys	Val	Val	Gln	Ile	Cys	Gly	Gly	Leu	Gly	Asn	Gln	Met
1				5				10					15		
Phe	Gln	Tyr	Ala	Phe	Ala	Lys	Ser	Leu	Gln	Lys	His	Ser	Asn	Thr	Pro
			20					25					30		
Val	Leu	Leu	Asp	Ile	Thr	Ser	Phe	Asp	Trp	Ser	Asp	Arg	Lys	Met	Gln
			35					40					45		

```

Ile Leu Leu Asp Glu Asp Lys Lys Tyr Leu Pro Lys Glu Thr Arg Glu
    195                      200                      205
Tyr Ile Arg Ser Ile Leu Ser Leu Ala Leu Lys Phe Asn Ser Leu Asp
    210                      215                      220
Asn Leu Lys Asp Lys Glu Tyr Leu Leu Asn Arg Gly Ala Arg Val Ser
    225                      230                      235                      240
Leu Val Gly Val Pro Phe Lys Arg Arg Ala Ser Leu Val Gln Val Ala
    245                      250                      255
Lys Asn Leu Asn Leu Ser Leu Glu Thr Leu Lys Ser Tyr Asn His Gln
    260                      265                      270
Phe Arg Tyr Asn Ile Leu Pro Ser Lys Asp Pro Thr Tyr Thr Ile Tyr
    275                      280                      285
Ile Pro Tyr Glu Lys Leu Ala Leu Phe Lys Gln Arg Gln Ile Lys Gln
    290                      295                      300
Asn Lys Asn Ile Gln Ala Ser Ser Lys Ser Pro Phe Ile Thr His Val
    305                      310                      315                      320
Val Leu Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val
    325                      330                      335
Ser Ile Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile
    340                      345                      350
Phe Ile His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala
    355                      360                      365
Thr Arg Glu Phe
    370

```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...510
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```

AAATGAGCTA AAATGAGCGT TTCATTTGAC AAATAAAGGG ATTGA ATG GCT TTT AAG      57
                                     Met Ala Phe Lys
                                     1

GTG GTG CAA ATT TGC GGA GGG CTT GGG AAT CAA ATG TTT CAA TAC GCT      105
Val Val Gln Ile Cys Gly Gly Leu Gly Asn Gln Met Phe Gln Tyr Ala
  5                      10                      15                      20

TTC GCT AAA AGT TTG CAA AAA CAC TCT AAT ACG CCT GTG CTG TTA GAT      153
Phe Ala Lys Ser Leu Gln Lys His Ser Asn Thr Pro Val Leu Leu Asp

```

```

CCT AAA GAA ACC CTA TCT TCT ATC GCT AAA CGC TAT CAA GTC AGT ATT      1065
Pro Lys Glu Thr Leu Ser Ser Ile Ala Lys Arg Tyr Gln Val Ser Ile
      325                      330                      335

TCC AAT ATC CAA TTA GCC AAT GAT CTC AAA GAT TCT AAT ATT TTT ATC      1113
Ser Asn Ile Gln Leu Ala Asn Asp Leu Lys Asp Ser Asn Ile Phe Ile
      340                      345                      350

CAC CAG CGT TTA ATC ATC CCC ACC AAC AAA AAA TTA CTC GCT ACA AGG      1161
His Gln Arg Leu Ile Ile Pro Thr Asn Lys Lys Leu Leu Ala Thr Arg
      355                      360                      365                      370

GAA TTT TAATGGGTTT GGCGTTGGAA AAAGTTTGTT TTTTAGGCGT TATTTTTTTTG AT  1219
Glu Phe

TA                                                                    1221

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```

Met Ser Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe
 1           5           10           15
Val Thr Leu Leu Leu Ala Ser Leu Gly His Ala Lys Met Ala Phe Glu
      20           25           30
Ser Asp Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly
      35           40           45
Phe Leu Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu
      50           55           60
Glu Trp Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile
65           70           75           80
Pro Ile Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe
      85           90           95
Leu Phe Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser
      100          105          110
Arg Lys Lys Ala Val Gly Ile Trp Gln Phe Met Pro Ser Thr Ala Lys
      115          120          125
Glu Leu Gly Leu Lys Val Asn His Tyr Ile Asp Glu Arg Arg Asp Pro
      130          135          140
Ile Lys Ser Thr Gln Ala Ala Ile Thr Tyr Leu Lys Arg Leu Tyr Lys
145          150          155          160
Gln Thr Gly Glu Trp Tyr Leu Val Ala Met Ala Tyr Asn Tyr Gly Leu
      165          170          175
Arg Lys Val Gln Asn Ala Ile Lys Ala Ala Gly Thr Ser Asp Ile Lys
      180          185          190

```

Leu	Ala	Met	Ala	Glu	Ser	Lys	Phe	Ser	Ser	Arg	Ala	Tyr	Ser	Arg	Lys		
100						105					110						
AAA	GCG	GTA	GGG	ATT	TGG	CAA	TTC	ATG	CCA	AGC	ACG	GCT	AAA	GAA	TTA	441	
Lys	Ala	Val	Gly	Ile	Trp	Gln	Phe	Met	Pro	Ser	Thr	Ala	Lys	Glu	Leu		
115					120					125					130		
GGG	CTT	AAG	GTC	AAT	CAT	TAC	ATT	GAT	GAA	AGA	AGA	GAT	CCC	ATT	AAA	489	
Gly	Leu	Lys	Val	Asn	His	Tyr	Ile	Asp	Glu	Arg	Arg	Asp	Pro	Ile	Lys		
				135					140					145			
AGC	ACT	CAA	GCG	GCG	ATC	ACT	TAT	TTG	AAA	CGG	CTC	TAC	AAG	CAA	ACC	537	
Ser	Thr	Gln	Ala	Ala	Ile	Thr	Tyr	Leu	Lys	Arg	Leu	Tyr	Lys	Gln	Thr		
			150					155					160				
GGA	GAG	TGG	TAT	TTG	GTC	GCT	ATG	GCG	TAT	AAT	TAC	GGC	TTA	CGC	AAG	585	
Gly	Glu	Trp	Tyr	Leu	Val	Ala	Met	Ala	Tyr	Asn	Tyr	Gly	Leu	Arg	Lys		
	165						170					175					
GTT	CAA	AAC	GCT	ATT	AAA	GCC	GCC	GGC	ACT	TCG	GAC	ATT	AAA	ATT	TTG	633	
Val	Gln	Asn	Ala	Ile	Lys	Ala	Ala	Gly	Thr	Ser	Asp	Ile	Lys	Ile	Leu		
	180					185					190						
TTG	GAT	GAA	GAT	AAG	AAA	TAC	CTC	CCT	AAA	GAA	ACA	CGA	GAG	TAT	ATC	681	
Leu	Asp	Glu	Asp	Lys	Lys	Tyr	Leu	Pro	Lys	Glu	Thr	Arg	Glu	Tyr	Ile		
195					200					205					210		
CGC	TCC	ATT	CTA	AGC	CTA	GCG	TTA	AAA	TTC	AAC	AGC	CTA	GAC	AAC	CTC	729	
Arg	Ser	Ile	Leu	Ser	Leu	Ala	Leu	Lys	Phe	Asn	Ser	Leu	Asp	Asn	Leu		
				215					220					225			
AAA	GAT	AAA	GAA	TAT	CTG	CTC	AAT	CGT	GGG	GCG	AGG	GTG	AGT	TTA	GTG	777	
Lys	Asp	Lys	Glu	Tyr	Leu	Leu	Asn	Arg	Gly	Ala	Arg	Val	Ser	Leu	Val		
			230					235					240				
GGC	GTC	CCG	TTT	AAA	AGG	CGT	GCT	TCT	TTA	GTC	CAA	GTA	GCC	AAA	AAT	825	
Gly	Val	Pro	Phe	Lys	Arg	Arg	Ala	Ser	Leu	Val	Gln	Val	Ala	Lys	Asn		
		245					250					255					
TTG	AAT	TTG	AGT	TTG	GAA	ACC	TTA	AAA	TCC	TAC	AAC	CAC	CAA	TTC	CGT	873	
Leu	Asn	Leu	Ser	Leu	Glu	Thr	Leu	Lys	Ser	Tyr	Asn	His	Gln	Phe	Arg		
	260					265					270						
TAT	AAC	ATT	CTG	CCT	TCT	AAA	GAC	CCC	ACT	TAT	ACC	ATT	TAT	ATC	CCT	921	
Tyr	Asn	Ile	Leu	Pro	Ser	Lys	Asp	Pro	Thr	Tyr	Thr	Ile	Tyr	Ile	Pro		
275					280					285					290		
TAT	GAA	AAA	CTC	GCT	CTT	TTC	AAA	CAA	CGC	CAG	ATC	AAA	CAA	AAT	AAA	969	
Tyr	Glu	Lys	Leu	Ala	Leu	Phe	Lys	Gln	Arg	Gln	Ile	Lys	Gln	Asn	Lys		
				295					300					305			
AAC	ATT	CAA	GCC	AGT	TCA	AAA	AGC	CCT	TTT	ATC	ACC	CAT	GTG	GTC	TTA	1017	
Asn	Ile	Gln	Ala	Ser	Ser	Lys	Ser	Pro	Phe	Ile	Thr	His	Val	Val	Leu		
			310					315					320				

130		135		140
Lys Ile Glu Gly Thr	Lys Ile Thr Phe Gly Glu	Ala Gly Ala Glu Tyr		
145	150	155	160	
Lys Lys Met Met	Ala Lys Ala			
	165			

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1167
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

TTATAATCAA AGCTATTTTA AAAGCTGAAT AGCTATAGTT ATTAGGATGC G ATG TCA	57
Met Ser	
1	
AAA AGA ATG AAG TGT TTT AGT CAA AAA TGG TTG GTT TTT TTT GTT ACC	105
Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe Val Thr	
5 10 15	
CTT TTA TTG GCT TCT TTA GGC CAT GCG AAA ATG GCT TTT GAA TCC GAT	153
Leu Leu Leu Ala Ser Leu Gly His Ala Lys Met Ala Phe Glu Ser Asp	
20 25 30	
ATT GAC ACC AAA GCG CTA GAG GCT TTT GGG GTT AAT GCG GGC TTT TTA	201
Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly Phe Leu	
35 40 45 50	
TCC CAA ATG CCC AAC GCT TTA AAA AAA ATG AAT AAA GAA GAA GAA TGG	249
Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu Glu Trp	
55 60 65	
AAG AGA CTT GTC AAA AGA TTT GAT GTG AAT TAC CAG TTC ATC CCC ATC	297
Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile Pro Ile	
70 75 80	
ATT AAA AAC ATG CTC ATA GAA GCG AGC GTG CCG CAA GAA TTT TTA TTT	345
Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe Leu Phe	
85 90 95	
TTA GCC ATG GCC GAG TCT AAA TTT TCA TCA AGG GCT TAT AGC AGG AAA	393


```

Asn Glu Lys Arg Asp Phe Lys Val Gly Glu Ser Val Phe Thr Thr Ala
  80                      85                      90

ATT CAA ATT TGC ACG CAT TTA GGG TGT ATC CCC ACT TAT CAA GAT GAA      397
Ile Gln Ile Cys Thr His Leu Gly Cys Ile Pro Thr Tyr Gln Asp Glu
  95                      100                      105                      110

GAA AAA GGC TTT TTA TGC CCA TGC CAT GGG GGG CGT TTC ACT TCT GAT      445
Glu Lys Gly Phe Leu Cys Pro Cys His Gly Gly Arg Phe Thr Ser Asp
                      115                      120                      125

GGC GTG AAT ATT GCC GGC ACT CCC CCT CCA CGC CCT TTT GAT ATC CCG      493
Gly Val Asn Ile Ala Gly Thr Pro Pro Pro Arg Pro Phe Asp Ile Pro
                      130                      135                      140

CCT TTT AAA ATT GAA GGC ACT AAG ATC ACT TTT GGT GAA GCC GGG GCT      541
Pro Phe Lys Ile Glu Gly Thr Lys Ile Thr Phe Gly Glu Ala Gly Ala
                      145                      150                      155

GAA TAC AAG AAA ATG ATG GCT AAA GCG TAAGGAGAGT TTAATGGCAG AGATAAA      595
Glu Tyr Lys Lys Met Met Lys Ala
                      160                      165

AAAAGCGAAA AATTTAGGCG AATGG      620

```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

Met Ala Asp Ile Gln Arg Arg Asp Phe Leu Gly Met Ser Leu Ala Ser
  1                      5                      10                      15
Val Thr Ala Ile Gly Ala Ile Ala Ser Leu Val Ala Met Lys Lys Thr
                      20                      25                      30
Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr Ile Asp
                      35                      40                      45
Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp Arg Gly
                      50                      55                      60
Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe Asn Glu
                      65                      70                      75                      80
Lys Arg Asp Phe Lys Val Gly Glu Ser Val Phe Thr Thr Ala Ile Gln
                      85                      90                      95
Ile Cys Thr His Leu Gly Cys Ile Pro Thr Tyr Gln Asp Glu Glu Lys
                      100                      105                      110
Gly Phe Leu Cys Pro Cys His Gly Gly Arg Phe Thr Ser Asp Gly Val
                      115                      120                      125
Asn Ile Ala Gly Thr Pro Pro Pro Arg Pro Phe Asp Ile Pro Pro Phe

```

```

Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu Leu
385                      390                      395                      400
Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly His
                      405                      410                      415
Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp Val
                      420                      425                      430
Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu Ile
                      435                      440                      445
Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn Ser
                      450                      455                      460
Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val
465                      470                      475

```

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 68...568
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

TGTAAGATAG GGATTTGCTA GGCCTTTAGT CGTTAAAAGG TAATTATCAT TAAGGAGTTT      60
TTTAATC ATG GCA GAT ATT CAA AGG CGT GAT TTT TTA GGA ATG AGC CTT      109
      Met Ala Asp Ile Gln Arg Arg Asp Phe Leu Gly Met Ser Leu
        1                      5                      10

GCT AGT GTT ACA GCT ATA GGG GCT ATA GCG AGT CTG GTA GCG ATG AAA      157
Ala Ser Val Thr Ala Ile Gly Ala Ile Ala Ser Leu Val Ala Met Lys
15                      20                      25                      30

AAG ACT TGG GAT CCG CTT CCA AGC GTT GTT TCA GCC GGT TTT ACG ACC      205
Lys Thr Trp Asp Pro Leu Pro Ser Val Val Ser Ala Gly Phe Thr Thr
                      35                      40                      45

ATA GAT GTG GCG AAT ATG CAA GAA GGG CAG TTT TCC ACC GTG GAA TGG      253
Ile Asp Val Ala Asn Met Gln Glu Gly Gln Phe Ser Thr Val Glu Trp
                      50                      55                      60

CGT GGG AAA CCG GTC TAT ATC CTC AAG CGT TCT AAA AAA GAG GGC TTT      301
Arg Gly Lys Pro Val Tyr Ile Leu Lys Arg Ser Lys Lys Glu Gly Phe
65                      70                      75

AAT GAA AAG CGC GAT TTT AAA GTT GGC GAG AGC GTT TTT ACC ACA GCC      349

```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn Pro
 1           5           10           15
Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser Pro
           20           25           30
His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Lys Pro Arg
           35           40           45
Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr Leu
           50           55           60
Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp Glu
65           70           75           80
Lys Leu Ser Leu Glu Thr Thr Leu Asn Pro Asn Arg Pro Thr Ile Pro
           85           90           95
Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Ser His
           100          105          110
Pro His Gln Met Pro Ser Leu Asn Ala Pro Met Gln Lys Pro Gln Asn
           115          120          125
Lys Pro His Ser Ser Gln Gln Pro Ser Gln Asn Phe Ser Tyr Pro Glu
           130          135          140
Pro Lys Leu Gly Ser Lys Asn Ser Lys Asn Ser Leu Leu Gln Pro Leu
145          150          155          160
Ala Ile Pro Ser Lys Ile Ser Pro Thr Asn Glu Thr Gln Thr Pro Thr
           165          170          175
Asn Asp Thr Lys Pro Pro Leu Lys His Ser Ser Glu Asp Gln Glu Ser
           180          185          190
Asn Leu Phe Ile Thr Pro Pro Thr Glu Lys Thr Leu Pro Asn Asn Thr
           195          200          205
Ser Asn Ala Asp Ile Ser Glu Asn Asn Glu Ser Asn Glu Asn Lys Asp
           210          215          220
Asn Val Glu Lys Gln Ala Ile Arg Asp Ala Asn Ile Lys Glu Phe Ala
225          230          235          240
Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg Pro
           245          250          255
Ser Ile Leu Lys Arg Val Asp Glu Asp Lys Gln Thr Ala Thr Asp Ile
           260          265          270
Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile Ile
           275          280          285
Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu Glu
           290          295          300
Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala Arg
305          310          315          320
Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly Thr
           325          330          335
Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp Glu
           340          345          350
Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu Arg
           355          360          365
Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser Glu
           370          375          380

```

Ile Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu	
290 295 300	
GAG CCA CAA ACT TTT GAA GCT AAA AAT AAT TTC GCC ATT CTT CAA GCC	1022
Glu Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala	
305 310 315	
AGA AGC TCT ACA GAA AAA TGC AAA AGG GCT AGA GCA AGA AAA GAC GGC	1070
Arg Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly	
320 325 330 335	
ACG ACT AGG CAA TGC TAT CTA ATA GAA GAG CCT TTA AAA CAA GCA TGG	1118
Thr Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp	
340 345 350	
GAG AGT GAG TAT GAA ATC ACC ACG CAA TTA GTG AAA GCC ATT TAT GAG	1166
Glu Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu	
355 360 365	
CGC CCC AAA CAA GAC GAT CAA GTA GAG CCG ACT TTT TAT GAA ACC AGC	1214
Arg Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser	
370 375 380	
GAA TTG GCT TAT TCT TCC ACA CGA AAA AGC GAA ATA ACG CAC AAT GAA	1262
Glu Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu	
385 390 395	
TTG AAT TTG AAT GAA AAA TTC ATG GAA TTT GTG GAA GTG TAT GAG GGG	1310
Leu Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly	
400 405 410 415	
CAT TAT TTA AAC GAT ATA ATT AAA GAG AGC AGT GAA TAT AAA GAA TGG	1358
His Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp	
420 425 430	
GTT AAA AAC CAT GTG CGC TTT AAA GAA GGG GTG TGC ATG GCT TTA GAA	1406
Val Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu	
435 440 445	
ATA GAA GAA CAG CCA CGA GCT AAA AGC ACG CCT TTG AGT ATT GAA AAC	1454
Ile Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn	
450 455 460	
TCT CGT GTG GTA TGT GTC AAA AAG GGG AAT TAT TTA TTC AAC GAA GTT T	1503
Ser Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val	
465 470 475	
AAGATGGTGG CTTGAGGCGG AATCGAACCA CCGACACGAA GATTTTC	1550

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

65	70	75	
GAA AAA CTT TCT TTA GAA ACA ACC TTA AAC CCT AAC CGC CCT ACT ATC			350
Glu Lys Leu Ser Leu Glu Thr Thr Leu Asn Pro Asn Arg Pro Thr Ile			
80	85	90	95
CCT AGA AAC ACC CAG ATT GTT TTT TCT TCA AAA GAA TTG AAA GAG TCG			398
Pro Arg Asn Thr Gln Ile Val Phe Ser Ser Lys Glu Leu Lys Glu Ser			
100	105		110
CAC CCG CAC CAA ATG CCT TCT TTA AAC GCG CCC ATG CAA AAA CCA CAA			446
His Pro His Gln Met Pro Ser Leu Asn Ala Pro Met Gln Lys Pro Gln			
115	120		125
AAC AAA CCC CAT TCA TCG CAA CAA CCT TCT CAA AAC TTT TCT TAC CCA			494
Asn Lys Pro His Ser Ser Gln Gln Pro Ser Gln Asn Phe Ser Tyr Pro			
130	135		140
GAG CCC AAA CTA GGC TCT AAA AAC TCT AAA AAC AGC CTT TTA CAG CCT			542
Glu Pro Lys Leu Gly Ser Lys Asn Ser Lys Asn Ser Leu Leu Gln Pro			
145	150		155
TTA GCA ATT CCT AGC AAA ATA AGT CCC ACT AAC GAA ACT CAA ACG CCA			590
Leu Ala Ile Pro Ser Lys Ile Ser Pro Thr Asn Glu Thr Gln Thr Pro			
160	165	170	175
ACA AAC GAC ACT AAA CCC CCT TTA AAG CAT TCT TCA GAA GAT CAA GAA			638
Thr Asn Asp Thr Lys Pro Pro Leu Lys His Ser Ser Glu Asp Gln Glu			
180	185		190
AGC AAC CTC TTT ATA ACG CCA CCC ACT GAA AAA ACG CTC CCT AAC AAC			686
Ser Asn Leu Phe Ile Thr Pro Pro Thr Glu Lys Thr Leu Pro Asn Asn			
195	200		205
ACC TCT AAC GCT GAT ATT AGT GAA AAC AAT GAA AGC AAT GAG AAT AAA			734
Thr Ser Asn Ala Asp Ile Ser Glu Asn Asn Glu Ser Asn Glu Asn Lys			
210	215		220
GAT AAT GTG GAA AAA CAA GCC ATT AGA GAT GCT AAT ATT AAA GAA TTT			782
Asp Asn Val Glu Lys Gln Ala Ile Arg Asp Ala Asn Ile Lys Glu Phe			
225	230		235
GCA TGC GGG AAG TGG GTC TAT GAC GAT GAA AAT TTA CAA GCC TAC CGC			830
Ala Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg			
240	245	250	255
CCA AGC ATT TTA AAA CGC GTT GAT GAA GAC AAA CAA ACT GCA ACA GAT			878
Pro Ser Ile Leu Lys Arg Val Asp Glu Asp Lys Gln Thr Ala Thr Asp			
260	265		270
ATT ACC CCT TGC GAT TAC AGC ACC GCT GAA AAT AAA AGC GGT AAA ATC			926
Ile Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile			
275	280		285
ATT ACC CCC TAT ACT AAA ATC TCC GTT CAT AAA ACA GAG CCT TTA GAA			974

65		70		75		80
Asp Thr Ala Pro	Pro Leu Asp Thr Ala	Ala Gln Lys Gln Glu Thr Lys				
	85	90		95		
Gln Glu Gln Glu	Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro Pro					
	100	105		110		
Val Gln Asn Asn	Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys Lys					
	115	120		125		
Pro Leu Glu Tyr	Lys Val Ala Val Ser Gly Val Asn Val Arg Ala Phe					
	130	135		140		
Pro Ser Thr Lys	Gly Lys Ile Leu Gly Leu Leu Lys Asn Lys Ser					
145	150		155		160	
Val Lys Val Leu	Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe Ser					
	165		170		175	
His Glu Thr Lys	Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala Glu					
	180	185		190		

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...1502
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

TTATGACTTT TACTAAACCT TTTTSTAAGC TATAATCCAA AAATCTAAAA TAAAAAGGAA	60
TAAGC ATG AAA AAA TCC CTT TGT CTG TCT TTC TTT CTG ACT TTC TCT AAC	110
Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn	
1 5 10 15	
CCT CTT CAA GCC CTT GTG ATC GAG CTT TTA GAA GAA ATC AAA ACT TCG	158
Pro Leu Gln Ala Leu Val Ile Glu Leu Leu Glu Glu Ile Lys Thr Ser	
20 25 30	
CCG CAT AAA GGC ACT TTT AAG GCT AAA GTC CTT GAT TCT AAA AAA CCA	206
Pro His Lys Gly Thr Phe Lys Ala Lys Val Leu Asp Ser Lys Lys Pro	
35 40 45	
AGA CAA GTT TTA GGC GTT TAT AAT ATC TCC CCA CAC AAA AAA CTC ACG	254
Arg Gln Val Leu Gly Val Tyr Asn Ile Ser Pro His Lys Lys Leu Thr	
50 55 60	
CTC ACT ATC ACC CAC ATA TCC ACT GCA ATC GTC TAT CAA CCC CTT GAT	302
Leu Thr Ile Thr His Ile Ser Thr Ala Ile Val Tyr Gln Pro Leu Asp	

AAA GAC ACA GCG CCG CCT TTA GAC ACA GCC GCG CAA AAA CAA GAA ACT	349
Lys Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr	
80 85 90 95	
AAA CAA GAG CAA GAA AAA GAA AAC GAG CCT AAA CAA GAT AGC GTC CCG	397
Lys Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro	
100 105 110	
CCC GTT CAA AAC AAT CAA AAA ACC CCT ACA ACC CCC TTA ATG GGA AAA	445
Pro Val Gln Asn Asn Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys	
115 120 125	
AAA CCT TTA GAG TAT AAA GTC GCA GTC AGT GGC GTG AAT GTG CGC GCT	493
Lys Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala	
130 135 140	
TTT CCC AGC ACA AAA GGT AAA ATC TTG GGA TTG CTT TTA AAA AAT AAA	541
Phe Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Leu Lys Asn Lys	
145 150 155	
AGC GTG AAA GTT TTA GAA ATC CAA AAC GAT TGG GCT GAA ATT GAA TTT	589
Ser Val Lys Val Leu Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe	
160 165 170 175	
TCT CAC GAA ACA AAG GGC TAT GTG TTT TTA AAA CTT TTA AAA AAG GCT	637
Ser His Glu Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala	
180 185 190	
GAA TGAAAGAATA ATGAAATTAA AATCTTTTGG GGTTTTGTGA AATCCCATTA	690
Glu	

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Lys Thr Glu Met Lys Ser Ser Leu Lys Leu Phe Met Arg Pro Leu	
1 5 10 15	
Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Val His Ala Ala	
20 25 30	
Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Ile Ser Pro Asn Val	
35 40 45	
Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys Gln	
50 55 60	
Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr Lys	

```

Val Ser Lys Lys Leu Phe Lys Glu Glu Asn Ala Arg Val Ile Ala Leu
      1700              1705              1710
Lys Gly Glu Pro Ala Ile Ala Glu Pro Val Leu Leu Gly Ile Thr Arg
      1715              1720              1725
Ala Ala Ile Gly Ser Asp Ser Ile Ile Ser Ala Ala Ser Phe Gln Glu
      1730              1735              1740
Thr Thr Lys Val Leu Thr Glu Ala Ser Ile Ala Met Lys Lys Asp Phe
      745              1750              1755              1760
Leu Glu Asp Leu Lys Glu Asn Val Val Leu Gly Arg Met Ile Pro Val
      1765              1770              1775
Gly Thr Gly Met Tyr Lys Asn Lys Lys Ile Val Leu Arg Ala Leu Glu
      1780              1785              1790
Asp Asn Ser Lys Phe
      1795

```

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 65...640
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

TAAGCGATTT GCTCTGTGTG GTGATTGACC CTAGGATTGA TTTTGAAAAG CGTTGAGGGT      60
AGGA ATG AAA ACT GAG ATG AAA TCT TCT TTA AAA CTT TTT ATG CGG CCT      109
  Met Lys Thr Glu Met Lys Ser Ser Leu Lys Leu Phe Met Arg Pro
    1              5              10              15

TTG TTG GTG GTT TTA GCG TTC ATG TTG TTG TAT GCT TTA GTG CAT GCT      157
Leu Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Val His Ala
      20              25              30

GCG CTT GGT TTT TAT GTA AAA AAA GAC AGC GCT CCA ATA AGC CCA AAT      205
Ala Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Ile Ser Pro Asn
      35              40              45

GTA GAA AAA ACC GAG ACA GAG CGT CAA AAC GGC GTG CTT TCG CCC AAA      253
Val Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys
      50              55              60

CAA GAA GAA GCC AAC GCA ACC ACA ACT GCC ACA GAA GAA AGC CCC ACC      301
Gln Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr
      65              70              75

```


1250	1255	1260
Pro Phe Asp Gly Glu Leu Arg Ile Glu Thr Val Tyr Glu Glu Val Val		
265	1270	1275
Val Ser Val Lys Asn Gly Asp Gln Glu Ala Lys Phe Val Leu Arg Arg		1280
	1285	1290
Ser Asp Ile Val Lys Pro Ser Glu Leu Ala Gly Val Gly Gly Lys Ile		1295
	1300	1305
Glu Gly Lys Val Tyr Leu Pro Tyr Ala Ser Gly His Lys Val His Lys		1310
	1315	1320
Gly Gly Ser Ile Ala Asp Ile Ile Gln Glu Gly Trp Asn Val Pro Asn		1325
	1330	1335
Arg Ile Pro Tyr Ala Ser Glu Leu Leu Val Lys Asp Asn Asp Pro Ile		1340
345	1350	1355
Ala Gln Asp Val Tyr Ala Lys Glu Lys Gly Val Ile Lys Tyr Tyr Val		1360
	1365	1370
Leu Glu Ala Asn His Leu Glu Arg Thr His Gly Ile Lys Lys Gly Asp		1375
	1380	1385
Met Val Ser Glu Lys Gly Leu Phe Ala Val Ile Ala Asp Asp Asn Gly		1390
	1395	1400
Arg Glu Ala Ala Arg His Tyr Ile Ala Arg Gly Ser Glu Ile Leu Ile		1405
	1410	1415
Asp Asp Asn Ser Glu Val Ser Thr Asn Ser Val Ile Ser Lys Pro Thr		1420
425	1430	1435
Thr Asn Thr Phe Lys Thr Ile Ala Thr Trp Asp Pro Tyr Asn Thr Pro		1440
	1445	1450
Ile Ile Ala Asp Phe Lys Gly Lys Val Gly Phe Val Asp Val Ile Ala		1455
	1460	1465
Gly Val Thr Val Ala Glu Lys Glu Asp Glu Asn Thr Gly Ile Thr Ser		1470
	1475	1480
Leu Val Val Asn Asp Tyr Ile Pro Ser Gly Tyr Lys Pro Ser Leu Phe		1485
	1490	1495
Leu Glu Gly Ala Asn Gly Glu Glu Met Arg Tyr Phe Leu Glu Pro Lys		1500
505	1510	1515
Thr Ser Ile Ala Ile Ser Asp Gly Ser Ser Val Glu Gln Ala Glu Val		1520
	1525	1530
Leu Ala Lys Ile Pro Lys Ala Thr Val Lys Ser Arg Asp Ile Thr Gly		1535
	1540	1545
Gly Leu Pro Arg Val Ser Glu Leu Phe Glu Ala Arg Lys Pro Lys Pro		1550
	1555	1560
Lys Asp Val Ala Ile Leu Ser Glu Val Asp Gly Ile Val Ser Phe Gly		1565
	1570	1575
Lys Pro Ile Arg Asn Lys Glu His Ile Ile Val Thr Ser Lys Asp Gly		1580
585	1590	1595
Arg Ser Met Asp Tyr Phe Val Asp Lys Gly Lys Gln Ile Leu Val His		1600
	1605	1610
Ala Asp Glu Phe Val His Ala Gly Glu Ala Met Thr Asp Gly Val Ile		1615
	1620	1625
Ser Ser His Asp Ile Leu Arg Ile Ser Gly Glu Lys Glu Leu Tyr Lys		1630
	1635	1640
Tyr Ile Val Ser Glu Val Gln Val Tyr Arg Arg Gln Gly Val Ser		1645
	1650	1655
Ile Ala Asp Lys His Ile Glu Ile Ile Val Ser Gln Met Leu Arg Gln		1660
665	1670	1675
Val Arg Ile Leu Asp Ser Gly Asp Ser Lys Phe Ile Glu Gly Asp Leu		1680
	1685	1690
		1695

Lys Gly Glu His Lys Leu Phe Ser Ser Val Asn Glu Ile Ile Thr Ala
 820 825 830
 Ile Asp Thr Lys Glu Leu Asp Ile His Ala Lys Ile Arg Val Leu Asp
 835 840 845
 Gln Gly Asn Ile Ile Ala Thr Ser Ala Gly Arg Met Ile Ile Lys Ser
 850 855 860
 Ile Leu Pro Asp Phe Ile Pro Thr Asp Leu Trp Asn Arg Pro Met Lys
 865 870 875 880
 Lys Lys Asp Ile Gly Val Leu Val Asp Tyr Val His Lys Val Gly Gly
 885 890 895
 Ile Gly Ile Thr Ala Thr Phe Leu Asp Asn Leu Lys Thr Leu Gly Phe
 900 905 910
 Arg Tyr Ala Thr Lys Ala Gly Ile Ser Ile Ser Met Glu Asp Ile Ile
 915 920 925
 Thr Pro Lys Asp Lys Gln Lys Met Val Glu Lys Ala Lys Val Glu Val
 930 935 940
 Lys Lys Ile Gln Gln Gln Tyr Asp Gln Gly Leu Leu Thr Asp Gln Glu
 945 950 955 960
 Arg Tyr Asn Lys Ile Ile Asp Thr Trp Thr Glu Val Asn Asp Lys Met
 965 970 975
 Ser Lys Glu Met Met Thr Ala Ile Ala Gln Asp Lys Glu Gly Phe Asn
 980 985 990
 Ser Ile Tyr Met Met Ala Asp Ser Gly Ala Arg Gly Ser Ala Ala Gln
 995 1000 1005
 Ile Arg Gln Leu Ser Ala Met Arg Gly Leu Met Thr Lys Pro Asp Gly
 1010 1015 1020
 Ser Ile Ile Glu Thr Pro Ile Ile Ser Asn Phe Lys Glu Gly Leu Asn
 025 1030 1035 1040
 Val Leu Glu Tyr Phe Asn Ser Thr His Gly Ala Arg Lys Gly Leu Ala
 1045 1050 1055
 Asp Thr Ala Leu Lys Thr Ala Asn Ala Gly Tyr Leu Thr Arg Lys Leu
 1060 1065 1070
 Ile Asp Val Ser Gln Asn Val Lys Val Val Ser Asp Asp Cys Gly Thr
 1075 1080 1085
 His Glu Gly Ile Glu Ile Thr Asp Ile Ala Val Gly Ser Glu Leu Ile
 1090 1095 1100
 Glu Pro Leu Glu Glu Arg Ile Phe Gly Arg Val Leu Leu Glu Asp Val
 105 1110 1115 1120
 Ile Asp Pro Ile Thr Asn Glu Ile Leu Leu Tyr Ala Asp Thr Leu Ile
 1125 1130 1135
 Asp Glu Glu Gly Ala Lys Lys Val Val Glu Ala Gly Ile Lys Ser Ile
 1140 1145 1150
 Thr Ile Arg Thr Pro Val Thr Cys Lys Ala Pro Lys Gly Val Cys Ala
 1155 1160 1165
 Lys Cys Tyr Gly Leu Asn Leu Gly Glu Gly Lys Met Ser Tyr Pro Gly
 1170 1175 1180
 Glu Ala Val Gly Val Val Ala Ala Gln Ser Ile Gly Glu Pro Gly Thr
 185 1190 1195 1200
 Gln Leu Thr Leu Arg Thr Phe His Val Gly Gly Thr Ala Ser Arg Ser
 1205 1210 1215
 Gln Asp Glu Arg Glu Ile Val Ala Ser Lys Glu Gly Phe Val Arg Phe
 1220 1225 1230
 Tyr Asn Leu Arg Thr Tyr Thr Asn Lys Glu Gly Lys Asn Ile Ile Ala
 1235 1240 1245
 Asn Arg Arg Asn Ala Ser Ile Leu Val Val Glu Pro Lys Ile Lys Ala

370	375	380
Arg Arg Phe Arg Met Gly His Ile Glu Leu Ala Thr Pro Val Ala His		
385	390	395
Ile Trp Tyr Val Asn Ser Leu Pro Ser Arg Ile Gly Thr Leu Leu Gly		400
	405	410
Val Lys Met Lys Asp Leu Glu Arg Val Leu Tyr Tyr Glu Ala Tyr Ile		415
	420	425
Val Lys Glu Pro Gly Glu Ala Ala Tyr Asp Asn Glu Gly Thr Lys Leu		430
	435	440
Val Met Lys Tyr Asp Ile Leu Asn Glu Glu Gln Tyr Gln Asn Ile Ser		445
	450	455
Arg Arg Tyr Glu Asp Arg Gly Phe Val Ala Gln Met Gly Gly Glu Ala		460
465	470	475
Ile Lys Asp Leu Leu Glu Glu Ile Asp Leu Ile Thr Leu Leu Gln Ser		480
	485	490
Leu Lys Glu Glu Val Lys Asp Thr Asn Ser Asp Ala Lys Lys Lys Lys		495
	500	505
Leu Ile Lys Arg Leu Lys Val Val Glu Ser Phe Leu Asn Ser Gly Asn		510
	515	520
Arg Pro Glu Trp Met Met Leu Thr Val Leu Pro Val Leu Pro Pro Asp		525
	530	535
Leu Arg Pro Leu Val Ala Leu Asp Gly Gly Lys Phe Ala Val Ser Asp		540
545	550	555
Val Asn Glu Leu Tyr Arg Arg Val Ile Asn Arg Asn Gln Arg Leu Lys		560
	565	570
Arg Leu Met Glu Leu Gly Ala Pro Glu Ile Ile Val Arg Asn Glu Lys		575
	580	585
Arg Met Leu Gln Glu Ala Val Asp Val Leu Phe Asp Asn Gly Arg Ser		590
	595	600
Thr Asn Ala Val Lys Gly Ala Asn Lys Arg Pro Leu Lys Ser Leu Ser		605
	610	615
Glu Ile Ile Lys Gly Lys Gln Gly Arg Phe Arg Gln Asn Leu Leu Gly		620
625	630	635
Lys Arg Val Asp Phe Ser Gly Arg Ser Val Ile Val Val Gly Pro Asn		640
	645	650
Leu Lys Met Asp Glu Cys Gly Leu Pro Lys Asn Met Ala Leu Glu Leu		655
	660	665
Phe Lys Pro His Leu Leu Ser Lys Leu Glu Glu Arg Gly Tyr Ala Thr		670
	675	680
Thr Leu Lys Gln Ala Lys Arg Met Ile Glu Gln Lys Ser Asn Glu Val		685
	690	695
Trp Glu Cys Leu Gln Glu Ile Thr Glu Gly Tyr Pro Val Leu Leu Asn		700
705	710	715
Arg Ala Pro Thr Leu His Lys Gln Ser Ile Gln Ala Phe His Pro Lys		720
	725	730
Leu Ile Asp Gly Lys Ala Ile Gln Leu His Pro Leu Val Cys Ser Ala		735
	740	745
Phe Asn Ala Asp Phe Asp Gly Asp Gln Met Ala Val His Val Pro Leu		750
	755	760
Ser Gln Glu Ala Ile Ala Glu Cys Lys Val Leu Met Leu Ser Ser Met		765
	770	775
Asn Ile Leu Leu Pro Ala Ser Gly Lys Ala Val Ala Ile Pro Ser Gln		780
785	790	795
Asp Met Val Leu Gly Leu Tyr Tyr Leu Ser Leu Glu Lys Ser Gly Val		800
	805	810
		815

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

```

Met Ala Gly Arg His Gly Asn Lys Gly Ile Val Ser Asn Ile Val Pro
 1           5           10           15
Val Ala Asp Met Pro Tyr Thr Ala Asp Gly Glu Pro Val Asp Ile Val
           20           25           30
Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln Ile Leu
           35           40           45
Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln Ile Ala
           50           55           60
Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu Arg Ala
65           70           75           80
Lys Met Leu Glu Xaa Ala Asn Ala Ile Asn Glu Lys Asp Pro Leu Thr
           85           90           95
Ile His Ala Leu Glu Asn Cys Ser Asp Glu Glu Leu Leu Glu Tyr Ala
           100          105          110
Lys Asp Trp Ser Lys Gly Val Lys Met Ala Ile Pro Val Phe Glu Gly
           115          120          125
Ile Ser Gln Glu Lys Phe Tyr Lys Leu Phe Glu Leu Ala Lys Ile Ala
           130          135          140
Met Asp Gly Lys Met Asp Leu Tyr Asp Gly Arg Thr Gly Glu Lys Met
145          150          155          160
Arg Glu Arg Val Asn Val Gly Tyr Met Tyr Met Ile Lys Leu His His
           165          170          175
Leu Val Asp Glu Lys Val His Ala Arg Ser Thr Gly Pro Tyr Ser Leu
           180          185          190
Val Thr His Gln Pro Val Gly Gly Lys Ala Leu Phe Gly Gly Gln Arg
           195          200          205
Phe Gly Glu Met Glu Val Trp Ala Leu Glu Ala Tyr Gly Ala Ala His
           210          215          220
Thr Leu Lys Glu Met Leu Thr Ile Lys Ser Asp Asp Ile Arg Gly Arg
225          230          235          240
Glu Asn Ala Tyr Arg Ala Ile Ala Lys Gly Glu Gln Val Gly Glu Ser
           245          250          255
Glu Ile Pro Glu Thr Phe Tyr Val Leu Thr Lys Glu Leu Gln Ser Leu
           260          265          270
Ala Leu Asp Ile Asn Ile Phe Gly Asp Asp Val Asp Glu Asp Gly Ala
           275          280          285
Pro Lys Pro Ile Val Ile Lys Glu Asp Asp Arg Pro Lys Asp Phe Ser
           290          295          300
Ser Phe Gln Leu Thr Leu Ala Ser Pro Glu Lys Ile His Ser Trp Ser
305          310          315          320
Tyr Gly Glu Val Lys Lys Pro Glu Thr Ile Asn Tyr Arg Thr Leu Lys
           325          330          335
Pro Glu Arg Asp Gly Leu Phe Cys Met Lys Ile Phe Gly Pro Thr Lys
           340          345          350
Asp Tyr Glu Cys Leu Cys Gly Lys Tyr Lys Lys Pro Arg Phe Lys Asp
           355          360          365
Ile Gly Thr Cys Glu Lys Cys Gly Val Ala Ile Thr His Ser Lys Val

```

(2) INFORMATION FOR SEO ID NO:308:

(A) LENGTH: 1797 amino acids

-518-

His Gly Ile Lys Lys Gly Asp Met Val Ser Glu Lys Gly Leu Phe Ala	
1390 1395 1400	
GTG ATA GCT GAT GAT AAT GGT AGG GAA GCC GCT CGC CAT TAT ATC GCT	4637
Val Ile Ala Asp Asp Asn Gly Arg Glu Ala Ala Arg His Tyr Ile Ala	
1405 1410 1415	
AGG GGT TCT GAG ATC TTG ATT GAT GAT AAT AGT GAA GTG AGC ACT AAT	4685
Arg Gly Ser Glu Ile Leu Ile Asp Asp Asn Ser Glu Val Ser Thr Asn	
1420 1425 1430	
AGC GTG ATT TCT AAA CCC ACG ACT AAC ACT TTC AAA ACG ATT GCC ACA	4733
Ser Val Ile Ser Lys Pro Thr Thr Asn Thr Phe Lys Thr Ile Ala Thr	
1435 1440 1445	
TGG GAT CCT TAC AAC ACC CCT ATC ATT GCG GAC TTT AAA GGT AAG GTG	4781
Trp Asp Pro Tyr Asn Thr Pro Ile Ile Ala Asp Phe Lys Gly Lys Val	
1450 1455 1460 1465	
GGT TTT GTG GAT GTT ATC GCA GGG GTT ACG GTC GCT GAA AAA GAA GAC	4829
Gly Phe Val Asp Val Ile Ala Gly Val Thr Val Ala Glu Lys Glu Asp	
1470 1475 1480	
GAA AAT ACC GGT ATC ACA AGC TTA GTG GTG AAT GAT TAC ATT CCA AGC	4877
Glu Asn Thr Gly Ile Thr Ser Leu Val Val Asn Asp Tyr Ile Pro Ser	
1485 1490 1495	
GGA TAC AAA CCA AGC TTG TTT TTA GAG GGG GCT AAT GGC GAA GAG ATG	4925
Gly Tyr Lys Pro Ser Leu Phe Leu Glu Gly Ala Asn Gly Glu Glu Met	
1500 1505 1510	
CGT TAT TTC CTA GAG CCA AAA ACC TCT ATC GCC ATT AGC GAT GGC TCT	4973
Arg Tyr Phe Leu Glu Pro Lys Thr Ser Ile Ala Ile Ser Asp Gly Ser	
1515 1520 1525	
AGC GTG GAG CAA GCT GAA GTG TTA GCG AAA ATC CCT AAA GCG ACC GTT	5021
Ser Val Glu Gln Ala Glu Val Leu Ala Lys Ile Pro Lys Ala Thr Val	
1530 1535 1540 1545	
AAA TCT AGG GAT ATT ACC GGG GGT CTC CCA AGG GTT TCG GAA CTC TTT	5069
Lys Ser Arg Asp Ile Thr Gly Gly Leu Pro Arg Val Ser Glu Leu Phe	
1550 1555 1560	
GAA GCG AGA AAA CCC AAG CCT AAA GAT GTG GCG ATC CTT TCT GAA GTT	5117
Glu Ala Arg Lys Pro Lys Pro Lys Asp Val Ala Ile Leu Ser Glu Val	
1565 1570 1575	
GAT GGG ATT GTG AGT TTT GGC AAA CCC ATT CGC AAT AAA GAA CAC ATC	5165
Asp Gly Ile Val Ser Phe Gly Lys Pro Ile Arg Asn Lys Glu His Ile	
1580 1585 1590	
ATC GTA ACT TCT AAA GAT GGC CGT TCC ATG GAT TAT TTT GTG GAT AAA	5213
Ile Val Thr Ser Lys Asp Gly Arg Ser Met Asp Tyr Phe Val Asp Lys	
1595 1600 1605	

1165	1170	1175	
GGC AAG ATG AGT TAT CCG GGT GAA GCG GTG GGC GTG GTA GCC GCG CAA			3965
Gly Lys Met Ser Tyr Pro Gly Glu Ala Val Gly Val Val Ala Ala Gln			
1180	1185	1190	
TCT ATT GGG GAG CCT GGA ACG CAG CTC ACT TTA AGG ACT TTC CAT GTG			4013
Ser Ile Gly Glu Pro Gly Thr Gln Leu Thr Leu Arg Thr Phe His Val			
1195	1200	1205	
GGC GGG ACA GCG AGC AGG AGT CAG GAT GAG CGC GAA ATC GTA GCG AGC			4061
Gly Gly Thr Ala Ser Arg Ser Gln Asp Glu Arg Glu Ile Val Ala Ser			
1210	1215	1220	1225
AAA GAA GGT TTT GTG CGT TTT TAC AAC CTT AGG ACT TAC ACG AAT AAA			4109
Lys Glu Gly Phe Val Arg Phe Tyr Asn Leu Arg Thr Tyr Thr Asn Lys			
1230	1235	1240	
GAG GGT AAA AAC ATT ATC GCT AAC CGC CGT AAC GCT TCT ATT TTA GTG			4157
Glu Gly Lys Asn Ile Ile Ala Asn Arg Arg Asn Ala Ser Ile Leu Val			
1245	1250	1255	
GTA GAG CCT AAG ATT AAA GCG CCT TTT GAT GGG GAA TTA CGC ATT GAA			4205
Val Glu Pro Lys Ile Lys Ala Pro Phe Asp Gly Glu Leu Arg Ile Glu			
1260	1265	1270	
ACG GTT TAT GAA GAA GTC GTT GTG AGC GTG AAA AAT GGC GAT CAA GAA			4253
Thr Val Tyr Glu Glu Val Val Ser Val Lys Asn Gly Asp Gln Glu			
1275	1280	1285	
GCT AAA TTT GTT TTA AGG AGA AGC GAT ATT GTC AAG CCA AGC GAA TTA			4301
Ala Lys Phe Val Leu Arg Arg Ser Asp Ile Val Lys Pro Ser Glu Leu			
1290	1295	1300	1305
GCC GGC GTT GGC GGT AAG ATT GAG GGG AAA GTG TAT TTG CCT TAT GCT			4349
Ala Gly Val Gly Gly Lys Ile Glu Gly Lys Val Tyr Leu Pro Tyr Ala			
1310	1315	1320	
AGT GGG CAT AAG GTG CAT AAG GGG GGA AGT ATC GCT GAT ATT ATC CAA			4397
Ser Gly His Lys Val His Lys Gly Gly Ser Ile Ala Asp Ile Ile Gln			
1325	1330	1335	
GAG GGC TGG AAT GTG CCT AAT CGC ATC CCT TAT GCG AGC GAA TTG CTA			4445
Glu Gly Trp Asn Val Pro Asn Arg Ile Pro Tyr Ala Ser Glu Leu Leu			
1340	1345	1350	
GTC AAG GAT AAT GAC CCT ATT GCG CAA GAT GTG TAT GCC AAA GAA AAA			4493
Val Lys Asp Asn Asp Pro Ile Ala Gln Asp Val Tyr Ala Lys Glu Lys			
1355	1360	1365	
GGC GTA ATC AAA TAC TAT GTT TTA GAG GCT AAC CAT TTA GAG CGC ACC			4541
Gly Val Ile Lys Tyr Tyr Val Leu Glu Ala Asn His Leu Glu Arg Thr			
1370	1375	1380	1385
CAT GGG ATC AAA AAG GGC GAT ATG GTG AGT GAA AAA GGC TTG TTT GCG			4589

GGG CTG CTC ACT GAC CAA GAG CGT TAC AAT AAG ATC ATT GAC ACT TGG	3293
Gly Leu Leu Thr Asp Gln Glu Arg Tyr Asn Lys Ile Ile Asp Thr Trp	
955 960 965	
ACT GAA GTC AAT GAC AAA ATG AGT AAA GAA ATG ATG ACC GCT ATC GCG	3341
Thr Glu Val Asn Asp Lys Met Ser Lys Glu Met Met Thr Ala Ile Ala	
970 975 980 985	
CAA GAT AAA GAG GGC TTT AAC TCT ATT TAT ATG ATG GCA GAT AGC GGC	3389
Gln Asp Lys Glu Gly Phe Asn Ser Ile Tyr Met Met Ala Asp Ser Gly	
990 995 1000	
GCA AGG GGT AGC GCG GCG CAA ATC CGT CAG CTT TCA GCG ATG AGG GGT	3437
Ala Arg Gly Ser Ala Ala Gln Ile Arg Gln Leu Ser Ala Met Arg Gly	
1005 1010 1015	
CTT ATG ACA AAG CCG GAC GGC AGT ATC ATT GAA ACG CCC ATT ATT TCT	3485
Leu Met Thr Lys Pro Asp Gly Ser Ile Ile Glu Thr Pro Ile Ile Ser	
1020 1025 1030	
AAC TTT AAA GAG GGG TTG AAT GTC TTA GAA TAC TTC AAT TCC ACG CAT	3533
Asn Phe Lys Glu Gly Leu Asn Val Leu Glu Tyr Phe Asn Ser Thr His	
1035 1040 1045	
GGC GCT AGA AAG GGC TTA GCG GAT ACA GCG CTA AAA ACA GCC AAT GCG	3581
Gly Ala Arg Lys Gly Leu Ala Asp Thr Ala Leu Lys Thr Ala Asn Ala	
1050 1055 1060 1065	
GGG TAT TTG ACC AGA AAG CTC ATT GAT GTT TCG CAA AAT GTC AAG GTG	3629
Gly Tyr Leu Thr Arg Lys Leu Ile Asp Val Ser Gln Asn Val Lys Val	
1070 1075 1080	
GTG TCT GAT GAT TGC GGC ACG CAT GAA GGG ATT GAA ATC ACG GAT ATT	3677
Val Ser Asp Asp Cys Gly Thr His Glu Gly Ile Glu Ile Thr Asp Ile	
1085 1090 1095	
GCG GTG GGG AGT GAG CTG ATT GAA CCT TTA GAA GAG CGT ATT TTT GGG	3725
Ala Val Gly Ser Glu Leu Ile Glu Pro Leu Glu Glu Arg Ile Phe Gly	
1100 1105 1110	
CGC GTT TTA TTA GAA GAT GTG ATC GAT CCC ATT ACG AAT GAA ATC TTG	3773
Arg Val Leu Leu Glu Asp Val Ile Asp Pro Ile Thr Asn Glu Ile Leu	
1115 1120 1125	
CTT TAT GCG GAC ACT TTG ATT GAT GAA GAG GGT GCT AAA AAG GTG GTT	3821
Leu Tyr Ala Asp Thr Leu Ile Asp Glu Glu Gly Ala Lys Lys Val Val	
1130 1135 1140 1145	
GAA GCC GGG ATT AAA TCC ATT ACG ATC CGC ACC CCA GTA ACT TGT AAA	3869
Glu Ala Gly Ile Lys Ser Ile Thr Ile Arg Thr Pro Val Thr Cys Lys	
1150 1155 1160	
GCG CCA AAG GGC GTG TGC GCG AAA TGC TAT GGC TTG AAT TTG GGC GAA	3917
Ala Pro Lys Gly Val Cys Ala Lys Cys Tyr Gly Leu Asn Leu Gly Glu	

ATT CAA GCG TTC CAT CCA AAG CTG ATT GAC GGC AAA GCG ATC CAA TTG	2621
Ile Gln Ala Phe His Pro Lys Leu Ile Asp Gly Lys Ala Ile Gln Leu	
730 735 740 745	
CAC CCG TTA GTG TGT TCA GCG TTC AAC GCC GAT TTT GAC GGG GAC CAA	2669
His Pro Leu Val Cys Ser Ala Phe Asn Ala Asp Phe Asp Gly Asp Gln	
750 755 760	
ATG GCG GTG CAT GTG CCT TTA AGC CAG GAA GCG ATC GCT GAA TGC AAG	2717
Met Ala Val His Val Pro Leu Ser Gln Glu Ala Ile Ala Glu Cys Lys	
765 770 775	
GTG CTG ATG CTA AGC TCT ATG AAT ATC CTT TTG CCT GCT AGC GGT AAG	2765
Val Leu Met Leu Ser Ser Met Asn Ile Leu Leu Pro Ala Ser Gly Lys	
780 785 790	
GCC GTA GCC ATT CCT AGC CAA GAT ATG GTT TTA GGG CTT TAT TAT CTT	2813
Ala Val Ala Ile Pro Ser Gln Asp Met Val Leu Gly Leu Tyr Tyr Leu	
795 800 805	
TCT TTA GAA AAG AGC GGG GTC AAG GGC GAG CAT AAG CTT TTT TCT AGC	2861
Ser Leu Glu Lys Ser Gly Val Lys Gly Glu His Lys Leu Phe Ser Ser	
810 815 820 825	
GTG AAT GAA ATC ATC ACC GCC ATT GAC ACG AAA GAA TTA GAC ATC CAC	2909
Val Asn Glu Ile Ile Thr Ala Ile Asp Thr Lys Glu Leu Asp Ile His	
830 835 840	
GCA AAG ATT AGG GTT TTA GAT CAA GGG AAT ATT ATC GCT ACG AGT GCA	2957
Ala Lys Ile Arg Val Leu Asp Gln Gly Asn Ile Ile Ala Thr Ser Ala	
845 850 855	
GGG CGC ATG ATC ATT AAG TCC ATT TTG CCT GAT TTT ATC CCT ACG GAT	3005
Gly Arg Met Ile Ile Lys Ser Ile Leu Pro Asp Phe Ile Pro Thr Asp	
860 865 870	
TTG TGG AAC AGA CCC ATG AAG AAA AAA GAT ATT GGC GTG CTT GTG GAT	3053
Leu Trp Asn Arg Pro Met Lys Lys Lys Asp Ile Gly Val Leu Val Asp	
875 880 885	
TAT GTG CAT AAA GTT GGC GGT ATC GGT ATT ACT GCA ACC TTT TTG GAT	3101
Tyr Val His Lys Val Gly Gly Ile Gly Ile Thr Ala Thr Phe Leu Asp	
890 895 900 905	
AAT TTA AAA ACG CTT GGC TTT AGG TAT GCG ACT AAG GCT GGT ATT TCT	3149
Asn Leu Lys Thr Leu Gly Phe Arg Tyr Ala Thr Lys Ala Gly Ile Ser	
910 915 920	
ATC TCT ATG GAG GAT ATT ATC ACG CCA AAA GAC AAG CAA AAA ATG GTG	3197
Ile Ser Met Glu Asp Ile Ile Thr Pro Lys Asp Lys Gln Lys Met Val	
925 930 935	
GAA AAA GCC AAA GTA GAG GTT AAA AAA ATC CAG CAA CAA TAC GAT CAA	3245
Glu Lys Ala Lys Val Glu Val Lys Lys Ile Gln Gln Gln Tyr Asp Gln	
940 945 950	

TCT GAT GCG AAA AAG AAA AAA CTC ATT AAG CGT TTG AAA GTG GTA GAA	1949
Ser Asp Ala Lys Lys Lys Lys Leu Ile Lys Arg Leu Lys Val Val Glu	
510 515 520	
AGC TTT TTA AAT TCT GGT AAT AGG CCT GAA TGG ATG ATG CTC ACG GTT	1997
Ser Phe Leu Asn Ser Gly Asn Arg Pro Glu Trp Met Met Leu Thr Val	
525 530 535	
TTA CCG GTA TTG CCA CCG GAT TTA AGG CCT TTA GTC GCG CTA GAT GGC	2045
Leu Pro Val Leu Pro Pro Asp Leu Arg Pro Leu Val Ala Leu Asp Gly	
540 545 550	
GGG AAG TTT GCA GTC AGC GAT GTG AAT GAA TTG TAT CGT CGT GTC ATC	2093
Gly Lys Phe Ala Val Ser Asp Val Asn Glu Leu Tyr Arg Arg Val Ile	
555 560 565	
AAT CGT AAC CAA CGC TTG AAA CGC TTA ATG GAG CTT GGA GCG CCA GAA	2141
Asn Arg Asn Gln Arg Leu Lys Arg Leu Met Glu Leu Gly Ala Pro Glu	
570 575 580 585	
ATC ATT GTG CGC AAT GAA AAA AGG ATG TTG CAA GAA GCC GTG GAT GTG	2189
Ile Ile Val Arg Asn Glu Lys Arg Met Leu Gln Glu Ala Val Asp Val	
590 595 600	
CTT TTT GAT AAC GGC CGC AGC ACT AAT GCG GTT AAA GGG GCT AAC AAA	2237
Leu Phe Asp Asn Gly Arg Ser Thr Asn Ala Val Lys Gly Ala Asn Lys	
605 610 615	
CGC CCT TTA AAA TCG CTC AGT GAA ATC ATT AAA GGC AAG CAG GGG CGT	2285
Arg Pro Leu Lys Ser Leu Ser Glu Ile Ile Lys Gly Lys Gln Gly Arg	
620 625 630	
TTC AGG CAA AAC CTT TTA GGT AAG CGC GTG GAT TTT TCA GGC AGA AGC	2333
Phe Arg Gln Asn Leu Leu Gly Lys Arg Val Asp Phe Ser Gly Arg Ser	
635 640 645	
GTG ATT GTG GTT GGG CCT AAT CTC AAA ATG GAT GAA TGC GGG TTG CCT	2381
Val Ile Val Val Gly Pro Asn Leu Lys Met Asp Glu Cys Gly Leu Pro	
650 655 660 665	
AAA AAC ATG GCG TTA GAA CTC TTC AAA CCG CAT TTG TTA TCC AAG CTT	2429
Lys Asn Met Ala Leu Glu Leu Phe Lys Pro His Leu Leu Ser Lys Leu	
670 675 680	
GAA GAG AGA GGC TAT GCC ACC ACG CTC AAA CAG GCT AAA CGC ATG ATT	2477
Glu Glu Arg Gly Tyr Ala Thr Thr Leu Lys Gln Ala Lys Arg Met Ile	
685 690 695	
GAG CAA AAA AGC AAT GAA GTA TGG GAG TGC TTG CAA GAA ATC ACA GAG	2525
Glu Gln Lys Ser Asn Glu Val Trp Glu Cys Leu Gln Glu Ile Thr Glu	
700 705 710	
GGG TAT CCG GTG CTA CTC AAC CGC GCT CCT ACC TTG CAC AAG CAA TCC	2573
Gly Tyr Pro Val Leu Leu Asn Arg Ala Pro Thr Leu His Lys Gln Ser	
715 720 725	

Asp Val Asp Glu Asp Gly Ala Pro Lys Pro Ile Val Ile Lys Glu Asp	
285 290 295	
GAC AGG CCT AAA GAC TTT AGC TCT TTC CAG CTC ACA CTA GCT AGC CCT	1325
Asp Arg Pro Lys Asp Phe Ser Ser Phe Gln Leu Thr Leu Ala Ser Pro	
300 305 310	
GAA AAA ATC CAT TCT TGG AGT TAT GGG GAA GTT AAA AAG CCA GAA ACG	1373
Glu Lys Ile His Ser Trp Ser Tyr Gly Glu Val Lys Lys Pro Glu Thr	
315 320 325	
ATC AAT TAT CGC ACC CTA AAA CCT GAA CGA GAC GGC TTG TTT TGC ATG	1421
Ile Asn Tyr Arg Thr Leu Lys Pro Glu Arg Asp Gly Leu Phe Cys Met	
330 335 340 345	
AAA ATC TTT GGC CCC ACT AAA GAT TAT GAA TGC TTG TGC GGC AAA TAC	1469
Lys Ile Phe Gly Pro Thr Lys Asp Tyr Glu Cys Leu Cys Gly Lys Tyr	
350 355 360	
AAA AAG CCT CGC TTC AAA GAC ATT GGC ACA TGC GAA AAA TGC GGC GTG	1517
Lys Lys Pro Arg Phe Lys Asp Ile Gly Thr Cys Glu Lys Cys Gly Val	
365 370 375	
GCG ATC ACG CAC TCC AAA GTC AGG CGT TTT AGA ATG GGC CAT ATT GAA	1565
Ala Ile Thr His Ser Lys Val Arg Arg Phe Arg Met Gly His Ile Glu	
380 385 390	
TTG GCC ACT CCT GTA GCG CAT ATC TGG TAT GTT AAT TCC TTG CCT AGC	1613
Leu Ala Thr Pro Val Ala His Ile Trp Tyr Val Asn Ser Leu Pro Ser	
395 400 405	
CGT ATC GGC ACG CTT TTA GGC GTT AAG ATG AAA GAC TTA GAG CGC GTG	1661
Arg Ile Gly Thr Leu Leu Gly Val Lys Met Lys Asp Leu Glu Arg Val	
410 415 420 425	
TTG TAT TAT GAA GCT TAT ATC GTT AAA GAA CCA GGC GAA GCC GCT TAT	1709
Leu Tyr Tyr Glu Ala Tyr Ile Val Lys Glu Pro Gly Glu Ala Ala Tyr	
430 435 440	
GAC AAT GAA GGC ACT AAG CTT GTG ATG AAA TAC GAT ATT TTG AAT GAA	1757
Asp Asn Glu Gly Thr Lys Leu Val Met Lys Tyr Asp Ile Leu Asn Glu	
445 450 455	
GAG CAG TAT CAA AAT ATC TCA CGA AGA TAC GAA GAC AGG GGC TTT GTA	1805
Glu Gln Tyr Gln Asn Ile Ser Arg Arg Tyr Glu Asp Arg Gly Phe Val	
460 465 470	
GCG CAA ATG GGC GGT GAA GCG ATC AAG GAT TTG TTA GAA GAA ATT GAT	1853
Ala Gln Met Gly Gly Glu Ala Ile Lys Asp Leu Leu Glu Glu Ile Asp	
475 480 485	
TTG ATC ACC TTA TTG CAG AGT TTG AAA GAA GAA GTG AAA GAC ACC AAT	1901
Leu Ile Thr Leu Leu Gln Ser Leu Lys Glu Glu Val Lys Asp Thr Asn	
490 495 500 505	

60	65	70	
TTT GCC AAA GAA TTG CGT GCT AAA ATG CTA GAA AWC GCT AAC GCT ATT			653
Phe Ala Lys Glu Leu Arg Ala Lys Met Leu Glu Xaa Ala Asn Ala Ile			
75	80	85	
AAT GAA AAA GAC CCC TTG ACA ATC CAT GCG CTT GAG AAT TGT TCT GAT			701
Asn Glu Lys Asp Pro Leu Thr Ile His Ala Leu Glu Asn Cys Ser Asp			
90	95	100	105
GAA GAG CTT TTG GAA TAC GCA AAA GAT TGG AGC AAG GGC GTT AAG ATG			749
Glu Glu Leu Leu Glu Tyr Ala Lys Asp Trp Ser Lys Gly Val Lys Met			
110	115	120	
GCT ATC CCT GTG TTT GAA GGC ATC TCG CAA GAA AAA TTT TAT AAG CTA			797
Ala Ile Pro Val Phe Glu Gly Ile Ser Gln Glu Lys Phe Tyr Lys Leu			
125	130	135	
TTT GAA TTA GCT AAG ATC GCT ATG GAT GGC AAA ATG GAT CTG TAT GAC			845
Phe Glu Leu Ala Lys Ile Ala Met Asp Gly Lys Met Asp Leu Tyr Asp			
140	145	150	
GGA CGC ACA GGC GAG AAA ATG AGG GAG CGC GTG AAT GTG GGC TAC ATG			893
Gly Arg Thr Gly Glu Lys Met Arg Glu Arg Val Asn Val Gly Tyr Met			
155	160	165	
TAT ATG ATC AAA CTC CAC CAT TTA GTG GAT GAA AAA GTC CAT GCC AGA			941
Tyr Met Ile Lys Leu His His Leu Val Asp Glu Lys Val His Ala Arg			
170	175	180	185
AGC ACA GGC CCT TAT AGC TTA GTA ACG CAC CAG CCC GTG GGG GGT AAA			989
Ser Thr Gly Pro Tyr Ser Leu Val Thr His Gln Pro Val Gly Gly Lys			
190	195	200	
GCG CTC TTT GGG GGT CAA AGG TTT GGG GAA ATG GAA GTG TGG GCC TTG			1037
Ala Leu Phe Gly Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Leu			
205	210	215	
GAA GCT TAT GGC GCA GCG CAC ACT CTA AAA GAA ATG CTC ACC ATT AAA			1085
Glu Ala Tyr Gly Ala Ala His Thr Leu Lys Glu Met Leu Thr Ile Lys			
220	225	230	
TCC GAT GAT ATT AGA GGC AGA GAG AAC GCT TAT AGG GCT ATC GCT AAA			1133
Ser Asp Asp Ile Arg Gly Arg Glu Asn Ala Tyr Arg Ala Ile Ala Lys			
235	240	245	
GGT GAG CAA GTG GGC GAG AGT GAA ATC CCT GAG ACT TTC TAT GTT TTG			1181
Gly Glu Gln Val Gly Glu Ser Glu Ile Pro Glu Thr Phe Tyr Val Leu			
250	255	260	265
ACT AAA GAA TTG CAA TCG CTC GCT TTG GAT ATT AAT ATT TTT GGG GAC			1229
Thr Lys Glu Leu Gln Ser Leu Ala Leu Asp Ile Asn Ile Phe Gly Asp			
270	275	280	
GAT GTG GAT GAG GAT GGA GCA CCT AAA CCC ATT GTC ATT AAA GAA GAT			1277

Glu	Ala	Leu	Leu	Lys	Glu	Ala	Ala	Glu	Lys	Arg	Arg	Glu	Ile	Ile	Ala
65					70				75						80
Glu	Ala	Ile	Gln	Lys	Ala	Thr	Glu	Ser	Tyr	Asp	Ala	Val	Ile	Lys	Gln
			85					90						95	
Lys	Glu	Asn	Glu	Leu	Asn	Gln	Glu	Phe	Glu	Ala	Phe	Ala	Lys	Gln	Leu
			100				105						110		
Gln	Asn	Glu	Lys	Gln	Ala	Leu	Lys	Glu	Gln	Leu	Gln	Ala	Gln	Met	Pro
		115				120					125				
Val	Phe	Glu	Asp	Glu	Leu	Asn	Lys	Arg	Val	Ala	Met	Gly	Leu	Gly	Ser
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 387...5777
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AAGCTTGATA	TGGAGCATTT	TGATCGCTTG	ACCATGCTCA	ATAGAGAAGA	ATTGTTGCGC	60
GTTACTCGCT	CCTTTCTCAA	GCGATTTTAG	AAGAGCCTTT	CAGCCATAAC	GGCAAGGATT	120
ATAAAGAAGG	CGATCAAATC	CCTAAAGAAG	AAATCGCTTC	AATCAACCGC	TTCACCTTGG	180
CTAGTTTGGT	CAAAAAGTAT	TCTAAAGAAG	TGCAAAACCA	CTATGAAATC	ACTAAAAACA	240
ATTTCTTAGA	GCAAAAGAAA	GTTTTGGGCG	AAGAGCATGA	AGAAAAGCTT	TCTATTTTAG	300
AAAAAGATGA	TATTTTGCCT	AATGGCGTGA	TCAAAAAAGT	CAAGCTCTAT	ATCGCTACAA	360
AACGAAAGCT	TAAAGTGGGC	GATAAA	ATG	GCA	GGA	AGG
			Met	Ala	Gly	Arg
			1			5
ATT	GTG	TCT	AAT	ATC	GTG	CCG
Ile	Val	Ser	Asn	Ile	Val	Pro
10			15			20
						25
GGC	GAG	CCT	GTA	GAT	ATT	GTT
Gly	Glu	Pro	Val	Asp	Ile	Val
		30				35
						40
ATG	AAT	ATC	GGG	CAG	ATT	TTA
Met	Asn	Ile	Gly	Gln	Ile	Leu
		45				50
						55
GAA	TTT	GGG	AAG	CAA	ATC	GCT
Glu	Phe	Gly	Lys	Gln	Ile	Ala
						605

TTA	TTG	TTA	TGG	GCG	ATG	AAT	GTT	TGG	GTG	TAT	AGG	CCT	TTG	TTG	GCT	153
Leu	Leu	Leu	Trp	Ala	Met	Asn	Val	Trp	Val	Tyr	Arg	Pro	Leu	Leu	Ala	
20						25					30					
TTT	ATG	GAT	AAC	AGA	CAG	GCA	GAG	ATA	AAG	GAT	AGC	TTG	GCT	AAA	ATC	201
Phe	Met	Asp	Asn	Arg	Gln	Ala	Glu	Ile	Lys	Asp	Ser	Leu	Ala	Lys	Ile	
35					40				45					50		
AAA	ACG	GAT	AAT	GCC	CAA	AGT	GTG	GAG	ATT	GGC	CAT	CAA	ATT	GAG	GCT	249
Lys	Thr	Asp	Asn	Ala	Gln	Ser	Val	Glu	Ile	Gly	His	Gln	Ile	Glu	Ala	
				55				60						65		
CTT	CTT	AAA	GAA	GCG	GCT	GAA	AAA	CGC	AGA	GAA	ATA	ATA	GCA	GAA	GCG	297
Leu	Leu	Lys	Glu	Ala	Ala	Glu	Lys	Arg	Arg	Glu	Ile	Ile	Ala	Glu	Ala	
		70						75					80			
ATT	CAA	AAA	GCC	ACA	GAG	TCC	TAT	GAC	GCT	GTG	ATC	AAG	CAA	AAA	GAG	345
Ile	Gln	Lys	Ala	Thr	Glu	Ser	Tyr	Asp	Ala	Val	Ile	Lys	Gln	Lys	Glu	
	85						90					95				
AAC	GAA	CTC	AAT	CAA	GAG	TTT	GAA	GCG	TTT	GCG	AAG	CAA	TTA	CAA	AAT	393
Asn	Glu	Leu	Asn	Gln	Glu	Phe	Glu	Ala	Phe	Ala	Lys	Gln	Leu	Gln	Asn	
100						105					110					
GAA	AAG	CAA	GCG	CTA	AAA	GAG	CAG	TTG	CAA	GCG	CAA	ATG	CCG	GTA	TTT	441
Glu	Lys	Gln	Ala	Leu	Lys	Glu	Gln	Leu	Gln	Ala	Gln	Met	Pro	Val	Phe	
115					120					125				130		
GAA	GAC	GAG	TTA	AAC	AAG	CGT	GTG	GCT	ATG	GGT	TTA	GGG	AGT	TGATGAATG		492
Glu	Asp	Glu	Leu	Asn	Lys	Arg	Val	Ala	Met	Gly	Leu	Gly	Ser			
				135					140							
TTTGTAGTTA	AAATGGTGTT	AGGGTTTTTG	ATCCTTTTA													531

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met	Asn	Ile	Ser	Val	Asn	Pro	Tyr	Leu	Met	Ala	Val	Val	Phe	Val	Val	
1				5				10					15			
Phe	Val	Leu	Leu	Leu	Trp	Ala	Met	Asn	Val	Trp	Val	Tyr	Arg	Pro	Leu	
		20					25					30				
Leu	Ala	Phe	Met	Asp	Asn	Arg	Gln	Ala	Glu	Ile	Lys	Asp	Ser	Leu	Ala	
	35					40					45					
Lys	Ile	Lys	Thr	Asp	Asn	Ala	Gln	Ser	Val	Glu	Ile	Gly	His	Gln	Ile	
50					55					60						

```

Lys Gln Asn Lys Glu Met Ser Glu Leu Leu Thr Lys Leu Ser Gln Asp
  130                135                140
Leu Val Ser Gln Ile Ala Leu Ile Gln Lys Ala Leu Lys Glu Gln Glu
 145                150                155                160
Glu Lys Ala Glu Lys Pro Leu Lys Ser Asn Ala Pro Ala Asn Lys Thr
                165                170                175
Pro Ser Leu Lys Ala Glu Ser Pro Lys Asn Gln Glu Gly Lys Thr Gln
                180                185                190
Glu Lys Ala Lys Ile Glu Phe Asp Lys Asp Leu Ser Lys Gln Lys Glu
 195                200                205
Ile Phe Gln Glu Ala Leu Ser Phe Phe Lys Asn Lys Ser Tyr Ala Glu
 210                215                220
Ala Lys Glu Arg Leu Leu Trp Leu Glu Ala Asn Ser Tyr Arg Leu Tyr
 225                230                235                240
Tyr Val Arg Tyr Val Leu Gly Glu Val Ala Tyr Gly Glu Lys Arg Tyr
                245                250                255
Arg Glu Ala Ile Lys Tyr Tyr Lys Glu Ser Ala Leu Leu Asn Lys Lys
                260                265                270
Ala Ser Tyr Met Pro Val Leu Leu Trp His Thr Ala Trp Ser Phe Lys
 275                280                285
Lys Ile Lys Asp Asp Gln Asn Tyr Tyr Lys Phe Leu Asn Thr Leu Gln
 290                295                300
His Leu Tyr Pro Ser Ser Glu Gln Ala Lys Met Ala Gln Lys Ile Leu
 305                310                315                320
Glu Asn Lys Glu Lys His His His Ala Lys Pro
                325                330

```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...483
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```

AACAAATGCG AGTTTCAAAT ATTTTGTAGG ATTTTAGGAA AGAAATAGGT T ATG AAT      57
                                     Met Asn
                                     1

ATA TCG GTT AAC CCC TAT TTA ATG GCG GTC GTT TTT GTG GTG TTT GTG      105
Ile Ser Val Asn Pro Tyr Leu Met Ala Val Val Phe Val Val Phe Val
      5                10                15

```

```

TAT TAT GTG CGT TAT GTT CTT GGA GAA GTG GCT TAT GGG GAA AAG AGA      830
Tyr Tyr Val Arg Tyr Val Leu Gly Glu Val Ala Tyr Gly Glu Lys Arg
240                               245                               250                               255

TAC AGA GAA GCG ATC AAG TAT TAC AAA GAG AGC GCT CTT TTA AAC AAA      878
Tyr Arg Glu Ala Ile Lys Tyr Tyr Lys Glu Ser Ala Leu Leu Asn Lys
                               260                               265                               270

AAA GCG TCT TAC ATG CCT GTG CTT TTG TGG CAT ACG GCA TGG TCG TTT      926
Lys Ala Ser Tyr Met Pro Val Leu Leu Trp His Thr Ala Trp Ser Phe
                               275                               280                               285

AAA AAA ATC AAA GAC GAT CAA AAC TAT TAT AAA TTT TTA AAC ACT TTG      974
Lys Lys Ile Lys Asp Asp Gln Asn Tyr Tyr Lys Phe Leu Asn Thr Leu
                               290                               295                               300

CAA CAC TTG TAT CCT TCA AGC GAA CAA GCT AAA ATG GCG CAA AAA ATC      1022
Gln His Leu Tyr Pro Ser Ser Glu Gln Ala Lys Met Ala Gln Lys Ile
                               305                               310                               315

TTA GAA AAC AAG GAG AAA CAC CAC CAT GCA AAA CCA TGATTTAGAG TCAATC  1074
Leu Glu Asn Lys Glu Lys His His His Ala Lys Pro
320                               325                               330

AAACAAGCCG CTTTGATTGA ATATGAAGTG AGAGAACA      1112

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```

Met Lys Arg Leu Phe Phe Ile Pro Phe Ile Ala Pro Phe Phe Leu Asn
 1             5             10             15
Gly Glu Pro Ser Ala Phe Asp Leu Gln Ser Gly Ala Thr Lys Lys Glu
                20                25                30
Leu Lys Gln Leu Gln Ile Asn Ser Lys Asn Phe Ser Asn Ile Leu Thr
                35                40                45
Lys Ile His Ser Gln Val Glu Ala Asn Thr Gln Ala Gln Glu Gly Leu
                50                55                60
Arg Ser Val Tyr Glu Gly Gln Ala Asn Lys Ile Lys Asp Leu Asn Asn
        65                70                75                80
Ala Ile Leu Ser Gln Glu Glu Ser Leu Arg Ala Leu Lys Ala Ser Gln
                85                90                95
Glu Val Gln Ala Asn Thr Leu Lys Gln Gln Ser Gln Thr Leu Glu Asp
                100                105                110
Leu Arg Asn Glu Ile His Ala Asn Gln Gln Ala Ile Gln Gln Leu Asp
        115                120                125

```


Asn	Gly	Glu	Pro	Ser	Ala	Phe	Asp	Leu	Gln	Ser	Gly	Ala	Thr	Lys	Lys	
			20						25					30		
GAA	CTC	AAG	CAG	TTG	CAA	ATC	AAT	AGT	AAG	AAT	TTT	TCT	AAT	ATT	TTG	206
Glu	Leu	Lys	Gln	Leu	Gln	Ile	Asn	Ser	Lys	Asn	Phe	Ser	Asn	Ile	Leu	
			35					40				45				
ACC	AAA	ATC	CAT	TCG	CAA	GTA	GAG	GCT	AAC	ACT	CAA	GCT	CAA	GAG	GGT	254
Thr	Lys	Ile	His	Ser	Gln	Val	Glu	Ala	Asn	Thr	Gln	Ala	Gln	Glu	Gly	
		50					55				60					
TTG	AGA	AGC	GTT	TAT	GAG	GGG	CAG	GCT	AAT	AAG	ATT	AAA	GAT	CTC	AAT	302
Leu	Arg	Ser	Val	Tyr	Glu	Gly	Gln	Ala	Asn	Lys	Ile	Lys	Asp	Leu	Asn	
	65					70					75					
AAC	GCT	ATC	CTT	TCC	CAA	GAA	GAA	TCC	TTA	CGA	GCC	TTA	AAA	GCT	TCG	350
Asn	Ala	Ile	Leu	Ser	Gln	Glu	Glu	Ser	Leu	Arg	Ala	Leu	Lys	Ala	Ser	
80					85				90					95		
CAA	GAA	GTG	CAG	GCT	AAC	ACG	CTT	AAG	CAG	CAA	TCG	CAA	ACT	TTA	GAG	398
Gln	Glu	Val	Gln	Ala	Asn	Thr	Leu	Lys	Gln	Gln	Ser	Gln	Thr	Leu	Glu	
			100					105					110			
GAT	TTG	AGG	AAT	GAG	ATT	CAC	GCT	AAC	CAG	CAA	GCT	ATC	CAG	CAG	TTA	446
Asp	Leu	Arg	Asn	Glu	Ile	His	Ala	Asn	Gln	Gln	Ala	Ile	Gln	Gln	Leu	
			115					120					125			
GAC	AAG	CAA	AAT	AAA	GAG	ATG	AGT	GAA	TTA	TTG	ACC	AAG	TTA	AGC	CAG	494
Asp	Lys	Gln	Asn	Lys	Glu	Met	Ser	Glu	Leu	Leu	Thr	Lys	Leu	Ser	Gln	
		130					135					140				
GAT	TTG	GTT	TCA	CAA	ATC	GCC	TTA	ATC	CAA	AAA	GCT	CTC	AAA	GAA	CAA	542
Asp	Leu	Val	Ser	Gln	Ile	Ala	Leu	Ile	Gln	Lys	Ala	Leu	Lys	Glu	Gln	
	145					150					155					
GAG	GAA	AAA	GCT	GAA	AAG	CCG	CTC	AAA	TCA	AAC	GCT	CCG	GCT	AAT	AAA	590
Glu	Glu	Lys	Ala	Glu	Lys	Pro	Leu	Lys	Ser	Asn	Ala	Pro	Ala	Asn	Lys	
160					165				170					175		
ACC	CCC	TCT	TTG	AAA	GCC	GAA	TCC	CCA	AAA	AAT	CAA	GAG	GGA	AAA	ACT	638
Thr	Pro	Ser	Leu	Lys	Ala	Glu	Ser	Pro	Lys	Asn	Gln	Glu	Gly	Lys	Thr	
			180					185					190			
CAA	GAA	AAG	GCG	AAA	ATT	GAG	TTT	GAT	AAA	GAC	TTG	TCT	AAG	CAA	AAA	686
Gln	Glu	Lys	Ala	Lys	Ile	Glu	Phe	Asp	Lys	Asp	Leu	Ser	Lys	Gln	Lys	
			195					200					205			
GAG	ATC	TTT	CAA	GAA	GCT	CTG	TCT	TTT	TTT	AAA	AAT	AAA	TCC	TAT	GCA	734
Glu	Ile	Phe	Gln	Glu	Ala	Leu	Ser	Phe	Phe	Lys	Asn	Lys	Ser	Tyr	Ala	
	210					215						220				
GAA	GCC	AAA	GAG	CGT	TTG	TTG	TGG	TTA	GAA	GCC	AAT	AGT	TAC	AGA	CTT	782
Glu	Ala	Lys	Glu	Arg	Leu	Leu	Trp	Leu	Glu	Ala	Asn	Ser	Tyr	Arg	Leu	
	225					230					235					

Ile Ser Lys Ile His
65

GAATATCAA

319

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys Phe
 1             5             10             15
Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe Lys
          20             25             30
Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys Lys
          35             40             45
Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln Ile
          50             55             60
Ser Lys Ile His
65

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...1058
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

AAAACTAGA GAGTGGTTATA AAGAAAACAG AAGAGTGGAT GTCAAATTAA TGAAGTAATT      60
CTAGG ATG AAA AGG CTT TTT TTT ATC CCT TTT ATC GCT CCC TTT TTT CTC      110
  Met Lys Arg Leu Phe Phe Ile Pro Phe Ile Ala Pro Phe Phe Leu
    1             5             10             15

AAT GGG GAG CCT TCA GCG TTT GAT TTG CAA AGT GGG GCT ACC AAA AAA      158

```

```

Thr Glu Lys Gly Tyr Thr Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr
   130               135               140
Met Glu Gly Arg Gly Val Pro Ser Asn Tyr Val Lys Ala Thr Glu Cys
 145               150               155               160
Phe Arg Lys Ala Met His Lys Gly Asn Val Glu Ala Tyr Ile Leu Leu
               165               170               175
Gly Asp Ile Tyr Tyr Ser Gly Asn Asp Gln Leu Gly Ile Glu Pro Asp
               180               185               190
Lys Asp Lys Ala Ile Val Tyr Tyr Lys Met Ala Ala Asp Met Ser Ser
               195               200               205
Ser Arg Ala Tyr Glu Gly Leu Ala Glu Ser Tyr Gln Tyr Gly Leu Gly
 210               215               220
Val Glu Lys Asp Lys Lys Lys Ala Glu Glu Tyr Met Gln Lys Ala Cys
 225               230               235               240
Asp Phe Asp Ile Asp Lys Asn Cys Lys Lys Lys Asn Thr Ser Ser Arg
               245               250               255

```

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...269
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

TGGGGGTTGT GGTTCCTCAT GTTCGCATGG GTAGTAAGGT ATAGGAGTAT TTAAAAGGCA      60
AGGTC ATG AAT AGT TCT AAT CTC AAA AAT TGG CTA TTC CCT ACC ATT TGC      110
  Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys
    1               5               10               15

TTT TTT TTA TTT TGT TAT ATT TTA ATT TTT TTA ATG TTC TTT ATG TTT      158
Phe Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe
    20               25               30

AAA AGT TTG CAA TCG CAA TCG TTT GGC TCT GTG GCA GAA ACC GGA AAA      206
Lys Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys
    35               40               45

AAA CCC ATC ACC ACC ACC AAG AAA TTT GGT AAG GAA TTG CAA AAA CAG      254
Lys Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln
    50               55               60

ATT TCA AAA ATC CAT TAACTTTTTT TCTTTTTTGC CGATACTTGC TGTAATGGAA T      310

```

TTT AGA AAA GCG ATG CAT AAG GGT AAT GTA GAA GCT TAT ATC CTT TTA 586
Phe Arg Lys Ala Met His Lys Gly Asn Val Glu Ala Tyr Ile Leu Leu
165 170 175

GGG GAT ATT TAT TAT AGT GGG AAT GAT CAA TTG GGT ATT GAG CCA GAC 634
Gly Asp Ile Tyr Tyr Ser Gly Asn Asp Gln Leu Gly Ile Glu Pro Asp
180 185 190

AAA GAT AAG GCG ATT GTC TAT TAT AAA ATG GCG GCT GAT ATG AGC TCT 682
Lys Asp Lys Ala Ile Val Tyr Tyr Lys Met Ala Ala Asp Met Ser Ser
195 200 205

TCT AGA GCT TAT GAA GGG TTA GCA GAG TCT TAT CAG TAT GGG TTA GGC 730
Ser Arg Ala Tyr Glu Gly Leu Ala Glu Ser Tyr Gln Tyr Gly Leu Gly
210 215 220

GTG GAA AAA GAT AAG AAA AAG GCT GAA GAA TAC ATG CAA AAA GCA TGC 778
Val Glu Lys Asp Lys Lys Lys Ala Glu Glu Tyr Met Gln Lys Ala Cys
225 230 235 240

GAT TTT GAC ATT GAT AAA AAT TGT AAG AAA AAG AAC ACT TCA AGC CGA 826
Asp Phe Asp Ile Asp Lys Asn Cys Lys Lys Lys Asn Thr Ser Ser Arg
245 250 255

TAACTCTCAA ACTTGGGCTT GATTAGGATT TTTGTTTTAT TTTAAGTAGC ATG 879

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu
1 5 10 15
Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn
20 25 30
Tyr Ile Tyr Xaa Gly Glu Glu Ala Tyr Asn Asn Lys Glu Tyr Glu Arg
35 40 45
Ala Ala Ser Phe Tyr Lys Ser Ala Ile Lys Asn Gly Glu Pro Leu Ala
50 55 60
Tyr Val Leu Leu Gly Ile Met Tyr Glu Asn Gly Arg Gly Val Pro Lys
65 70 75 80
Asp Glu Lys Lys Ala Ala Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp
85 90 95
Ile Pro Arg Gly Tyr Asn Asn Leu Gly Val Met Tyr Lys Glu Gly Arg
100 105 110
Gly Val Pro Lys Asp Glu Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala
115 120 125

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 59...826

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

TTTTAAGATT GGTAGCCATT GGCATTATGT TTGATCTTAT TAAAGCAGAG GAGTAACA      58

ATG GGA TAC GCA AGC AAA TTA GCC TTG AAG ATT TGT TTG GCA AGT TTA      106
Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu
  1             5             10             15

TGT TTA TTT AGC GCT CTT GGT GCA GAA CAC CTT GAA CAA AAA AGG AAC      154
Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn
          20             25             30

TAT ATT TAT AAM GGG GAG GAA GCC TAT AAT AAT AAG GAA TAT GAG CGG      202
Tyr Ile Tyr Xaa Gly Glu Glu Ala Tyr Asn Asn Lys Glu Tyr Glu Arg
          35             40             45

GCG GCT TCT TTT TAT AAG AGC GCG ATT AAA AAT GGC GAG CCG CTT GCT      250
Ala Ala Ser Phe Tyr Lys Ser Ala Ile Lys Asn Gly Glu Pro Leu Ala
          50             55             60

TAT GTT CTT TTA GGG ATC ATG TAT GAA AAT GGT AGG GGT GTG CCT AAA      298
Tyr Val Leu Leu Gly Ile Met Tyr Glu Asn Gly Arg Gly Val Pro Lys
          65             70             75             80

GAT GAA AAG AAA GCG GCT GAA TAT TTT CAA AAA GCG GTT GAT AAC GAT      346
Asp Glu Lys Lys Ala Ala Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp
          85             90             95

ATA CCT AGA GGG TAT AAC AAT TTA GGC GTG ATG TAT AAA GAG GGT AGA      394
Ile Pro Arg Gly Tyr Asn Asn Leu Gly Val Met Tyr Lys Glu Gly Arg
          100             105             110

GGT GTG CCT AAA GAT GAA AAG AAA GCC GTG GAG TAT TTT AGA ATA GCT      442
Gly Val Pro Lys Asp Glu Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala
          115             120             125

ACC GAG AAG GGC TAT ACT AAC GCC TAT ATA AAC TTA GGC ATC ATG TAT      490
Thr Glu Lys Gly Tyr Thr Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr
          130             135             140

ATG GAG GGT AGG GGA GTT CCA AGC AAC TAT GTG AAA GCG ACA GAG TGC      538
Met Glu Gly Arg Gly Val Pro Ser Asn Tyr Val Lys Ala Thr Glu Cys
          145             150             155             160

```

80	85	90	95	
TAC AGC AAT GGG TGT CAT TTG CTA GGG AAT TTA TAT TAC AGC GGG CAA				457
Tyr Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln				
	100	105	110	
GGC GTG TCC CAA AAC ACC AAT AAA GCC CTA CAA TAC TAC TCT AAA GCG				505
Gly Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala				
	115	120	125	
TGC GAT TTG AAA TAC GCT GAA GGG TGC GCG ACT TAGGGGGGAT TTATCATGAT				558
Cys Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr				
	130	135		
GGTAAAGTGG TAACTAGGGA TTTTAAAAAA GCGGTGGAAT AT				600

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Met	Leu	Glu	Asn	Val	Lys	Lys	Ser	Phe	Phe	Arg	Val	Leu	Cys	Leu	Gly	1	5	10	15
Ala	Leu	Cys	Leu	Gly	Gly	Leu	Met	Ala	Glu	Gln	Asp	Pro	Lys	Glu	Leu	20	25	30	
Val	Gly	Leu	Gly	Ala	Lys	Ser	Tyr	Lys	Glu	Lys	Asp	Phe	Thr	Gln	Ala	35	40	45	
Lys	Lys	Tyr	Phe	Glu	Lys	Ala	Cys	Asp	Leu	Lys	Glu	Asn	Ser	Gly	Cys	50	55	60	
Phe	Asn	Leu	Gly	Val	Leu	Tyr	Tyr	Gln	Gly	Gln	Gly	Val	Glu	Lys	Asn	65	70	75	80
Leu	Lys	Lys	Ala	Ala	Ser	Phe	Tyr	Ala	Lys	Ala	Cys	Asp	Leu	Asn	Tyr	85	90	95	
Ser	Asn	Gly	Cys	His	Leu	Leu	Gly	Asn	Leu	Tyr	Tyr	Ser	Gly	Gln	Gly	100	105	110	
Val	Ser	Gln	Asn	Thr	Asn	Lys	Ala	Leu	Gln	Tyr	Tyr	Ser	Lys	Ala	Cys	115	120	125	
Asp	Leu	Lys	Tyr	Ala	Glu	Gly	Cys	Ala	Thr							130	135		

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```

Ile Ile Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr
      115              120              125
Ser His Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys
      130              135              140
Ala Tyr Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe
      145              150              155              160
Thr Gln Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile
              165              170              175
Asp Arg Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg
      180              185

```

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 125...538
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

CAAAGAGTGG GATAAAATCA CAGAAATTTG TAAGAGAGCG CTAGCTTTAA GATAACAAAA      60
AGATCATGGC ATTTTGTATT TGCTTAATAA CACTATAATA AAATTTTTAA TAAGGAGATA      120
CATC ATG TTA GAA AAT GTC AAA AAG TCC TTT TTT AGG GTT TTG TGC TTG      169
  Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu
    1              5              10              15

GGT GCG TTG TGT TTA GGG GGG CTA ATG GCA GAG CAA GAC CCT AAA GAG      217
Gly Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu
    20              25              30

CTT GTG GGT TTG GGG GCA AAG AGC TAC AAA GAG AAA GAT TTC ACT CAA      265
Leu Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln
    35              40              45

GCG AAG AAA TAT TTT GAG AAA GCG TGC GAT TTG AAA GAA AAT AGC GGG      313
Ala Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly
    50              55              60

TGT TTT AAT TTA GGG GTG CTT TAT TAT CAA GGG CAA GGG GTG GAA AAG      361
Cys Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys
    65              70              75

AAC TTG AAA AAA GCC GCC TCC TTT TAC GCT AAA GCT TGC GAT TTG AAT      409
Asn Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn

```

85	90	95	
GTG AGC ATC ACG CAA AAA AGC GGC GAT TAT GGA GCG GAT TTG ATT ATA			392
Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu Ile Ile			
100	105	110	
GAA AAA GAC GGC ATC AAG TGG GCG GTT CAA GTC AAA CGC TAC TCG CAT			440
Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr Ser His			
115	120	125	130
AAA GTT TCG CCC AAA GCC ATT CAA GAG GTG GTC TCT TCT AAA GCT TAT			488
Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys Ala Tyr			
	135	140	145
TAC GCT TGC GAA AAA GCT TGC GTG ATC ACC AAC AGC TAT TTC ACG CAA			536
Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe Thr Gln			
	150	155	160
GCC GCT CAA AAA CTG GCT CAA GCT AAC GAA GTG CTC TTG ATT GAC AGA			584
Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile Asp Arg			
	165	170	175
GAC GAA TGG GTC AGG TTT TTG AAC GAA AAG AGA TGAACCGATC CCATCAGATC			637
Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg			
180	185		
GTGTGTTCTC AAGTTCTTTT AAAATTTTGT CGT			670

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met	Lys	Lys	Ile	Ala	Phe	Phe	Ile	Phe	Val	Ile	Leu	Phe	Ser	Val	Gly
1				5					10					15	
Ile	Tyr	Leu	Ile	Trp	His	Val	Leu	Leu	Glu	Lys	Ala	Leu	Glu	Leu	Lys
		20						25					30		
Leu	Ala	Thr	Ser	Ala	Asn	Asp	Leu	Leu	Lys	Leu	Leu	Ala	Ile	Leu	
		35					40				45				
Gly	Val	Phe	Ser	Met	Leu	Val	Leu	Phe	Gln	Gly	Ile	Ile	Ser	Ser	Tyr
	50					55				60					
Lys	Lys	Arg	Gln	Leu	Lys	Arg	Ile	Leu	Gln	Lys	Ile	Asp	Ala	Met	Asn
65				70						75				80	
Gly	Phe	Glu	Phe	Glu	Glu	Tyr	Ser	Lys	Ile	Phe	Phe	Thr	Ser	Lys	Gly
			85					90						95	
Phe	Glu	Val	Ser	Ile	Thr	Gln	Lys	Ser	Gly	Asp	Tyr	Gly	Ala	Asp	Leu
			100					105						110	


```

Leu Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu
  50                      55                      60
Phe Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu
  65                      70                      75                      80
Phe Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg
                      85                      90                      95
Ser Tyr Asp Phe Asp Asp Gly Lys
                      100

```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...617
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

GTTTAGAAAA GCGTTTGAAC GCTATAAAAA ATGCAGAGTG GCTTTAAGGC ATG AAA      56
                                     Met Lys
                                     1

AAG ATT GCA TTT TTT ATT TTT GTC ATT TTG TTT TCG GTA GGG ATT TAT      104
Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly Ile Tyr
      5                      10                      15

TTA ATT TGG CAT GTT TTA TTG GAA AAA GCC CTA GAA TTG AAA TTA GCA      152
Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys Leu Ala
      20                      25                      30

ACC TCA GCT AAT GAT TTG CTT TTA AAA TTG TTG GCA ATT CTT GGC GTT      200
Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu Gly Val
      35                      40                      45                      50

TTT TCA ATG TTA GTG CTT TTT CAA GGC ATT ATT TCT TCG TAT AAG AAG      248
Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr Lys Lys
                      55                      60                      65

CGC CAA CTC AAA CGC ATT TTA CAA AAA ATA GAC GCC ATG AAC GGC TTT      296
Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn Gly Phe
                      70                      75                      80

GAA TTT GAA GAA TAT TCC AAA ATC TTT TTC ACT TCA AAG GGT TTT GAA      344
Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly Phe Glu

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

AAAGAAGGTT TGAAAAGCTT TTTTAAAAGG CTTTGAAGT ATTTGGGGTA GGCTTGA ATG      60
                                         Met
                                         1

AAA GTG CAA AAT TTT ATC CAT TTT TCT GTT GTG GTA GGG TTT TTT TTG      108
Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe Leu
                    5                      10                      15

GGG TTA GTG TTT TCG GTG TTG AAA TTC AAT GAG CCA GAG AGC ATT TTA      156
Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile Leu
                20                      25                      30

TTA TGG ACG GTG TTA TCC ACG CTT GGG GGG TAC TTG ATT GCG TTG TTG      204
Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu Leu
                35                      40                      45

TTT GCG TCT ATT TTT ATC GCT TGC ACG GAT TTG GAT ATT TGT CTT TTT      252
Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu Phe
                50                      55                      60                      65

GAC AAA AAA GGC ACT GAA GAG AGT TTG CTT CGT TTC AAC CAT GAG TTT      300
Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu Phe
                    70                      75                      80

AAA AAC AGA GAA AAA GAA GTG GCT AGT ATT TTA GAA TAC ATT AGA AGT      348
Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg Ser
                    85                      90                      95

TAT GAT TTT GAT GAT GGA AAA TAGAATGCCC AAAGGAATTC AAAAAACTGA AACA      403
Tyr Asp Phe Asp Asp Gly Lys
                100

AGCGAAAAAA ATATAGAA      421

```

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```

Met Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe
 1                      5                      10                      15
Leu Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile
                20                      25                      30
Leu Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu
                35                      40                      45

```

```

AGGGACTCGC TCGTGGCGTT ACTGCCCACG CCGGCTAACA CTTTC ATG CGC GAA TTT 117
                                     Met Arg Glu Phe
                                     1

GAG GGC GTT TTA GTG TTT TTG CAA GTT TCT ATG GCG ATT TCA ATG CAA 165
Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala Ile Ser Met Gln
  5                10                15                20

CGC ATG TGC TCT TTG TGG GTG AGC GTG GCG GAT TCT CCT GTC GTG CCA 213
Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser Pro Val Val Pro
          25                30                35

ACA GGC ACG CAT GCG TCC ATG CCC TGAAAAATTT GGCGCTTGAT CAAGGTTTCA 267
Thr Gly Thr His Ala Ser Met Pro
          40

TAAGCGGCCT CATCAACGCT CAA 290

```

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```

Met Arg Glu Phe Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala
  1                5                10                15
Ile Ser Met Gln Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser
          20                25                30
Pro Val Val Pro Thr Gly Thr His Ala Ser Met Pro
    35                40

```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...369
- (D) OTHER INFORMATION:

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Met Pro Ala Leu Ser Arg Ser Tyr Gly Val Val Leu Ile Phe Ile Thr
 1           5           10           15
Gln Ser Asn Ala Leu Ile Glu Lys Tyr Tyr Gly Arg Glu Asp Ala Arg
      20           25           30
Ile Val Asn Ser Thr Val Ala Tyr Lys Ile Ile Phe Lys Met Asp Asp
      35           40           45
Leu Glu Tyr Ala Lys Gln Val Ser Glu Glu Val Gly Lys Met Thr Arg
      50           55           60
Lys Thr Arg Ser His Ser Thr Glu Lys Gly Gln Leu Ile Thr Gly Gly
65           70           75           80
Thr Ser Ser Ile Gly Lys Glu Ala Trp Asp Leu Leu Ser Ala Gln Asp
      85           90           95
Ile Met Asn Ile Asp Lys Asp Glu Val Ile Val Leu Val Ser Gly His
      100          105          110
Lys Ala Lys Pro Leu Lys Leu Lys Ala Asn Tyr Tyr Phe Lys Asn Lys
      115          120          125
Glu Leu Leu Ser Arg Ile Asn Trp Glu Val Lys Pro Asn Glu Glu Val
      130          135          140
Phe
145

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 106...237
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TAAGGGCTTA CGCATAAAAT CGCATCCGCG CCGATTTTTT GAGCGAACTT TGCTAAAGAA 60

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 145...579

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

GCGTTCAATA GAATGCTTTA GTTAGGAAGC TCCTTGCTTT AGCAAGGNGT GGTTTCACTG      60
AAAGAGAGTA AGAAATTTGA AGAAAGGGTT TATCTTTTTT TAGATGAATT TGTGCGTTTT      120
GGTAAATTGC CTTTTTTATT AGAA ATG CCA GCA TTA AGT AGG AGC TAT GGT      171
                Met Pro Ala Leu Ser Arg Ser Tyr Gly
                  1                      5

GTG GTT TTA ATT TTT ATC ACG CAA TCC AAC GCT CTT ATT GAA AAA TAT      219
Val Val Leu Ile Phe Ile Thr Gln Ser Asn Ala Leu Ile Glu Lys Tyr
10                      15                      20                      25

TAC GGC AGA GAA GAT GCA AGA ATT GTT AAT AGC ACC GTG GCT TAC AAA      267
Tyr Gly Arg Glu Asp Ala Arg Ile Val Asn Ser Thr Val Ala Tyr Lys
                30                      35                      40

ATA ATT TTC AAA ATG GAT GAT TTA GAA TAC GCT AAA CAG GTG AGC GAA      315
Ile Ile Phe Lys Met Asp Asp Leu Glu Tyr Ala Lys Gln Val Ser Glu
                45                      50                      55

GAA GTC GGT AAG ATG ACT AGA AAA ACA CGA AGC CAC TCT ACA GAA AAA      363
Glu Val Gly Lys Met Thr Arg Lys Thr Arg Ser His Ser Thr Glu Lys
                60                      65                      70

GGA CAA CTC ATT ACC GGA GGG ACT TCT AGT ATA GGT AAA GAG GCG TGG      411
Gly Gln Leu Ile Thr Gly Gly Thr Ser Ser Ile Gly Lys Glu Ala Trp
                75                      80                      85

GAC TTA TTG AGC GCG CAA GAT ATT ATG AAT ATT GAT AAA GAT GAA GTG      459
Asp Leu Leu Ser Ala Gln Asp Ile Met Asn Ile Asp Lys Asp Glu Val
                90                      95                      100                      105

ATC GTT TTA GTA AGC GGT CAT AAG GCT AAA CCC TTA AAA TTA AAA GCG      507
Ile Val Leu Val Ser Gly His Lys Ala Lys Pro Leu Lys Leu Lys Ala
                110                      115                      120

AAT TAT TAT TTC AAA AAC AAA GAA TTA CTC TCT CGT ATT AAC TGG GAA      555
Asn Tyr Tyr Phe Lys Asn Lys Glu Leu Ser Arg Ile Asn Trp Glu
                125                      130                      135

GTC AAG CCC AAT GAA GAA GTG TTT TGATGGATTA AAAAAAGTTTG CATGAGTATT      609
Val Lys Pro Asn Glu Glu Val Phe
                140                      145

TTTTAATTGC TTTTTTAAAA AT      631

```

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 112...252
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

ATGCCTGCCA TTTCATAGCC TAAATTTTCT TTAGAGCCGA ATTGATAAGC GGCTTTTAAG      60
ACTTCTTTTTT GCTTAGCGTT AAAATCTTTA ATATTGTCGC AATTGGTCAT C ATG ACT      117
                                     Met Thr
                                     1

TTA GTA ACG GGC GAT TTG GGC TTG TTT TTA ACC CCT TTA GCG GGC TTA      165
Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala Gly Leu
      5              10              15

GGC TCT GTT TTA GTG GGG CTT TCT GTT GCG GCT AAA CTT AAA GAT GCA      213
Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys Asp Ala
      20              25              30

CTT AAG GCT GTG CCT AGC CAT AAG GCT TTA AAG ATG GTG TGAGTGAGTG GG      264
Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val
      35              40              45

GTTAAATGTT TCAAAACGCC TACCTTTTGT ATTAAGAAAT AACTA      310

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

Met Thr Leu Val Thr Gly Asp Leu Gly Leu Phe Leu Thr Pro Leu Ala
  1              5              10              15
Gly Leu Gly Ser Val Leu Val Gly Leu Ser Val Ala Ala Lys Leu Lys
      20              25              30
Asp Ala Leu Lys Ala Val Pro Ser His Lys Ala Leu Lys Met Val
      35              40              45

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

AAG GTC GCT CAA AAA GAA TTT GGT AGC GTT TGT GCG TTA AGG TAGTTTTAT 642
 Lys Val Ala Gln Lys Glu Phe Gly Ser Val Cys Ala Leu Arg
 175 180

AGCATTCTAG CGAGCATGTT TAAGGCATGC TCTACGCTTT TATT 686

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met	Val	Leu	Ile	Ala	Leu	Leu	Gly	Val	Phe	Ser	Ser	Val	Ser	Leu	Ser	1	5	10	15
Ala	Lys	Ser	Leu	Leu	Arg	Asp	Asp	Gly	Ile	Leu	Val	Ser	Asp	Leu	Lys	20	25	30	
Gly	Met	Lys	Ser	Glu	Leu	Ser	Asp	Ala	Pro	Ala	Trp	Val	Phe	Glu	Asp	35	40	45	
Ala	Lys	Ala	Pro	Tyr	Glu	Glu	Met	Gly	Val	Ala	Tyr	Ile	Pro	Val	Asn	50	55	60	
Asn	Lys	Tyr	Leu	Gly	Ile	Glu	Gln	Ala	Thr	Leu	Asn	Ala	Lys	Leu	Ser	65	70	75	80
Leu	Ile	Val	Val	Phe	His	Glu	Ile	Met	Met	Lys	Tyr	Lys	Lys	Arg	Phe	85	90	95	
Met	Glu	Gln	Phe	His	Glu	Ser	Glu	Gln	Thr	Thr	Thr	Asn	Ile	Ser	Tyr	100	105	110	
Ala	Ile	Tyr	Asn	Tyr	Leu	Ala	Thr	Lys	Ile	Gln	Val	Ser	Asn	Thr	Tyr	115	120	125	
Thr	Asn	Leu	Lys	Ser	Glu	Val	Ala	Val	Val	Lys	Ile	Lys	Leu	Val	Gly	130	135	140	
Cys	Gln	Ile	Glu	Gln	Ile	Lys	Arg	Tyr	Leu	Lys	Ala	Ser	Val	Glu	Asn	145	150	155	160
Leu	Asn	Asp	Asn	Glu	Ile	Ala	Tyr	Ile	Ala	Lys	Val	Ala	Gln	Lys	Glu	165	170	175	
Phe	Gly	Ser	Val	Cys	Ala	Leu	Arg									180			

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 82...633
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

TGTGATTAAA CAAAATCAAA AACTTTTAA CTATAATCAA ACCTAAATTA AAGTTCAAGG	60
AGTGGCATT TGTTTAAAAG A ATG GTT TTA ATC GCT CTT TTA GGG GTG TTT	111
Met Val Leu Ile Ala Leu Leu Gly Val Phe	
1 5 10	
TCA AGC GTT TCA TTA AGC GCT AAG AGT CTT TTA AGA GAT GAT GGG ATT	159
Ser Ser Val Ser Leu Ser Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile	
15 20 25	
TTA GTC TCT GAT TTA AAG GGC ATG AAA TCA GAA CTA TCT GAT GCT CCT	207
Leu Val Ser Asp Leu Lys Gly Met Lys Ser Glu Leu Ser Asp Ala Pro	
30 35 40	
GCT TGG GTT TTT GAA GAC GCT AAA GCC CCC TAC GAA GAA ATG GGC GTG	255
Ala Trp Val Phe Glu Asp Ala Lys Ala Pro Tyr Glu Glu Met Gly Val	
45 50 55	
GCG TAT ATC CCT GTT AAT AAT AAA TAT TTA GGG ATT GAG CAA GCG ACC	303
Ala Tyr Ile Pro Val Asn Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr	
60 65 70	
TTA AAC GCT AAA TTG AGT CTG ATC GTG GTT TTT CAT GAA ATC ATG ATG	351
Leu Asn Ala Lys Leu Ser Leu Ile Val Val Phe His Glu Ile Met Met	
75 80 85 90	
AAG TAT AAA AAA CGC TTC ATG GAG CAA TTC CAT GAG TCC GAG CAG ACG	399
Lys Tyr Lys Lys Arg Phe Met Glu Gln Phe His Glu Ser Glu Gln Thr	
95 100 105	
ACT ACG AAT ATC AGT TAC GCT ATC TAT AAT TAT CTA GCG ACT AAG ATC	447
Thr Thr Asn Ile Ser Tyr Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile	
110 115 120	
CAG GTA TCC AAC ACC TAC ACG AAT TTA AAA TCG GAG GTG GCG GTG GTG	495
Gln Val Ser Asn Thr Tyr Thr Asn Leu Lys Ser Glu Val Ala Val Val	
125 130 135	
AAA ATC AAG CTA GTG GGT TGT CAG ATT GAG CAA ATC AAA AGG TAT TTA	543
Lys Ile Lys Leu Val Gly Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu	
140 145 150	
AAA GCG AGC GTT GAA AAC CTT AAC GAT AAT GAA ATC GCT TAC ATC GCT	591
Lys Ala Ser Val Glu Asn Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala	
155 160 165 170	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```

Met Lys Arg Arg Asp Phe Ile Lys Thr Thr Thr Leu Gly Ala Thr Gly
 1           5           10           15
Ala Val Leu Gly Ala Gln Ile Leu Gln Ala Glu Glu Ser Lys Gly Ser
          20           25           30
Val Ala Lys Tyr Lys Ile Glu Ala Gln Tyr Ser Ile Asp Phe Asp Ser
          35           40           45
Ala Glu His Thr Ser Leu Phe Ile Pro Met Pro Ser Val Val Ala Ser
          50           55           60
Asn Val His Leu Gln Gly Asn His Ala Ser Tyr Lys Ser Met Leu Asn
65           70           75           80
Phe Gly Val Pro Tyr Leu Gln Val Asp Phe Leu Lys Ser Thr Gln Lys
          85           90           95
Lys Gln Val His Leu Ser Tyr Glu Ile Ala Ser Tyr Gln Leu Asn Glu
          100          105          110
Arg Leu Phe Glu Thr Ser Asp Phe Val Ala Met Gly Arg Tyr Glu Arg
          115          120          125
Asp Asp Ala Ser Val Ala Asn Ile Ala Asn Gln Leu Lys Gly Thr Thr
          130          135          140
Pro Lys Glu Ser Val Arg Asn Phe Tyr Ala Phe Ile Lys His Glu Met
145          150          155          160
Pro Lys Arg Gln Lys Ala Leu Glu Gly Lys Glu Asn Leu Pro Lys Arg
          165          170          175
Glu Ser Leu Pro Trp Phe Ala Thr Ile Ser Lys Glu Ser Met Phe Val
          180          185          190
Ser Leu Cys His Ala Cys Gly Ile Lys Ser Ala Glu Val Gln Gly Leu
          195          200          205
Lys Leu Gly Gln Asn Ser Val Val Lys Asn Ala Pro Arg Val Glu Val
          210          215          220
Tyr Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys
225          230          235          240
Glu Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser
          245          250          255
Ala Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg
          260          265          270
Asp Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr
          275          280          285
Thr Ile Val
          290

```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

TTG TTT GAA ACG AGC GAT TTT GTA GCA ATG GGG CGT TAT GAA AGA GAC	443
Leu Phe Glu Thr Ser Asp Phe Val Ala Met Gly Arg Tyr Glu Arg Asp	
115 120 125	
GAT GCG AGC GTG GCT AAC ATT GCC AAC CAG CTT AAG GGA ACA ACC CCT	491
Asp Ala Ser Val Ala Asn Ile Ala Asn Gln Leu Lys Gly Thr Thr Pro	
130 135 140 145	
AAA GAA AGC GTT CGC AAT TTT TAT GCG TTC ATC AAG CAT GAG ATG CCT	539
Lys Glu Ser Val Arg Asn Phe Tyr Ala Phe Ile Lys His Glu Met Pro	
150 155 160	
AAG AGA CAG AAG GCT TTA GAG GGT AAA GAA AAT TTA CCT AAG CGT GAG	587
Lys Arg Gln Lys Ala Leu Glu Gly Lys Glu Asn Leu Pro Lys Arg Glu	
165 170 175	
AGT TTG CCC TGG TTT GCA ACC ATT TCA AAA GAG AGC ATG TTT GTG TCC	635
Ser Leu Pro Trp Phe Ala Thr Ile Ser Lys Glu Ser Met Phe Val Ser	
180 185 190	
TTA TGC CAT GCG TGC GGG ATT AAA AGC GCT GAA GTG CAA GGC TTG AAA	683
Leu Cys His Ala Cys Gly Ile Lys Ser Ala Glu Val Gln Gly Leu Lys	
195 200 205	
CTG GGT CAA AAC AGC GTG GTG AAA AAC GCT CCT AGA GTG GAA GTG TAT	731
Leu Gly Gln Asn Ser Val Val Lys Asn Ala Pro Arg Val Glu Val Tyr	
210 215 220 225	
TTG AAA GAT TCA TTT CTA GCG TTT GAT TTT CAA AAT AAT CAC AAG GAA	779
Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys Glu	
230 235 240	
GTT TTT ATC CCG TTG AAT CGT CAT AAA GAC ATG CAG TTA GAT TCT GCC	827
Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser Ala	
245 250 255	
TTA TTG GCG ACT TTT GGC GAT GCT TTT GCC CTT GTG GAT GGT AGG GAT	875
Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg Asp	
260 265 270	
TTA GGC AAT TAC GAG AGC AAA CTT TTT GAA AAA AGA GTG TCC TAT ACG	923
Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr Thr	
275 280 285	
ATT GTC TAAAGGCATG AAATCTAGGA ATATTCCTTG ATAGCGGGCT TTCCTTTTGA GG	981
Ile Val	
290	

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

Ala Ile Leu His

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 57...929
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

GTCCTATTTT TTCATTCATT CAACGAATTT AAAAATTACA ATAAAGAGTT ATAGTT ATG      59
                                     Met
                                     1

AAA CGA AGG GAT TTT ATT AAA ACG ACT ACT TTA GGC GCT ACA GGT GCT      107
Lys Arg Arg Asp Phe Ile Lys Thr Thr Leu Gly Ala Thr Gly Ala
          5                      10                      15

GTT TTA GGA GCA CAG ATT TTG CAG GCA GAA GAA AGT AAA GGG AGT GTT      155
Val Leu Gly Ala Gln Ile Leu Gln Ala Glu Glu Ser Lys Gly Ser Val
      20                      25                      30

GCA AAA TAT AAA ATA GAA GCT CAA TAC AGC ATT GAT TTT GAT TCT GCA      203
Ala Lys Tyr Lys Ile Glu Ala Gln Tyr Ser Ile Asp Phe Asp Ser Ala
      35                      40                      45

GAA CAC ACT TCA CTT TTC ATT CCC ATG CCG AGT GTT GTA GCG AGC AAT      251
Glu His Thr Ser Leu Phe Ile Pro Met Pro Ser Val Val Ala Ser Asn
      50                      55                      60                      65

GTG CAT TTA CAA GGC AAT CAT GCT AGC TAT AAA AGC ATG CTC AAT TTT      299
Val His Leu Gln Gly Asn His Ala Ser Tyr Lys Ser Met Leu Asn Phe
          70                      75                      80

GGA GTG CCT TAT TTG CAA GTG GAT TTT TTA AAA AGC ACT CAA AAA AAG      347
Gly Val Pro Tyr Leu Gln Val Asp Phe Leu Lys Ser Thr Gln Lys Lys
          85                      90                      95

CAA GTC CAT TTG TCT TAT GAG ATC GCT AGC TAT CAA TTG AAT GAG CGT      395
Gln Val His Leu Ser Tyr Glu Ile Ala Ser Tyr Gln Leu Asn Glu Arg
      100                      105                      110

```

```

                210                215                220
AAC CCA TTG ACT TTA AAT CGC GCT TCA GCC GAA GAG ATT CAA GAT CAT      781
Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His
                225                230                235

GAA TGC GCG ATT TTG CAC TAAAGCGAGT TAGATTCTTA AGCTTGAGCG ATAACCTT    837
Glu Cys Ala Ile Leu His
                240

TAAAAAGCGT TAT                                                              850

```

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile Val Val
 1          5          10          15
Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile Val Phe
          20          25          30
Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys
          35          40          45
Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp Ile Asn
          50          55          60
Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser Gly Ile
65          70          75          80
Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu
          85          90          95
Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile
          100          105          110
Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser
          115          120          125
Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu Ala Arg
          130          135          140
Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro
145          150          155          160
Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg Val Thr
          165          170          175
Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn Lys Glu
          180          185          190
Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala Val Val
          195          200          205
Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe Asn Pro
          210          215          220
Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys
225          230          235          240

```

ACCACTATTG TAGAAAAATA ACAAGAGGGT TTGCAAAAAC TCTCATTAAA AACAAAGGAGC	60
AAAAAAG ATG AAA AAG GCG GGC TTT CTT TTT TTA GCG GTA ATG GCT ATC	109
Met Lys Lys Ala Gly Phe Leu Phe Leu Ala Val Met Ala Ile	
1 5 10	
GTT GTT ATG AGT TTA AAC GCT AAA GAT CCG AAT GTG TTG CGT AAG ATT	157
Val Val Met Ser Leu Asn Ala Lys Asp Pro Asn Val Leu Arg Lys Ile	
15 20 25 30	
GTT TTT GAG AAA TGT CTG CCT AAT TAT GAG AAA AAT CAG AAT CCT TCG	205
Val Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn Gln Asn Pro Ser	
35 40 45	
CCA TGC ATA GAA GTC AAA CCC GAT GCC GGC TAT GTG GTT TTA AAA GAT	253
Pro Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val Val Leu Lys Asp	
50 55 60	
ATT AAC GGC CCG TTG CAA TAT TTG TTG ATG CCA ACA ACT CAC ATT AGC	301
Ile Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr Thr His Ile Ser	
65 70 75	
GGT ATT GAA AGC CCT TTG TTA CTT GAT CCT TCT ACG CCT AAC TTT TTT	349
Gly Ile Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe	
80 85 90	
TAT TTA TCC TGG CAA GCG CGT GAT TTT ATG AGT AAA AAA TAC GGC CAA	397
Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln	
95 100 105 110	
CCC ATT CCT GAT TAT GCG ATT TCT TTG ACG ATT AAC TCT AGC AAA GGG	445
Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly	
115 120 125	
CGA TCG CAA AAC CAT TTT CAT ATC CAT ATC TCT TGC ATT AGT CTT GAA	493
Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu	
130 135 140	
GCA CGC AAA CAG CTG GAT AAT AAC CTA AAA AAA ATC AAC AGC CGT TGG	541
Ala Arg Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp	
145 150 155	
TCG CCA TTA CCG GGC GGT TTG AAT GGG CAT AAA TAC TTG GCG CGT CGG	589
Ser Pro Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg	
160 165 170	
GTA ACA GAG AGC GAG TTA GTG CAA AAA AGC CCG TTT GTC ATG CTT AAT	637
Val Thr Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn	
175 180 185 190	
AAA GAA GTG CCT AAT GCG TAC AAA CGC ATG GGG GAC TAT GGC TTA GCG	685
Lys Glu Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala	
195 200 205	
GTG GTG CAA CAA AGC GAT AAC TCC TTT GTC TTA TTA GCG ACA CAA TTT	733
Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe	

Thr	Asp	Asn	Asn	Lys	Glu	Tyr	Glu	Gly	Tyr	Glu	Gly	Leu	Ile	Lys	Arg	485	490	495
Leu	Leu	Thr	Glu	Phe	Pro	Leu	Lys	Glu	Pro	Ile	Val	Ser	Glu	Ser	Gln	500	505	510
Lys	Lys	Asp	Phe	Ile	Lys	Leu	Phe	Gly	Lys	Ile	Leu	Lys	Leu	Glu	Asn	515	520	525
Ile	Leu	Asn	Ser	Phe	Glu	Asn	Phe	Lys	Lys	Asp	Asp	Tyr	Ile	Asn	Pro	530	535	540
Arg	Asp	Phe	Gln	Asp	Tyr	Gln	Ser	Lys	Tyr	Leu	Asp	Phe	Tyr	Asp	Ala	545	550	555
Met	Arg	Ser	Glu	Lys	Gly	Lys	Asp	Lys	Glu	Glu	Ile	Asn	Asp	Asp	Leu	565	570	575
Ile	Phe	Glu	Ile	Glu	Leu	Ile	Lys	Gln	Val	Glu	Val	Asn	Ile	Asp	Tyr	580	585	590
Ile	Leu	Asn	Leu	Ile	Glu	Glu	Phe	Ala	Lys	Glu	His	Gly	Val	Glu	Ile	595	600	605
Gln	Gly	Val	Lys	Thr	Lys	Ile	Glu	Pro	Ile	Ile	Asn	Ser	Ser	Ile	Glu	610	615	620
Leu	Arg	Asn	Lys	Lys	Asp	Leu	Ile	Met	Asp	Phe	Ile	Asp	Lys	Tyr	Asn	625	630	635
Lys	Asp	Gln	Glu	Val	His	Ala	His	Phe	Gln	Asp	Tyr	Ile	His	Gln	Lys	645	650	655
Arg	Glu	Glu	Glu	Phe	Gln	Asn	Ile	Ile	Glu	Glu	Asn	Arg	Leu	Asn	Glu	660	665	670
Glu	Lys	Ala	Tyr	Ser	Phe	Met	Gln	His	Ala	Phe	Lys	Gly	Gly	Glu	Ile	675	680	685
Ser	Phe	Ser	Gly	Thr	Glu	Phe	Pro	Lys	Ile	Ile	Glu	Glu	Lys	Pro	Ser	690	695	700
Met	Phe	Gly	Lys	Asn	Ser	Arg	Tyr	Gln	Glu	Val	Lys	Glu	Lys	Val	Ala	705	710	715
Ala	Ser	Leu	Ser	Arg	Phe	Phe	His	Arg	Phe	Cys	Asp	Leu	Thr	Ser	Ala	725	730	735
Ile	Phe	Lys	Lys	Asn	Glu	Val	Lys	Lys	Asp	Glu	Val	Asn	Glu	Lys		740	745	750

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 68...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

	35					40					45				
Thr	Ala	Gln	Asn	Ser	Lys	Thr	Lys	Asn	Gln	Ser	Lys	Gly	Tyr	Ile	Trp
	50					55					60				
His	Thr	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ser	Phe	Lys	Ser	Ala	Thr
65					70					75					80
Leu	Ala	Lys	Glu	Leu	Glu	Ser	Val	Ser	Lys	Val	Leu	Phe	Val	Val	Asp
				85					90					95	
Arg	Lys	Asp	Leu	Asp	Tyr	Gln	Thr	Met	Lys	Glu	Tyr	Asp	Lys	Phe	Gln
			100					105					110		
Lys	Asp	Cys	Ala	Asn	Ser	Asn	Thr	Ser	Thr	Lys	Ile	Leu	Lys	Glu	Gln
		115					120					125			
Leu	Glu	Asp	Ser	Asn	Ala	Lys	Ile	Ile	Ile	Thr	Thr	Ile	Gln	Lys	Leu
	130					135					140				
Asp	Lys	Phe	Val	Lys	Ser	His	Lys	Gly	His	Ala	Ile	Phe	Asn	Glu	Glu
145					150					155					160
Val	Val	Met	Ile	Phe	Asp	Glu	Cys	His	Arg	Ser	Gln	Leu	Gly	Ser	Met
				165					170					175	
His	Gln	Ala	Ile	Thr	Lys	Ala	Phe	Lys	Lys	Tyr	His	Leu	Phe	Gly	Phe
		180						185					190		
Thr	Gly	Thr	Pro	Ile	Phe	Ala	Ala	Asn	Cys	Asp	Lys	Asn	Asn	Pro	Leu
	195						200					205			
Gly	Thr	Thr	Glu	Gln	Lys	Phe	Gly	Lys	Cys	Leu	His	Gln	Tyr	Thr	Ile
	210				215						220				
Ile	Asp	Ala	Ile	Arg	Asp	Lys	Asn	Val	Leu	Pro	Phe	Arg	Val	Glu	Tyr
225					230					235					240
His	Asn	Thr	Ile	Lys	Ala	Lys	Glu	Asp	Ile	Lys	Asp	Asn	Lys	Val	Arg
				245					250					255	
Ala	Val	Asp	Glu	Lys	Asn	Ala	Leu	Leu	Asp	Thr	Arg	Arg	Ile	Lys	Glu
			260					265					270		
Ile	Thr	Lys	Cys	Ile	Leu	Glu	Arg	Phe	Asn	Gln	Ala	Thr	Lys	Asn	Lys
	275						280					285			
Lys	Phe	Asn	Ser	Ile	Leu	Ala	Cys	Ser	Ser	Ile	Glu	Ala	Leu	Lys	Lys
	290					295					300				
Tyr	Tyr	Gln	Ala	Phe	Lys	Glu	Glu	Lys	His	Asp	Leu	Lys	Ile	Ala	Ala
305					310					315					320
Ile	Phe	Ser	Tyr	Ser	Ala	Asn	Glu	Glu	Ile	Asp	Thr	Leu	Glu	Asp	Glu
				325					330					335	
Asn	Asn	Glu	Ser	Ala	Cys	Arg	Leu	Asp	Lys	Ser	Ser	Arg	Asp	Phe	Leu
			340					345					350		
Glu	Gly	Ala	Ile	Ala	Asp	Tyr	Asn	Gly	Met	Phe	Gly	Val	Ser	Phe	Asp
	355						360					365			
Thr	Ser	Asp	Gln	Lys	Phe	Gln	Ser	Tyr	Tyr	Lys	Asp	Leu	Ser	Gln	Lys
	370					375					380				
Met	Lys	Glu	Arg	Lys	Ile	Asp	Leu	Leu	Met	Val	Val	Asn	Met	Phe	Leu
385					390					395					400
Thr	Gly	Phe	Asp	Ala	Thr	Arg	Leu	Asn	Thr	Leu	Trp	Val	Asp	Lys	Asn
				405					410					415	
Leu	Lys	Tyr	His	Gly	Leu	Ile	Gln	Ala	Phe	Ser	Arg	Ala	Asn	Arg	Ile
			420					425					430		
Leu	Asp	Ser	Val	Lys	Thr	His	Gly	Asn	Ile	Val	Cys	Phe	Arg	Asp	Leu
	435						440					445			
Glu	Gln	Asp	Leu	Asn	Asp	Ala	Leu	Met	Leu	Phe	Gly	Asn	Lys	Asp	Ala
	450					455					460				
Gln	Ser	Ile	Ala	Leu	Leu	Arg	Lys	Tyr	Glu	Asp	Tyr	Leu	Lys	Gly	Tyr
465					470					475					480

ATA GAG TTA AGG AAT AAA AAA GAT TTG ATC ATG GAT TTC ATT GAC AAA	2642
Ile Glu Leu Arg Asn Lys Lys Asp Leu Ile Met Asp Phe Ile Asp Lys	
625 630 635	
TAC AAC AAA GAC CAA GAA GTC CAT GCG CAT TTT CAA GAT TAT ATC CAC	2690
Tyr Asn Lys Asp Gln Glu Val His Ala His Phe Gln Asp Tyr Ile His	
640 645 650	
CAA AAA AGA GAA GAG GAA TTC CAA AAT ATC ATA GAA GAA AAC CGC TTG	2738
Gln Lys Arg Glu Glu Glu Phe Gln Asn Ile Ile Glu Glu Asn Arg Leu	
655 660 665 670	
AAT GAA GAA AAA GCC TAT TCG TTC ATG CAG CAT GCC TTT AAA GGG GGC	2786
Asn Glu Glu Lys Ala Tyr Ser Phe Met Gln His Ala Phe Lys Gly Gly	
675 680 685	
GAA ATC AGT TTT AGT GGG ACG GAA TTC CCT AAA ATC ATT GAA GAA AAA	2834
Glu Ile Ser Phe Ser Gly Thr Glu Phe Pro Lys Ile Ile Glu Glu Lys	
690 695 700	
CCC TCC ATG TTT GGT AAA AAT TCG CGC TAT CAA GAG GTG AAA GAA AAA	2882
Pro Ser Met Phe Gly Lys Asn Ser Arg Tyr Gln Glu Val Lys Glu Lys	
705 710 715	
GTC GCT GCA AGC CTT TCT CGT TTT TTC CAC CGC TTT TGT GAT CTC ACT	2930
Val Ala Ala Ser Leu Ser Arg Phe Phe His Arg Phe Cys Asp Leu Thr	
720 725 730	
AGC GCT ATA TTT AAG AAA AAT GAG GTT AAA AAA GAT GAG GTT AAT GAA	2978
Ser Ala Ile Phe Lys Lys Asn Glu Val Lys Lys Asp Glu Val Asn Glu	
735 740 745 750	
AAA TAGTTCATGA ACGCTTTTGC ATTAAGGCTC AAAAAAGCG CCGTTTAATG GATT	3035
Lys	

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met Asp Phe Ala Lys Ala Phe Phe Ala Lys Arg Ser Leu Leu Asn Val	
1 5 10 15	
Leu Thr Cys Tyr Cys Val Phe Thr Ser Glu Glu Val Leu Leu Val Met	
20 25 30	
Arg Pro Tyr Gln Ile Val Ala Ala Glu Arg Ile Leu Glu Lys Ile Lys	

TTT TTG ACC GGG TTT GAC GCT ACA AGG CTC AAC ACC CTT TGG GTG GAT	1970
Phe Leu Thr Gly Phe Asp Ala Thr Arg Leu Asn Thr Leu Trp Val Asp	
400 405 410	
AAA AAT CTC AAA TAC CAT GGG CTA ATT CAA GCT TTT TCA CGC GCA AAC	2018
Lys Asn Leu Lys Tyr His Gly Leu Ile Gln Ala Phe Ser Arg Ala Asn	
415 420 425 430	
CGC ATT TTA GAT AGC GTT AAA ACG CAT GGG AAT ATC GTG TGT TTT AGG	2066
Arg Ile Leu Asp Ser Val Lys Thr His Gly Asn Ile Val Cys Phe Arg	
435 440 445	
GAT TTA GAA CAG GAT TTG AAT GAC GCT CTC ATG CTT TTT GGC AAC AAG	2114
Asp Leu Glu Gln Asp Leu Asn Asp Ala Leu Met Leu Phe Gly Asn Lys	
450 455 460	
GAC GCT CAA TCT ATT GCG CTG TTA AGA AAA TAT GAA GAT TAT TTG AAA	2162
Asp Ala Gln Ser Ile Ala Leu Leu Arg Lys Tyr Glu Asp Tyr Leu Lys	
465 470 475	
GGC TAC ACG GAT AAC AAC AAA GAA TAC GAG GGC TAT GAG GGT TTG ATT	2210
Gly Tyr Thr Asp Asn Asn Lys Glu Tyr Glu Gly Tyr Glu Gly Leu Ile	
480 485 490	
AAA AGG CTT TTA ACC GAA TTC CCA TTA AAA GAG CCA ATC GTT TCA GAA	2258
Lys Arg Leu Leu Thr Glu Phe Pro Leu Lys Glu Pro Ile Val Ser Glu	
495 500 505 510	
AGC CAG AAA AAG GAT TTT ATT AAG CTT TTT GGC AAG ATT TTG AAA TTA	2306
Ser Gln Lys Lys Asp Phe Ile Lys Leu Phe Gly Lys Ile Leu Lys Leu	
515 520 525	
GAA AAT ATT TTA AAC AGC TTT GAA AAT TTC AAA AAA GAC GAT TAC ATC	2354
Glu Asn Ile Leu Asn Ser Phe Glu Asn Phe Lys Lys Asp Asp Tyr Ile	
530 535 540	
AAT CCC AGG GAT TTT CAA GAC TAT CAA AGC AAA TAC CTT GAT TTT TAC	2402
Asn Pro Arg Asp Phe Gln Asp Tyr Gln Ser Lys Tyr Leu Asp Phe Tyr	
545 550 555	
GAT GCA ATG AGA TCA GAA AAA GGG AAG GAT AAA GAA GAG ATT AAT GAT	2450
Asp Ala Met Arg Ser Glu Lys Gly Lys Asp Lys Glu Glu Ile Asn Asp	
560 565 570	
GAT TTG ATT TTT GAA ATT GAA CTC ATC AAA CAA GTG GAA GTC AAT ATT	2498
Asp Leu Ile Phe Glu Ile Glu Leu Ile Lys Gln Val Glu Val Asn Ile	
575 580 585 590	
GAC TAT ATT TTG AAT TTG ATT GAA GAG TTC GCT AAA GAG CAT GGG GTG	2546
Asp Tyr Ile Leu Asn Leu Ile Glu Glu Phe Ala Lys Glu His Gly Val	
595 600 605	
GAA ATC CAA GGC GTT AAA ACC AAA ATA GAG CCA ATC ATC AAC TCC AGC	2594
Glu Ile Gln Gly Val Lys Thr Lys Ile Glu Pro Ile Ile Asn Ser Ser	
610 615 620	

TCT ATG CAT CAA GCC ATC ACT AAA GCG TTT AAA AAA TAC CAC CTT TTT	1298
Ser Met His Gln Ala Ile Thr Lys Ala Phe Lys Lys Tyr His Leu Phe	
175 180 185 190	
GGC TTT ACT GGC ACG CCC ATT TTT GCA GCT AAT TGC GAT AAA AAC AAC	1346
Gly Phe Thr Gly Thr Pro Ile Phe Ala Ala Asn Cys Asp Lys Asn Asn	
195 200 205	
CCT TTA GGC ACG ACA GAG CAA AAG TTT GGG AAA TGC CTC CAC CAA TAC	1394
Pro Leu Gly Thr Thr Glu Gln Lys Phe Gly Lys Cys Leu His Gln Tyr	
210 215 220	
ACC ATT ATT GAT GCG ATC AGG GAT AAA AAC GTT TTG CCC TTT AGA GTG	1442
Thr Ile Ile Asp Ala Ile Arg Asp Lys Asn Val Leu Pro Phe Arg Val	
225 230 235	
GAA TAC CAC AAC ACC ATT AAA GCT AAA GAG GAC ATT AAG GAT AAT AAG	1490
Glu Tyr His Asn Thr Ile Lys Ala Lys Glu Asp Ile Lys Asp Asn Lys	
240 245 250	
GTT AGA GCG GTT GAT GAA AAA AAC GCC CTT TTG GAT ACT AGG AGG ATC	1538
Val Arg Ala Val Asp Glu Lys Asn Ala Leu Leu Asp Thr Arg Arg Ile	
255 260 265 270	
AAA GAA ATC ACT AAA TGC ATT TTA GAG CGT TTC AAT CAA GCC ACT AAA	1586
Lys Glu Ile Thr Lys Cys Ile Leu Glu Arg Phe Asn Gln Ala Thr Lys	
275 280 285	
AAT AAA AAA TTC AAT TCC ATT CTG GCA TGC TCT AGC ATA GAA GCG CTG	1634
Asn Lys Lys Phe Asn Ser Ile Leu Ala Cys Ser Ser Ile Glu Ala Leu	
290 295 300	
AAA AAA TAC TAC CAA GCC TTT AAA GAA GAA AAA CAC GAT CTT AAA ATC	1682
Lys Lys Tyr Tyr Gln Ala Phe Lys Glu Glu Lys His Asp Leu Lys Ile	
305 310 315	
GCT GCC ATT TTT AGC TAT AGC GCT AAT GAG GAA ATT GAC ACG CTA GAA	1730
Ala Ala Ile Phe Ser Tyr Ser Ala Asn Glu Glu Ile Asp Thr Leu Glu	
320 325 330	
GAT GAA AAC AAT GAA AGC GCT TGC CGG CTA GAC AAA AGC TCA AGG GAT	1778
Asp Glu Asn Asn Glu Ser Ala Cys Arg Leu Asp Lys Ser Ser Arg Asp	
335 340 345 350	
TTT TTA GAG GGC GCG ATT GCG GAT TAT AAT GGG ATG TTT GGC GTT TCT	1826
Phe Leu Glu Gly Ala Ile Ala Asp Tyr Asn Gly Met Phe Gly Val Ser	
355 360 365	
TTT GAC ACT TCG GAT CAA AAA TTC CAA AGT TAT TAC AAG GAT CTT TCT	1874
Phe Asp Thr Ser Asp Gln Lys Phe Gln Ser Tyr Tyr Lys Asp Leu Ser	
370 375 380	
CAA AAA ATG AAA GAG CGT AAA ATC GAT CTT TTA ATG GTG GTG AAC ATG	1922
Gln Lys Met Lys Glu Arg Lys Ile Asp Leu Leu Met Val Val Asn Met	
385 390 395	

GAAACGATCG	CAGAAAGCAA	TGAAAGCACG	GTAGTAGCGG	AATTTTCATAG	CAGTAATGAA	60
AAAAAAGCGC	TTATGAGAGC	GAAGCAGAGC	TAGAAAAGGGC	GTTTATTAAG	CTTTTAGAAA	120
AACAAGGCTA	TGAATTTAAA	AAAATCCACA	AAGAAGAAGA	ATTAAAAGAC	AATTTAAAAG	180
AGCAGTTAGA	AAAGCTTAAT	GATCATTCTT	TCACGCCTAA	AGAATGGGAC	ACTCTTTATT	240
CTCAATTCAT	CGCTAATAAA	AACGATGACT	ATAAGGCTAA	AACGAAAAAG	ATCCAAGAAG	300
ATCCGATTTT	TAATCTCACG	CTAGAGAACG	GGAAAACCAA	AAACATTAAA	ATCATTGATA	360
AGAAAAATAT	CCATAGAAAC	GCCTTGCAAG	TGATCCACCA	ATACAGCAAT	AAAGGGGGGA	420
AGTATCAAAA	CCGCTATGAT	GTGAGTATCC	TTGTGAATGG	CTTGCCTTTA	GTGCATGTGG	480
AATTGAAAAA	AAGAGGCGTG	GCGATCAGGG	AGGCGTTCAA	CCAGATCAAG	CGCTATAAAA	540
GGGATAGTTT	TAGCGCTGAA	GACGGGCTTT	TTGATTTTGT	GCAGATTTTT	GTCATCAGTA	600
ACGGCACGAG	CTCTAAATAC	TATTCAAACA	CCACAAGAAT	AGCCCAGCTG	GAAAAAAACC	660
ATAAAGCCGA	TACTTTTGAA	TTCACGAATT	ATTGGGCGGA	TAGCAAGAAT	CACAATATTG	720
AGGATTTA	ATG GAT TTT GCT AAG GCG TTT TTT GCA AAG CGC AGC CTT TTG					770
	Met Asp Phe Ala Lys Ala Phe Phe Ala Lys Arg Ser Leu Leu					
	1	5		10		
AAC GTT TTA ACG TGC TAT TGC GTT TTC ACA AGC GAA GAG GTT TTA TTG						818
Asn Val Leu Thr Cys Tyr Cys Val Phe Thr Ser Glu Glu Val Leu Leu						
15	20		25		30	
GTG ATG CGG CCT TAT CAA ATC GTG GCG GCC GAA AGG ATT TTG GAA AAG						866
Val Met Arg Pro Tyr Gln Ile Val Ala Ala Glu Arg Ile Leu Glu Lys						
	35		40		45	
ATC AAA ACC GCG CAA AAT AGT AAA ACG AAA AAT CAA AGC AAA GGC TAT						914
Ile Lys Thr Ala Gln Asn Ser Lys Thr Lys Asn Gln Ser Lys Gly Tyr						
	50		55		60	
ATC TGG CAC ACG ACA GGG AGC GGT AAA ACC CTA ACG AGC TTT AAA AGC						962
Ile Trp His Thr Thr Gly Ser Gly Lys Thr Leu Thr Ser Phe Lys Ser						
	65		70		75	
GCA ACG TTG GCT AAA GAA TTA GAG AGC GTT TCA AAA GTC TTG TTC GTG						1010
Ala Thr Leu Ala Lys Glu Leu Glu Ser Val Ser Lys Val Leu Phe Val						
	80		85		90	
GTG GAC AGG AAG GAT TTG GAC TAT CAA ACC ATG AAA GAA TAC GAT AAA						1058
Val Asp Arg Lys Asp Leu Asp Tyr Gln Thr Met Lys Glu Tyr Asp Lys						
95	100		105		110	
TTC CAA AAA GAT TGC GCT AAT TCC AAC ACA AGC ACT AAG ATT TTA AAA						1106
Phe Gln Lys Asp Cys Ala Asn Ser Asn Thr Ser Thr Lys Ile Leu Lys						
	115		120		125	
GAA CAG CTT GAA GAT TCT AAC GCT AAA ATC ATT ATC ACC ACG ATC CAA						1154
Glu Gln Leu Glu Asp Ser Asn Ala Lys Ile Ile Ile Thr Thr Ile Gln						
	130		135		140	
AAA TTA GAC AAA TTC GTT AAA TCC CAT AAA GGG CAT GCG ATT TTT AAT						1202
Lys Leu Asp Lys Phe Val Lys Ser His Lys Gly His Ala Ile Phe Asn						
	145		150		155	
GAA GAA GTT GTG ATG ATT TTT GAT GAA TGC CAC AGG AGT CAG TTA GGC						1250
Glu Glu Val Val Met Ile Phe Asp Glu Cys His Arg Ser Gln Leu Gly						
	160		165		170	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Arg Ala Phe Leu Lys Ile Leu Met Val Leu Ile Phe Met Ser Val
 1             5             10             15
Ala Tyr Ala Lys Asn Pro Ser Thr Leu Ser Lys Glu Glu Glu Val Leu
      20             25             30
Gln His Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn
      35             40             45
Glu Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn
      50             55             60
Trp Ala Leu Trp Val Tyr Glu Lys Pro Leu Lys Lys Glu Ile Tyr Met
65             70             75             80
Asn Asp Lys Glu Val Val Ile Tyr Glu Pro Asn Leu Phe Gln Ala Thr
      85             90             95
Ile Thr Pro Leu Lys Asp Lys Thr Asp Phe Phe Thr Ile Leu Lys Arg
      100            105            110
Leu Lys Lys Gln Asp Asp Gly Ser Phe Lys Thr Thr Ile Asn Lys Thr
      115            120            125
Thr Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe
      130            135            140
Lys Asp Gly Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu
145            150            155            160
Ile Asn Pro Thr Ile Ala Asn Glu Ile Phe Val Phe Lys Pro Lys Asp
      165            170            175
Glu Asn Ile Asp Ile Val Arg Gln
      180

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 729...2981
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

TCATGTAAAA TAAAGGGTTT TATTAAAGAT GAGAGATTGT TTTAAGGTTT GAATA ATG	58
Met	
1	
AGA GCT TTT TTA AAG ATT TTA ATG GTT TTG ATT TTT ATG AGC GTT GCT	106
Arg Ala Phe Leu Lys Ile Leu Met Val Leu Ile Phe Met Ser Val Ala	
5 10 15	
TAT GCT AAA AAT CCT TCA ACG CTT TCT AAA GAA GAA GAG GTT TTG CAG	154
Tyr Ala Lys Asn Pro Ser Thr Leu Ser Lys Glu Glu Val Leu Gln	
20 25 30	
CAT TTG CAA AGT TTT AGC GCG CAT TTC AAG CAG GTT TTA AAA AAT GAA	202
His Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn Glu	
35 40 45	
AAA CCT TTA GTT TAT TAC GGG GTT TTA AAG GCT AAA GCC CCT AAT TGG	250
Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn Trp	
50 55 60 65	
GCT TTA TGG GTT TAT GAA AAG CCT TTA AAA AAA GAA ATT TAC ATG AAC	298
Ala Leu Trp Val Tyr Glu Lys Pro Leu Lys Lys Glu Ile Tyr Met Asn	
70 75 80	
GAT AAA GAA GTG GTA ATT TAT GAG CCT AAT TTG TTT CAA GCG ACC ATC	346
Asp Lys Glu Val Val Ile Tyr Glu Pro Asn Leu Phe Gln Ala Thr Ile	
85 90 95	
ACG CCC TTA AAA GAC AAG ACG GAT TTT TTC ACC ATT CTC AAG CGT TTA	394
Thr Pro Leu Lys Asp Lys Thr Asp Phe Phe Thr Ile Leu Lys Arg Leu	
100 105 110	
AAA AAG CAA GAT GAC GGA TCT TTT AAA ACG ACT ATC AAC AAA ACC ACT	442
Lys Lys Gln Asp Asp Gly Ser Phe Lys Thr Thr Ile Asn Lys Thr Thr	
115 120 125	
TAT CGT TTG GTT TTT AAA GAC GGC AAG CCT TTT TCA TTG GAA TTT AAA	490
Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe Lys	
130 135 140 145	
GAT GGA ATG AAC AAT CTT GTA ACG ATC ACT TTT TCT CAA GCA GAA ATC	538
Asp Gly Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu Ile	
150 155 160	
AAC CCC ACC ATT GCT AAT GAA ATC TTT GTT TTT AAG CCT AAA GAT GAA	586
Asn Pro Thr Ile Ala Asn Glu Ile Phe Val Phe Lys Pro Lys Asp Glu	
165 170 175	
AAC ATT GAT ATT GTG CGC CAA TGATTTTAA TGATTCATTG CATCTTGTTA GCAA	641
Asn Ile Asp Ile Val Arg Gln	
180	
AAGTTAGCTA AAATAGAC	659

(2) INFORMATION FOR SEQ ID NO:278:

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

Met Gly Met Leu Ala Thr Val Ile Asn Ala Val Ala Met Gln Glu Ala
 1              5              10              15
Leu Glu His Ile Gly Leu Asp Thr Arg Val Gln Ser Ala Ile Glu Ile
      20              25              30
Lys Glu Ile Cys Glu Ser Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu
      35              40              45
Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe
      50              55              60
Phe Thr Thr Asp Thr Ala Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser
65              70              75              80
Asp Leu Ile Ile Lys Ala Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp
      85              90              95
Pro Asn Lys Phe Lys Asp Ala Lys Lys Leu Asp Thr Leu Ser Tyr Asn
      100             105             110
Asp Ala Leu Ile Gly Asp Ile Glu Val Met Asp Asp Thr Ala Ile Ser
      115             120             125
Leu Ala Lys Asp Asn Lys Leu Pro Ile Val Val Cys Asn Met Phe Lys
      130             135             140
Lys Gly Asn Leu Leu Gln Val Ile Lys His Gln Gln Gly Val Phe Ser
145             150             155             160
Met Val Lys

```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...607
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

GCAAAGATAA AAAACAAACG GGTTTTGGTG AAATTTTCTG GGGAAGCGTT AGCTGGNGGA      60
CAACCAGTTT GGGATTGACA TTCATGTGTT AGATCACATC GCTAAAGAGA TCAAAAGTTT      120
AGTGGAAAAC GATATTGAAG TGGGTATTGT GATTGGTGGA GGCAATATTA TTAGGGGGGT      180
TAGCGCGGCT CAAGGGGGGA TTATTAGGCG CACCAGTGGG GATTAT ATG GGC ATG      235
                                     Met Gly Met
                                     1

TTA GCC ACC GTG ATT AAT GCG GTA GCG ATG CAA GAA GCT TTA GAG CAT      283
Leu Ala Thr Val Ile Asn Ala Val Ala Met Gln Glu Ala Leu Glu His
      5                      10                      15

ATC GGC TTA GAC ACA AGG GTG CAG AGC GCG ATT GAA ATC AAA GAG ATT      331
Ile Gly Leu Asp Thr Arg Val Gln Ser Ala Ile Glu Ile Lys Glu Ile
      20                      25                      30                      35

TGT GAA AGT TAC ATT TAC AGA AAA GCG ATC AGG CAT TTA GAA AAG GGT      379
Cys Glu Ser Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu Glu Lys Gly
                        40                      45                      50

AGG GTG GTG ATT TTT GGC GCA GGC ACG GGA AAC CCG TTT TTC ACT ACG      427
Arg Val Val Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe Phe Thr Thr
                        55                      60                      65

GAT ACG GCT GCC ACT TTA AGA GCG ATT GAA ATT GGA TCG GAT TTA ATC      475
Asp Thr Ala Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser Asp Leu Ile
      70                      75                      80

ATT AAA GCG ACT AAA GTG GAT GGC ATT TAC GAC AAA GAT CCT AAC AAG      523
Ile Lys Ala Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp Pro Asn Lys
      85                      90                      95

TTT AAA GAC GCT AAA AAA TTA GAC ACT TTA AGC TAT AAC GAT GCC TTG      571
Phe Lys Asp Ala Lys Lys Leu Asp Thr Leu Ser Tyr Asn Asp Ala Leu
      100                      105                      110                      115

ATA GGG GAT ATT GAA GTG ATG GAC GAT ACC GCT ATT TCT TTA GCT AAA      619
Ile Gly Asp Ile Glu Val Met Asp Asp Thr Ala Ile Ser Leu Ala Lys
                        120                      125                      130

GAC AAT AAG CTC CCC ATT GTG GTG TGT AAC ATG TTC AAA AAA GGG AAT      667
Asp Asn Lys Leu Pro Ile Val Val Cys Asn Met Phe Lys Lys Gly Asn
                        135                      140                      145

TTA TTG CAA GTG ATC AAG CAC CAA CAA GGC GTA TTT TCT ATG GTA AAA T      716
Leu Leu Gln Val Ile Lys His Gln Gln Gly Val Phe Ser Met Val Lys
      150                      155                      160

AAGCCCTTTA ACATTGGATA GAACTCAAAA TAAAAGGATC AGTTTGAAAA AAGAG      771

```

```

Pro Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala
 130                      135                      140
Asp Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys
145                      150                      155                      160
Lys Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys
                      165                      170                      175
Ser Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys
                      180                      185                      190
Tyr Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu
                      195                      200                      205
Thr Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala
                      210                      215                      220
Ile Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu
225                      230                      235                      240
Arg Ala Lys Ala Glu Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala
                      245                      250                      255
Met Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu
                      260                      265                      270
Lys Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg
                      275                      280                      285
Leu Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser
                      290                      295                      300
Val Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala
305                      310                      315                      320
His Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe
                      325                      330                      335
Val Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu
                      340                      345                      350
Ser Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala
                      355                      360                      365
Gly Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile
                      370                      375                      380
Ile Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro
385                      390                      395                      400
Ile Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr
                      405                      410                      415
Lys Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr
                      420                      425                      430
Asn Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro
                      435                      440                      445

```

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 227...715
- (D) OTHER INFORMATION:


```

TAT TTA GGG GAT TGT GAG ATA GGG AAA AAC ACA AAT GTA GGG GCT GGC      1162
Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala Gly
   355                               360                               365

GTG ATC ACT TGC AAT TAC GAT GGT AAA AAG AAA CAC CAA ACA ATC ATC      1210
Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile Ile
   370                               375                               380                               385

GGT GAA AAT GTC TTT ATA GGG AGC GAT AGC CAG CTA GTC GCC CCC ATA      1258
Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro Ile
           390                               395                               400

AAT ATC GGC TCT AAT GTC TTA ATC GGC AGC GGC ACC ACT ATC ACT AAA      1306
Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr Lys
           405                               410                               415

GAC ATT CCT AGC GGT TCG TTG AGC CTT TCA CGC GCC CCT CAA ACC AAC      1354
Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr Asn
           420                               425                               430

ATT GAA AAC GGG TAT TTT AAG TTT TTT AAG AAA CCT TAATTTGTTT GAATAA  1406
Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro
   435                               440                               445

TGAAAAATCC TAAAAATATTA ATCATTTACT TTAA                                1440

```

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```

Met Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val
  1             5             10             15
Ile Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro
           20             25             30
Lys Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu
           35             40             45
Glu Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His
           50             55             60
Gln Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val
           65             70             75             80
Ile Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala
           85             90             95
Ile Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val
           100            105            110
Leu Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala
           115            120            125

```

TTA TTA GAA AGC AAG AAT AAC GCT ATA GGC TTA CTC CAT TTA GCT GAC Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala Asp 130 135 140 145	490
CCT AAA GGT TAT GGG CGC GTT GTT TTA GAA AAC CAT CAG GTT AAA AAG Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys Lys 150 155 160	538
ATT GTA GAA GAA AAG GAC GCT AAT GAT GAA GAA AAA GAA ATT AAA AGC Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys Ser 165 170 175	586
GTG AAT GCT GGC GTG TAT GGG TTT GAA AGG GAT TTT TTA GAA AAA TAC Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys Tyr 180 185 190	634
TTA CCC AAG CTC CAT GAC CAA AAC GCC CAA AAA GAA TAC TAC CTC ACG Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu Thr 195 200 205	682
GAT TTA ATC GCT CTA GGG ATC AAT GAA AAC GAA ACA ATT GAC GCT ATT Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala Ile 210 215 220 225	730
TTC TTA AAA GAA GAG TGT TTT TTA GGG GTG AAT AGC CAA ACA GAA AGG Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu Arg 230 235 240	778
GCG AAA GCT GAA GAA ATC ATG CTA GAA AGA CTG CGC AAA AAC GCC ATG Ala Lys Ala Glu Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala Met 245 250 255	826
GAC TTG GGG GTA GTG ATG CAA TTG CCT AAT AGC ATT TAT TTA GAA AAA Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu Lys 260 265 270	874
GGC GTG AGT TTT AAG GGG GAG TGC GTT TTA GAG CAA GGG GTG CGT TTG Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg Leu 275 280 285	922
ATT GGG AAT TGT TTG ATA GAA AAC GCG CAT ATT AAG GCT TAT AGC GTG Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser Val 290 295 300 305	970
ATA GAA GAG AGC CAG ATT GTT AAT AGC AGT GTG GGG CCG TTT GCC CAT Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala His 310 315 320	1018
GCG CGC CCT AAA AGC GTG ATT TGT AAT AGC CAT GTG GGG AAT TTT GTA Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe Val 325 330 335	1066
GAG ACT AAA AAC GCT AAA CTT CAA GGC ACT AAA GCA GGG CAT TTG AGC Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu Ser 340 345 350	1114

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...1390
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

GCAAAATTCT AGCCTTAAAT CTTTGATGAA ACGAAGTCAA ATTATAAGAT AAGGC ATG      58
                                         Met
                                         1

TTA AAA TTC CCT AAA ATG AGT TTA AGG ATT TTA ATG CTT TCT GTC ATC      106
Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val Ile
          5                      10                      15

ATA CTG GCC GCT GGT AAA GGC ACT CGC ATG CGT TCT AGC CTG CCT AAA      154
Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro Lys
          20                      25                      30

ACT TTA CAC ACC ATT TGT GGG GAG CCT ATG TTG TTT TAC ATT TTA GAA      202
Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu Glu
          35                      40                      45

ACG GCT TTT TCA ATC AGC GAT GAT GTG CAT CTT ATC TTA CAC CAC CAA      250
Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His Gln
          50                      55                      60                      65

CAA GAA CGC ATT AAA GAA GCG GTG TTG GAG CGT TTT AAG GGC GTC ATT      298
Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val Ile
          70                      75                      80

TTT CAC ACT CAA ATT GTG GAA AAA TAT TCA GGG ACA GGT GGG GCT ATC      346
Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala Ile
          85                      90                      95

ATG CAA AAA GAT AAA ACG CCT ATT TCT ACG AAA CAT GAG CGG GTT TTG      394
Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val Leu
          100                     105                     110

ATT TTG AAT GCG GAC ATG CCT TTA ATC ACT AAA GAC GCT CTC GCC CCC      442
Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala Pro
          115                     120                     125

```

Glu Leu Tyr Gly Gln Asp Phe Glu Lys Arg Tyr Leu Glu Tyr Glu Lys
 195 200 205
 Asp Pro Lys Ile Ile Lys Glu Tyr Ile Asn Ala Lys Asp Leu Trp Lys
 210 215 220
 Lys Ile Leu Met Asn Tyr Phe Glu Ala Gly Leu Pro Phe Leu Ala Phe
 225 230 235 240
 Lys Asp Asn Ala Asn Arg Cys Asn Pro Asn Ala His Ala Gly Ile Ile
 245 250 255
 Arg Ser Ser Asn Leu Cys Thr Glu Ile Phe Gln Asn Thr Ala Pro Asn
 260 265 270
 His Tyr Tyr Met Gln Ile Glu Tyr Thr Asp Gly Thr Ile Glu Phe Phe
 275 280 285
 Glu Glu Lys Glu Leu Val Thr Thr Asp Ser Asn Ile Thr Lys Cys Ala
 290 295 300
 Asn Lys Leu Thr Ser Thr Asp Ile Leu Lys Gly Lys Pro Ile Tyr Ile
 305 310 315 320
 Ala Thr Lys Val Ala Lys Asp Gly Gln Thr Ala Val Cys Asn Leu Ala
 325 330 335
 Ser Ile Asn Leu Ser Lys Ile Asn Thr Glu Glu Asp Ile Lys Arg Val
 340 345 350
 Val Pro Ile Met Val Arg Leu Leu Asp Asn Val Ile Asp Leu Asn Phe
 355 360 365
 Tyr Pro Asn Arg Lys Val Lys Ala Thr Asn Leu Gln Asn Arg Ala Ile
 370 375 380
 Gly Leu Gly Val Met Gly Glu Ala Gln Met Leu Ala Glu His Gln Ile
 385 390 395 400
 Ala Trp Gly Ser Lys Glu His Leu Glu Lys Ile Asp Ala Leu Met Glu
 405 410 415
 Gln Ile Ser Tyr His Ala Ile Asp Thr Ser Ala Asn Leu Ala Lys Glu
 420 425 430
 Lys Gly Val Tyr Lys Asp Phe Glu Asn Ser Glu Trp Ser Lys Gly Ile
 435 440 445
 Phe Pro Ile Asp Lys Ala Asn Asn Glu Ala Leu Lys Leu Thr Glu Lys
 450 455 460
 Gly Leu Phe Asn His Ala Cys Asp Trp Gln Gly Leu Arg Glu Lys Val
 465 470 475 480
 Lys Ala Asn Gly Met Arg Asn Gly Tyr Leu Met Ala Ile Ala Pro Thr
 485 490 495
 Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu Pro Ile
 500 505 510
 Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile Pro Val
 515 520 525
 Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr Ser Ala
 530 535 540
 Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Val Arg Gln
 545 550 555 560
 Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg Ile Glu
 565 570 575
 Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala Trp Lys
 580 585 590
 Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro Ser Ile
 595 600 605
 Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn Cys Gln
 610 615 620

ATA GAA AAC GCC AGC GGT AAA ACC TTG CAT GAC ATC TAC ACG CTC GCT 2317
 Ile Glu Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala
 575 580 585 590

TGG AAA TTA GGA CTC AAA TCC ACT TAT TAT TTG CGC AGC GAA AGC CCT 2365
 Trp Lys Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro
 595 600 605

AGC ATA GAT GAA AAA AGC GTG TTG GAT CGA TCG GTG GAG TGT TTT AAT 2413
 Ser Ile Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn
 610 615 620

TGC CAA TAATATAAGC TTAAATAAGC TAATCTTTGC TAAAATGAGA TTTAAAATTA TT 2471
 Cys Gln

TA 2473

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Met	Phe	Met	Ser	Ile	Ala	Met	Phe	Leu	Ala	Gln	Asn	Glu	Gln	Glu	Pro
1				5				10					15		
Asn	Lys	Ile	Ala	Leu	Glu	Phe	Tyr	Glu	Val	Leu	Ser	Lys	Phe	Glu	Ala
			20					25					30		
Met	Cys	Ala	Thr	Pro	Thr	Leu	Ala	Asn	Ala	Arg	Thr	Thr	Lys	His	Gln
		35				40				45					
Leu	Ser	Ser	Cys	Tyr	Ile	Gly	Ser	Thr	Pro	Asp	Asn	Ile	Glu	Gly	Ile
	50					55				60					
Phe	Asp	Ser	Tyr	Lys	Glu	Met	Ala	Leu	Leu	Ser	Lys	Tyr	Gly	Gly	Gly
65					70					75				80	
Ile	Gly	Trp	Asp	Phe	Ser	Leu	Val	Arg	Ser	Ile	Gly	Ser	Tyr	Ile	Asp
			85					90						95	
Gly	His	Lys	Asn	Ala	Ser	Ala	Gly	Thr	Ile	Pro	Phe	Leu	Lys	Ile	Ala
			100					105					110		
Asn	Asp	Val	Ala	Ile	Ala	Val	Asp	Gln	Leu	Gly	Thr	Arg	Lys	Gly	Ala
		115						120					125		
Ile	Ala	Val	Tyr	Leu	Glu	Ile	Trp	His	Ile	Asp	Val	Met	Glu	Phe	Ile
	130						135					140			
Asp	Leu	Arg	Lys	Asn	Ser	Gly	Asp	Glu	Arg	Arg	Ala	His	Asp	Leu	
145				150					155					160	
Phe	Pro	Ala	Leu	Trp	Val	Cys	Asp	Leu	Phe	Leu	Lys	Arg	Val	Leu	Glu
			165						170					175	
Asp	Ala	Met	Trp	Thr	Leu	Phe	Asp	Pro	Tyr	Glu	Cys	Lys	Asp	Leu	Thr
			180					185						190	

Arg Val Val Pro Ile Met Val Arg Leu Leu Asp Asn Val Ile Asp Leu	
355 360 365	
AAT TTC TAC CCT AAC CGC AAA GTC AAA GCC ACT AAT TTA CAA AAT AGG	1693
Asn Phe Tyr Pro Asn Arg Lys Val Lys Ala Thr Asn Leu Gln Asn Arg	
370 375 380	
GCC ATA GGG TTA GGG GTT ATG GGT GAA GCG CAA ATG CTC GCA GAA CAC	1741
Ala Ile Gly Leu Gly Val Met Gly Glu Ala Gln Met Leu Ala Glu His	
385 390 395	
CAA ATC GCT TGG GGG TCT AAA GAG CAT TTA GAA AAA ATT GAC GCT TTA	1789
Gln Ile Ala Trp Gly Ser Lys Glu His Leu Glu Lys Ile Asp Ala Leu	
400 405 410	
ATG GAG CAA ATC AGC TAC CAT GCG ATT GAC ACG AGC GCG AAT TTA GCG	1837
Met Glu Gln Ile Ser Tyr His Ala Ile Asp Thr Ser Ala Asn Leu Ala	
415 420 425 430	
AAA GAA AAA GGG GTT TAT AAG GAT TTT GAA AAT TCA GAA TGG AGT AAG	1885
Lys Glu Lys Gly Val Tyr Lys Asp Phe Glu Asn Ser Glu Trp Ser Lys	
435 440 445	
GGG ATT TTC CCC ATT GAT AAA GCC AAT AAT GAA GCC TTA AAG CTC ACC	1933
Gly Ile Phe Pro Ile Asp Lys Ala Asn Asn Glu Ala Leu Lys Leu Thr	
450 455 460	
GAA AAA GGG CTT TTT AAT CAC GCT TGC GAT TGG CAA GGT TTG AGG GAA	1981
Glu Lys Gly Leu Phe Asn His Ala Cys Asp Trp Gln Gly Leu Arg Glu	
465 470 475	
AAA GTC AAA GCC AAT GGC ATG CGT AAT GGC TAT TTA ATG GCG ATC GCT	2029
Lys Val Lys Ala Asn Gly Met Arg Asn Gly Tyr Leu Met Ala Ile Ala	
480 485 490	
CCC ACA AGC TCC ATT TCT ATT TTA GTA GGC ACA ACC CAA ACG ATT GAA	2077
Pro Thr Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu	
495 500 505 510	
CCC ATT TAT AAG AAA AAA TGG TTT GAA GAA AAT TTG AGC GGG CTT ATT	2125
Pro Ile Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile	
515 520 525	
CCT GTT GTG GTG CCT AAT TTG AAT GTA GAA ACC TGG AAT TTT TAC ACA	2173
Pro Val Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr	
530 535 540	
TCA GCC TAT GAT ATT GAC GCT AAA GAT TTG ATT AAA GCA GCG GCC GTG	2221
Ser Ala Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Ala Val	
545 550 555	
CGC CAA AAG TGG ATT GAT CAA GGC CAA AGC CTT AAT GTG TTT TTA CGC	2269
Arg Gln Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg	
560 565 570	

130	135	140	
TTC ATT GAT TTA AGG AAA AAT AGC GGC GAT GAA AGG CGA AGA GCG CAT			1021
Phe Ile Asp Leu Arg Lys Asn Ser Gly Asp Glu Arg Arg Arg Ala His			
145	150	155	
GAT TTA TTC CCG GCT CTT TGG GTG TGC GAT TTG TTT TTG AAA AGG GTT			1069
Asp Leu Phe Pro Ala Leu Trp Val Cys Asp Leu Phe Leu Lys Arg Val			
160	165	170	
TTA GAA GAT GCG ATG TGG ACT TTA TTT GAC CCT TAT GAG TGT AAG GAT			1117
Leu Glu Asp Ala Met Trp Thr Leu Phe Asp Pro Tyr Glu Cys Lys Asp			
175	180	185	190
TTG ACT GAG CTT TAT GGG CAG GAT TTT GAA AAA CGC TAT TTA GAG TAT			1165
Leu Thr Glu Leu Tyr Gly Gln Asp Phe Glu Lys Arg Tyr Leu Glu Tyr			
195	200	205	
GAA AAA GAT CCC AAG ATC ATT AAG GAA TAC ATT AAC GCT AAA GAT TTA			1213
Glu Lys Asp Pro Lys Ile Ile Lys Glu Tyr Ile Asn Ala Lys Asp Leu			
210	215	220	
TGG AAA AAA ATC TTA ATG AAT TAT TTT GAA GCC GGT TTG CCT TTC TTA			1261
Trp Lys Lys Ile Leu Met Asn Tyr Phe Glu Ala Gly Leu Pro Phe Leu			
225	230	235	
GCC TTT AAA GAT AAC GCC AAT CGG TGC AAC CCA AAC GCT CAT GCA GGA			1309
Ala Phe Lys Asp Asn Ala Asn Arg Cys Asn Pro Asn Ala His Ala Gly			
240	245	250	
ATC ATT CGA TCC AGC AAT CTA TGC ACG GAG ATT TTC CAA AAT ACC GCG			1357
Ile Ile Arg Ser Ser Asn Leu Cys Thr Glu Ile Phe Gln Asn Thr Ala			
255	260	265	270
CCT AAC CAC TAC TAC ATG CAA ATA GAA TAC ACC GAC GGC ACC ATA GAG			1405
Pro Asn His Tyr Tyr Met Gln Ile Glu Tyr Thr Asp Gly Thr Ile Glu			
275	280	285	
TTT TTT GAA GAA AAA GAG TTG GTA ACG ACA GAT AGT AAT ATC ACT AAA			1453
Phe Phe Glu Glu Lys Glu Leu Val Thr Thr Asp Ser Asn Ile Thr Lys			
290	295	300	
TGC GCT AAC AAG CTC ACT AGC ACC GAT ATT CTA AAG GGC AAG CCA ATC			1501
Cys Ala Asn Lys Leu Thr Ser Thr Asp Ile Leu Lys Gly Lys Pro Ile			
305	310	315	
TAT ATC GCT ACT AAA GTC GCT AAA GAC GGG CAA ACG GCG GTG TGC AAT			1549
Tyr Ile Ala Thr Lys Val Ala Lys Asp Gly Gln Thr Ala Val Cys Asn			
320	325	330	
CTG GCG AGC ATC AAT TTA AGC AAA ATC AAC ACT GAA GAA GAC ATT AAA			1597
Leu Ala Ser Ile Asn Leu Ser Lys Ile Asn Thr Glu Glu Asp Ile Lys			
335	340	345	350
AGG GTT GTG CCG ATC ATG GTC AGG CTT TTA GAC AAT GTG ATT GAT TTG			1645

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 548...2419

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GATACAATTC CAAATTTAAA AAACAAACGA TTTAATTCAA ATTTAAGGAA AAATTTTGAT	60
TACAGTGGTT AAACGAAACG GGCGCATTGA GCCTTTGGAC ATTACCAAAA TCCAAAAATA	120
CACTAAGGAC GCTACGGACA ATTTAGAGGG CGTGAGCCAA AGTGAGCTGG AAGTGGATGC	180
GAGGTTGCAA TTCAGGGACA AGATCACTAC TGAAGAAATC CAACAAACTT TGATTAAAAC	240
CGCTGTGGAT AAGATAGATA TTGACACGCC TAATTGGAGT TTTGTCGCCT CAAGGCTTTT	300
TTTGTATGAT TTATACCATA AAGTAAGTGG TTTTACAGGG TATAGGCATT TGAAAGAGTA	360
TTTTGAAAAC GCTGAAGAAA AGGGCCGCAT CCTTAAGGGC TTTAAGGAAA AATTTGATCT	420
AGAGTTTTTTA AATAGCCAGA TCAAGCCTGA AAGGGATTTT CAATTCAATT ATTTAGGGAT	480
TAAAACCTTG TATGATCGCT ATTTGTTAAA AGACGCTAAC AACAACCCTA TTGAATTGCC	540
CCAACAC ATG TTT ATG AGC ATT GCG ATG TTT TTA GCA CAA AAC GAA CAA	589
Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln	
1 5 10	
GAA CCC AAT AAA ATC GCC TTA GAA TTT TAT GAA GTT TTG AGC AAG TTT	637
Glu Pro Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe	
15 20 25 30	
GAA GCG ATG TGC GCG ACC CCC ACT CTA GCG AAC GCC CGC ACC ACC AAA	685
Glu Ala Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys	
35 40 45	
CAC CAG CTC AGC TCA TGC TAT ATT GGC AGC ACG CCG GAT AAT ATT GAG	733
His Gln Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu	
50 55 60	
GGG ATT TTT GAC AGC TAT AAG GAA ATG GCG CTG TTG TCC AAA TAC GGC	781
Gly Ile Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly	
65 70 75	
GGA GGG ATT GGC TGG GAT TTT TCT TTG GTG CGC TCT ATT GGG AGT TAT	829
Gly Gly Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr	
80 85 90	
ATT GAT GGG CAT AAA AAT GCG AGC GCT GGC ACG ATC CCT TTT TTA AAA	877
Ile Asp Gly His Lys Asn Ala Ser Ala Gly Thr Ile Pro Phe Leu Lys	
95 100 105 110	
ATC GCT AAC GAT GTG GCG ATT GCG GTG GAT CAA TTA GGC ACA CGA AAG	925
Ile Ala Asn Asp Val Ala Ile Ala Val Asp Gln Leu Gly Thr Arg Lys	
115 120 125	
GGC GCG ATT GCG GTG TAT TTG GAA ATT TGG CAC ATT GAT GTG ATG GAG	973
Gly Ala Ile Ala Val Tyr Leu Glu Ile Trp His Ile Asp Val Met Glu	

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```

Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser Ser Trp Val Gly
 1           5           10           15
Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile Ala Gln Ala Phe
          20           25           30
Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr Glu Gly Asp Met
          35           40           45
Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile Pro Lys Ile Pro
          50           55           60
Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu
65           70           75           80
Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro
          85           90           95
Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly
          100          105          110
Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe
          115          120          125
Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala
          130          135          140
Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn Pro Tyr Lys
145          150          155          160
Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His
          165          170          175
Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn Ile Ser Met
          180          185          190
Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn
          195          200          205
Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn Ser Ser Asp
          210          215          220
Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val Gly Ser Pro
225          230          235          240
Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser Leu Glu Met Asp
          245          250          255
Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg Trp Glu Arg Met
          260          265          270
Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys Lys Glu Asn Ala
          275          280          285
Thr His
290

```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2473 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

TTT GCC ATT GGA GGC GAT GAG GTG TTG TTC ACT AAT GAG GGT TTT TAT	445
Phe Ala Ile Gly Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr	
110 115 120	
TTG CAC CCT TTT GAG AGC GAC ACG GAC AAA AAT TAC ATC GCT AAA CAT	493
Leu His Pro Phe Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His	
125 130 135 140	
TAC CCT AAC GCC ATG ACA AAA GAA TTT ATG GGT AAA ATT TTT GTT TTA	541
Tyr Pro Asn Ala Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu	
145 150 155	
AAC CCT TAT AAA AAT GAG CAT CCG GGT ATC CAT TAC CAA AAA GAC AAT	589
Asn Pro Tyr Lys Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn	
160 165 170	
GAA ACC TTC CAC TTA ATG GAG CAA TTA GCC ACT CAA GGC GCA GAA GCT	637
Glu Thr Phe His Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala	
175 180 185	
AAT ATC AGC ATG CAA CTC ATT CAA ATG GAG GGC GAA AAG GTG TTT TAT	685
Asn Ile Ser Met Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr	
190 195 200	
AAG AAA ATC AAT GAC GAT GAA TTT TTC ATG ATC GGC GAC AAC AGA GAC	733
Lys Lys Ile Asn Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp	
205 210 215 220	
AAT TCT AGC GAC TCG CGC TTT TGG GGG AGT GTG GCT TAT AAA AAC ATC	781
Asn Ser Ser Asp Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile	
225 230 235	
GTG GGT TCG CCA TGG TTT GTT TAT TTC AGT TTG AGT TTA AAA AAT AGC	829
Val Gly Ser Pro Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser	
240 245 250	
CTA GAA ATG GAT GCA GAA AAT AAC CCT AAA AAA CGC TAT CTG GTG CGT	877
Leu Glu Met Asp Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg	
255 260 265	
TGG GAA CGC ATG TTT AAA AGC GTT GGA GGC TTA GAA AAA ATC ATT AAA	925
Trp Glu Arg Met Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys	
270 275 280	
AAA GAA AAC GCA ACG CAT TAAGGTTTTT TGTGCAATTT TTTGATTCTT CTTTAGAA	981
Lys Glu Asn Ala Thr His	
285 290	
AGTTTTTATTA CCAC	995

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

	420		425		430
Gln Glu Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu					
	435		440		445
Ala Gly Lys Lys					
450					

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 74...943
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GGCCTATGAC GATTGTCTCG CTTTGTAGAAA ACACTCTAAT CGCTTTTGAA AAACAACAAA	60
GGAAGGGATT TTA ATG AAA TTT TTA CGC TCT GTT TAT GCA TTT TGC TCC	109
Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser	
1 5 10	
AGT TGG GTA GGG ACG ATT GTT ATT GTG CTG TTG GTT ATC TTT TTT ATC	157
Ser Trp Val Gly Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile	
15 20 25	
GCG CAA GCC TTT ATC ATT CCC TCT CGC TCT ATG GTT GGC ACG CTC TAT	205
Ala Gln Ala Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr	
30 35 40	
GAG GGC GAC ATG CTC TTT GTC AAA AAG TTT TCT TAC GGC ATA CCC ATT	253
Glu Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile	
45 50 55 60	
CCT AAA ATC CCA TGG ATT GAG CTT CCT GTT ATG CCT GAT TTT AAA AAT	301
Pro Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn	
65 70 75	
AAC GGA CAT TTG ATA GAG GGG GAT CGC CCT AAG CGT GGC GAA GTG GTG	349
Asn Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val	
80 85 90	
GTG TTT ATC CCT CCC CAT GAA AAA AAG TCT TAC TAT GTT AAA AGG AAT	397
Val Phe Ile Pro Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn	
95 100 105	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```

Met Leu Arg Leu Leu Ile Gly Leu Leu Leu Met Ser Phe Ile Ser Leu
 1           5           10           15
Gln Ser Ala Ser Trp Gln Glu Pro Leu Arg Val Ser Ile Glu Phe Val
 20           25           30
Asp Leu Pro Lys Lys Ile Ile Arg Phe Pro Ala His Asp Leu Gln Val
 35           40           45
Gly Glu Phe Gly Phe Val Val Thr Lys Leu Ser Asp Tyr Glu Ile Val
 50           55           60
Asn Ser Glu Val Val Ile Ile Ala Val Glu Asn Gly Val Ala Thr Ala
 65           70           75           80
Lys Phe Arg Ala Phe Glu Ser Met Lys Gln Arg His Leu Pro Thr Pro
 85           90           95
Arg Met Val Ala Arg Lys Gly Asp Leu Val Tyr Phe Arg Gln Phe Asn
 100          105          110
Asn Gln Ala Phe Leu Ile Ala Pro Asn Asp Glu Leu Tyr Glu Gln Ile
 115          120          125
Arg Ala Thr Asn Thr Asp Ile Asn Phe Ile Ser Ser Asp Leu Leu Val
 130          135          140
Thr Phe Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu Arg Lys Ala
 145          150          155          160
Cys Asn Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr Thr Asn Thr
 165          170          175
Leu Asn Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu Lys Arg Glu
 180          185          190
Leu Asp Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe Phe Ser Arg
 195          200          205
Val Glu Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe Ser Gly Ser
 210          215          220
Gln Ser Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val Lys Lys Glu
 225          230          235          240
Lys Arg Lys Glu Val Arg Ile Lys Lys Arg Glu Glu Lys Ile Asp Ser
 245          250          255
Arg Glu Ile Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys Glu Pro Lys
 260          265          270
Lys Ala Asn Gln Gly Thr Gln Asn Ala Pro Thr Leu Glu Glu Lys Asn
 275          280          285
Tyr Gln Lys Ala Glu Arg Lys Leu Asp Ala Lys Glu Glu Arg Arg Tyr
 290          295          300
Leu Arg Asp Glu Arg Lys Lys Ala Lys Ala Thr Lys Lys Ala Met Glu
 305          310          315          320
Phe Glu Glu Arg Glu Lys Glu His Asp Glu Arg Asp Glu Gln Glu Thr
 325          330          335
Glu Gly Arg Arg Lys Ala Leu Glu Met Asp Lys Gly Asp Lys Lys Glu
 340          345          350
Glu Arg Val Lys Pro Lys Glu Asn Glu Arg Glu Ile Lys Gln Glu Ala
 355          360          365
Ile Lys Glu Pro Ser Asp Gly Asn Asn Ala Thr Gln Gln Gly Glu Lys
 370          375          380
Gln Asn Ala Pro Lys Glu Asn Asn Ala Gln Lys Glu Glu Asn Lys Pro
 385          390          395          400
Asn Ser Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala
 405          410          415
Lys Ala Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala Arg Glu His

```

AAA GCA GAG CGC AAA CTT GAT GCT AAA GAA GAA AGG CGT TAT TTG AGA	968
Lys Ala Glu Arg Lys Leu Asp Ala Lys Glu Glu Arg Arg Tyr Leu Arg	
295 300 305	
GAT GAA AGG AAA AAA GCC AAA GCC ACC AAA AAG GCT ATG GAA TTT GAA	1016
Asp Glu Arg Lys Lys Ala Lys Ala Thr Lys Lys Ala Met Glu Phe Glu	
310 315 320	
GAA AGA GAA AAA GAG CAT GAT GAA AGG GAC GAA CAA GAG ACT GAA GGA	1064
Glu Arg Glu Lys Glu His Asp Glu Arg Asp Glu Gln Glu Thr Glu Gly	
325 330 335	
AGA AGA AAA GCT TTA GAA ATG GAT AAA GGC GAT AAA AAA GAA GAA AGA	1112
Arg Arg Lys Ala Leu Glu Met Asp Lys Gly Asp Lys Lys Glu Glu Arg	
340 345 350	
GTC AAA CCC AAA GAA AAT GAG CGA GAA ATC AAG CAA GAA GCC ATT AAA	1160
Val Lys Pro Lys Glu Asn Glu Arg Glu Ile Lys Gln Glu Ala Ile Lys	
355 360 365 370	
GAG CCA AGT GAT GGA AAT AAC GCC ACC CAA CAA GGC GAA AAA CAA AAC	1208
Glu Pro Ser Asp Gly Asn Asn Ala Thr Gln Gln Gly Glu Lys Gln Asn	
375 380 385	
GCT CCT AAA GAG AAC AAC GCT CAA AAA GAA GAG AAT AAA CCA AAT TCT	1256
Ala Pro Lys Glu Asn Asn Ala Gln Lys Glu Glu Asn Lys Pro Asn Ser	
390 395 400	
AAA GAA GAA AAA CGC CGC TTG AAA GAA GAA AAG AAA AAA GCC AAA GCC	1304
Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala Lys Ala	
405 410 415	
GAA CAA AGA GCG AGA GAA TTT GAA CAA AGA GCG AGA GAG CAT CAA GAA	1352
Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala Arg Glu His Gln Glu	
420 425 430	
AGA GAT GAA AAA GAG CTT GAA GAG CGA AGA AAG GCG CTA GAA GCG GGT	1400
Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu Ala Gly	
435 440 445 450	
AAA AAA TAACATGTTA GACCAACAAC ACATCCAATA CTTTAAAAAC CTAGTAGGGG GA	1458
Lys Lys	
G	1459

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

GAA GTG GTC ATT ATT GCC GTT GAA AAT GGC GTC GCA ACG GCT AAA TTC	296
Glu Val Val Ile Ile Ala Val Glu Asn Gly Val Ala Thr Ala Lys Phe	
70 75 80	
AGA GCG TTT GAG TCT ATG AAA CAA AGG CAT TTA CCC ACT CCA AGA ATG	344
Arg Ala Phe Glu Ser Met Lys Gln Arg His Leu Pro Thr Pro Arg Met	
85 90 95	
GTC GCT AGA AAG GGT GAT TTA GTC TAT TTT AGG CAA TTC AAC AAC CAA	392
Val Ala Arg Lys Gly Asp Leu Val Tyr Phe Arg Gln Phe Asn Asn Gln	
100 105 110	
GCG TTT TTA ATC GCT CCT AAT GAT GAA CTC TAT GAG CAA ATC AGA GCG	440
Ala Phe Leu Ile Ala Pro Asn Asp Glu Leu Tyr Glu Gln Ile Arg Ala	
115 120 125 130	
ACT AAC ACC GAT ATT AAT TTT ATT AGT TCT GAT TTG TTG GTT ACT TTT	488
Thr Asn Thr Asp Ile Asn Phe Ile Ser Ser Asp Leu Leu Val Thr Phe	
135 140 145	
TTG AAT GGG TTT GAC CCA AAA ATC GCT AAT TTA AGG AAA GCG TGC AAC	536
Leu Asn Gly Phe Asp Pro Lys Ile Ala Asn Leu Arg Lys Ala Cys Asn	
150 155 160	
GTT TAT AGC GTG GGG GTG ATT TAT ATT GTA ACC ACC AAC ACG CTC AAT	584
Val Tyr Ser Val Gly Val Ile Tyr Ile Val Thr Thr Asn Thr Leu Asn	
165 170 175	
ATT TTA AGT TGT GAG AGT TTT GAA ATT TTA GAA AAA AGA GAG CTG GAT	632
Ile Leu Ser Cys Glu Ser Phe Glu Ile Leu Glu Lys Arg Glu Leu Asp	
180 185 190	
ACA AGC GGC GTT ACT AAA ACT TCC ACG CCG TTT TTT TCT AGG GTT GAG	680
Thr Ser Gly Val Thr Lys Thr Ser Thr Pro Phe Phe Ser Arg Val Glu	
195 200 205 210	
GGT ATT GAT GCA GGC ACG CTA GGG AAA CTT TTT TCA GGC AGT CAG TCT	728
Gly Ile Asp Ala Gly Thr Leu Gly Lys Leu Phe Ser Gly Ser Gln Ser	
215 220 225	
AAA AAT TAC TTC GCT TAC TAT GAC GCT TTA GTG AAG AAA GAA AAA CGC	776
Lys Asn Tyr Phe Ala Tyr Tyr Asp Ala Leu Val Lys Lys Glu Lys Arg	
230 235 240	
AAA GAA GTG AGG ATT AAA AAG AGG GAA GAA AAG ATT GAT TCT AGA GAA	824
Lys Glu Val Arg Ile Lys Lys Arg Glu Glu Lys Ile Asp Ser Arg Glu	
245 250 255	
ATT AAA CGA GAA ATC AAG CAA GAG GCC ATT AAA GAG CCT AAA AAA GCC	872
Ile Lys Arg Glu Ile Lys Gln Glu Ala Ile Lys Glu Pro Lys Lys Ala	
260 265 270	
AAT CAA GGC ACA CAA AAC GCT CCT ACT TTA GAA GAG AAA AAC TAC CAA	920
Asn Gln Gly Thr Gln Asn Ala Pro Thr Leu Glu Glu Lys Asn Tyr Gln	
275 280 285 290	

```

Leu Glu Asn Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Val Tyr
145                      150                      155                      160
Gly Ala Ser Ile Ser Gln Ala His Gln Phe Val Ala Thr Lys Asn Ala
                      165                      170                      175
Gln Ile Gly Phe Gly Ala Leu Ser Leu Met Asp Lys Lys Asp Lys Asn
                      180                      185                      190
Leu Ser Tyr Phe Ile Ile Asp Lys Ala Leu Tyr Asn Pro Ile Glu Gln
                      195                      200                      205
Ala Leu Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys Val
                      210                      215                      220
Phe Lys Asp Phe Leu Phe Ser Pro Lys Ala Arg Ala Ile Phe Lys Glu
225                      230                      235                      240
Tyr Gly Tyr Ile Val Asp
                      245

```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1406
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

AGCCATTTTA TGGCATTAA AAAAGTTTAA AAATGTTTAA AAGGAATTTT ATG TTA      56
                                   Met Leu
                                   1

AGG CTT TTG ATA GGA CTT CTT CTA ATG AGT TTT ATA AGC TTG CAA TCA      104
Arg Leu Leu Ile Gly Leu Leu Leu Met Ser Phe Ile Ser Leu Gln Ser
   5                      10                      15

GCC TCT TGG CAA GAA CCC TTA AGA GTG AGT ATA GAA TTT GTG GAT TTG      152
Ala Ser Trp Gln Glu Pro Leu Arg Val Ser Ile Glu Phe Val Asp Leu
  20                      25                      30

CCT AAA AAA ATC ATT CGT TTT CCG GCT CAT GAT TTG CAA GTG GGG GAG      200
Pro Lys Lys Ile Ile Arg Phe Pro Ala His Asp Leu Gln Val Gly Glu
 35                      40                      45                      50

TTT GGT TTT GTC GTT ACT AAA CTT TCA GAT TAT GAA ATC GTT AAT TCT      248
Phe Gly Phe Val Val Thr Lys Leu Ser Asp Tyr Glu Ile Val Asn Ser
   55                      60                      65

```

165	170	175	
GGC TTT GGA GCG TTA TCC TTG ATG GAT AAA AAA GAT AAA AAC CTC TCT			632
Gly Phe Gly Ala Leu Ser Leu Met Asp Lys Lys Asp Lys Asn Leu Ser			
180	185	190	
TAT TTC ATC ATT GAT AAA GCC CTT TAT AAC CCT ATT GAA CAA GCC TTG			680
Tyr Phe Ile Ile Asp Lys Ala Leu Tyr Asn Pro Ile Glu Gln Ala Leu			
195	200	205	210
ATT ATC ACT AAA AAT GGG GCT AAC AAC CCT TTA GCC AAA GTC TTT AAA			728
Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys Val Phe Lys			
215	220	225	
GAT TTT TTA TTC AGC CCT AAA GCC AGA GCT ATT TTT AAA GAA TAC GGC			776
Asp Phe Leu Phe Ser Pro Lys Ala Arg Ala Ile Phe Lys Glu Tyr Gly			
230	235	240	
TAT ATT GTG GAT TAAAACGCAT AAAAAAGGCG AGCAATGGAT CATGAGTTTT TGATT			833
Tyr Ile Val Asp			
245			
ACCATGCG			841

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met	Lys	Asn	Thr	Phe	Lys	Ala	Phe	Ala	Phe	Leu	Ile	Val	Phe	Phe	Ser
1				5				10					15		
Ser	Ala	Leu	Leu	Ala	Gln	Asp	Leu	Lys	Ile	Ala	Ala	Ala	Ala	Asn	Leu
		20					25					30			
Thr	Arg	Ala	Leu	Lys	Ala	Leu	Val	Lys	Glu	Phe	Gln	Lys	Glu	His	Pro
	35				40						45				
Lys	Asp	Thr	Val	Asn	Ile	Ser	Phe	Asn	Ser	Ser	Gly	Lys	Leu	Tyr	Ala
	50				55					60					
Gln	Ile	Ile	Gln	Asn	Ala	Pro	Phe	Asp	Leu	Phe	Ile	Ser	Ala	Asp	Met
65				70					75					80	
Ile	Arg	Pro	Lys	Lys	Leu	Tyr	Asp	Lys	Lys	Ile	Thr	Pro	Phe	Lys	Glu
			85					90					95		
Glu	Val	Tyr	Ala	Lys	Gly	Val	Leu	Val	Leu	Trp	Ser	Glu	Asp	Leu	Lys
			100				105					110			
Met	Asp	Ser	Leu	Glu	Ile	Leu	Lys	Asn	Pro	Lys	Ile	Lys	Arg	Ile	Ala
	115					120					125				
Met	Ala	Asn	Pro	Lys	Leu	Ala	Pro	Tyr	Gly	Lys	Ala	Ser	Met	Glu	Val
	130				135						140				

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...788
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

TACAAATAGG TATAATCACC AATTCCAATC ATTTAATCAA AGGGAGTTCT ATG AAA	56
Met Lys	
1	
AAT ACT TTC AAA GCG TTT GCC TTT TTA ATT GTA TTT TTT TCA AGC GCT	104
Asn Thr Phe Lys Ala Phe Ala Phe Leu Ile Val Phe Phe Ser Ser Ala	
5 10 15	
TTA TTA GCG CAG GAT TTA AAA ATC GCT GCT GCT GCT AAT CTT ACA CGC	152
Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Ala Asn Leu Thr Arg	
20 25 30	
GCT TTA AAA GCC CTT GTT AAA GAA TTT CAA AAA GAA CAC CCC AAA GAC	200
Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His Pro Lys Asp	
35 40 45 50	
ACT GTT AAT ATT AGC TTT AAT TCT TCA GGC AAA CTC TAC GCT CAA ATC	248
Thr Val Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr Ala Gln Ile	
55 60 65	
ATT CAA AAC GCC CCT TTT GAT TTA TTC ATT TCA GCA GAT ATG ATT AGA	296
Ile Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp Met Ile Arg	
70 75 80	
CCT AAA AAG CTT TAT GAT AAA AAA ATA ACC CCT TTT AAA GAA GAA GTC	344
Pro Lys Lys Leu Tyr Asp Lys Lys Ile Thr Pro Phe Lys Glu Glu Val	
85 90 95	
TAT GCT AAA GGC GTG TTG GTT TTA TGG AGT GAA GAT CTA AAA ATG GAT	392
Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asp Leu Lys Met Asp	
100 105 110	
TCT TTA GAA ATT CTT AAA AAT CCT AAA ATC AAG CGT ATC GCT ATG GCT	440
Ser Leu Glu Ile Leu Lys Asn Pro Lys Ile Lys Arg Ile Ala Met Ala	
115 120 125 130	
AAT CCT AAA CTA GCC CCT TAT GGA AAA GCC AGC ATG GAA GTC TTA GAG	488
Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu Val Leu Glu	
135 140 145	
AAT TTA AAA CTC ACT CCC AGT CTT AAA TCT AAA ATC GTT TAT GGC GCT	536
Asn Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Val Tyr Gly Ala	
150 155 160	
TCT ATT TCT CAA GCC CAT CAA TTT GTC GCT ACT AAA AAC GCT CAA ATA	584
Ser Ile Ser Gln Ala His Gln Phe Val Ala Thr Lys Asn Ala Gln Ile	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

```

Met Lys Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser
 1             5             10             15
Gly Ala Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln
          20             25             30
His Asn Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile
          35             40             45
Lys Gly Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu
          50             55             60
Pro Lys Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu
          65             70             75             80
Phe Glu Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys
          85             90             95
Gly Tyr Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp
          100            105            110
Ile Lys Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala
          115            120            125
Ile Leu Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys
          130            135            140
Val Ile Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro
          145            150            155            160
Lys Ser Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile
          165            170            175
Lys Ala Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly
          180            185            190
Phe Val Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp
          195            200            205
Gln Ala Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val
          210            215            220
His Ile Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys
          225            230            235            240
Val Ser Ser Glu Met Lys Lys Arg Lys
          245

```

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

AAG CAA GAG CCT AAA AAC AGC CAT TTA GTC GTT TTG ATC GAA CCT AAA	248
Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu Pro Lys	
55 60 65	
ATA GAG ATC AAT AAA GTT ATC CCT GAA AGT TAT CAA AAA GAG TTT GAG	296
Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu Phe Glu	
70 75 80	
AAG TCT TTG TTT CTC CAG TTG AGT AGT TTT TTA GAG AGA AAA GGC TAT	344
Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys Gly Tyr	
85 90 95	
AGC GTT TCG CAA TTT AAA GAT GCT AGC GAA ATC CCT CAA GAC ATC AAA	392
Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp Ile Lys	
100 105 110	
GAA AAA GCG TTG CTC GTT TTA CGC ATG GAT GGG AAT GTG GCT ATC TTG	440
Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala Ile Leu	
115 120 125 130	
GAA GAT ATT GTA GAA GAG AGC GAT GCG CTT AGC GAA GAA AAA GTG ATA	488
Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys Val Ile	
135 140 145	
GAC ATG TCT TCA GGG TAT TTG AAC TTG AAT TTT GTT GAG CCA AAA AGT	536
Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro Lys Ser	
150 155 160	
GAA GAT ATT ATC CAT AGT TTT GGT ATT GAT GTT TCA AAG ATT AAG GCT	584
Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile Lys Ala	
165 170 175	
GTG ATT GAA AGA GTG GAA TTG CGG CGC ACC AAT TCT GGA GGT TTT GTC	632
Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly Phe Val	
180 185 190	
CCC AAA ACT TTT GTG CAT AGG ATT AAG GAA ACC GAT CAT GAT CAA GCC	680
Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp Gln Ala	
195 200 205 210	
ATT AGA AAA ATC ATG AAT CAA GCC TAT CAC AAA GTG ATG GTG CAT ATT	728
Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val His Ile	
215 220 225	
ACC AAA GAG TTA AGC AAA AAA CAC ATG GAA CAT TAT GAA AAA GTT TCT	776
Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys Val Ser	
230 235 240	
AGT GAA ATG AAA AAA CGA AAG TAGTTTTTAA GAAACGAAAA GCTTAAAAAT CATT	831
Ser Glu Met Lys Lys Arg Lys	
245	
GAGAGCTATT TTTAAAAA	850

(2) INFORMATION FOR SEQ ID NO:264:

```

Gly Asn Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg
      100                      105                      110
Lys Lys Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe
      115                      120                      125
Thr Lys Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys
      130                      135                      140
Lys Ser Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val
      145                      150                      155                      160
Leu Glu Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val
      165                      170                      175
Asp Gly Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr
      180                      185                      190
Asp Ile Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala
      195                      200                      205
Lys Ile Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys
      210                      215                      220
Lys Phe Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr
      225                      230                      235

```

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...797
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

```

TTGGGTAAGA TTAGGAATTG ATTTTAAAGA AAAAGAAAGA AAGGAATTTA ATG AAA      56
                                     Met Lys
                                     1
AAA GGT AGT TTG GCA ATC GTT TTA GGA TCG CTA TTA GCG AGT GGG GCG      104
Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser Gly Ala
      5                      10                      15
TTT TAT ACG GCT CTA GCT GAT GGA ATG CCT GCA AAA CAG CAG CAC AAT      152
Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln His Asn
      20                      25                      30
AAT ACG GGC GAG TCA GTG GAG TTG CAT TTC CAC TAT CCT ATT AAA GGC      200
Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile Lys Gly
      35                      40                      45                      50

```

```

TCC AGC AAT AAC ACG AAT TTT AAA GGC GGT GGC TCG CAA AAA AAG AGC      488
Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys Lys Ser
              135                      140                      145

GAA GAT TTA GAG ATT GTG TTG AGC GCT CGA ATC ATT AAG GTG CTA GAA      536
Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val Leu Glu
              150                      155                      160

AAC GGG AAT TAT TTC ATC TAT GGG AAT AAG GAA GTG CTA GTG GAT GGG      584
Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val Asp Gly
              165                      170                      175

GAA AAG CAA ATC CTT AAG GTG AGT GGG GTG ATC CGC CCT TAT GAT ATT      632
Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr Asp Ile
              180                      185                      190

GAA AGG AAT AAC ACC ATC CAA TCC AAG TTT TTA GCC GAC GCT AAG ATT      680
Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala Lys Ile
              195                      200                      205                      210

GAA TAC ACG AAT TTA GGG CAT TTG AGC GAT TCC AAT AAG AAG AAA TTC      728
Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys Lys Phe
              215                      220                      225

GCT GCT GAT GCG ATG GAA ACC CAA ATG CCT TAT TAAAAAGAGC AAAGCCTAGC      781
Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr
              230                      235

ATGAGAGCGA TCGCTATTGT TTTAGCCAGA AGT      814

```

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```

Met Lys Lys Ala Leu Tyr Leu Gly Ala Val Ala Phe Ser Val Ala Phe
 1              5              10              15
Ser Met Ala Ser Ala Asn Glu Pro Lys Ile Asp Phe Asn Pro Pro Asn
              20              25              30
Tyr Val Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys
              35              40              45
Leu Gly Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg
              50              55              60
Arg Ala Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys
              65              70              75              80
Ala Ser Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly
              85              90              95

```

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...761
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TATAAGAGAG TATAATTCAA GGCTTAAAT AACTCAAGTA AGGCTAGTGG ATG AAA	56
Met Lys	
1	
AAA GCG CTT TAT TTA GGG GCT GTT GCG TTT AGC GTT GCA TTC AGC ATG	104
Lys Ala Leu Tyr Leu Gly Ala Val Ala Phe Ser Val Ala Phe Ser Met	
5 10 15	
GCA TCA GCC AAT GAG CCA AAA ATT GAT TTT AAC CCT CCC AAT TAT GTA	152
Ala Ser Ala Asn Glu Pro Lys Ile Asp Phe Asn Pro Pro Asn Tyr Val	
20 25 30	
GAA GAA ACC CCC TCT AAA GAA TTT ATC CCT GAA TTG AAC AAG TTA GGG	200
Glu Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys Leu Gly	
35 40 45 50	
AGT TTG TTT GGG CAG GGT GAG CGC CCC TTG TTT GCG GAC AGG AGG GCG	248
Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg Arg Ala	
55 60 65	
ATG AAG CCT AAC GAT TTG ATC ACA ATC ATT GTT TCT GAA AAA GCG AGC	296
Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys Ala Ser	
70 75 80	
GCG AAT TAT TCC AGC TCT AAA GAT TAT AAA AGC GCT TCA GGG GGT AAT	344
Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly Gly Asn	
85 90 95	
TCC ACG CCC CCA AGA CTC ACT TAT AAC GGG CTA GAT GAA AGA AAG AAA	392
Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg Lys Lys	
100 105 110	
AAA GAA GCG GAG TAT TTA GAC GAT AAG AAT AAT TAC AAT TTC ACC AAA	440
Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe Thr Lys	
115 120 125 130	

```

GAT GAT AAG ATC GTG TTT TTA GGC TCA GCG AAT TGG AGC AAA AAC GCT      488
Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys Asn Ala
          135                      140                      145

TTT GAA AAC AAT TAT GAA GTG CTT TTA AAA ACC GAT GAC ACA GAA ACG      536
Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr Glu Thr
          150                      155                      160

ATC CTC AAA GCC AAG AGC TAT TAC CAA AAG ATG TTA GGG AGT TGC GTT      584
Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser Cys Val
          165                      170                      175

GGG TTT TAAAAGCCCT TTAGAAGTGG TAATTATACC CCACATAAAA GGCAAAGACC CT      642
Gly Phe
          180

A                                                                    643

```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

Met Leu Asn Lys Phe Lys Lys Ile Val Gly Val Ser Val Leu Val Gly
 1          5          10          15
Cys Leu Gly Val Leu Gln Ala Lys Asn Ser Leu Phe Val Leu Pro Tyr
          20          25          30
Glu Gln Lys Asp Ala Leu Asn Ser Leu Val Ser Gly Ile Ser Asn Ala
          35          40          45
Arg Glu Ser Val Lys Ile Ala Ile Tyr Ser Phe Thr His Arg Asp Ile
          50          55          60
Ala Arg Ala Ile Lys Ser Val Ala Ser Arg Gly Ile Lys Val Gln Ile
65          70          75          80
Ile Tyr Asp Tyr Glu Ser Asn His His Asn Lys Gln Ser Thr Ile Gly
          85          90          95
Tyr Leu Asp Lys Tyr Pro Asn Thr Lys Val Cys Leu Leu Lys Gly Leu
          100         105         110
Lys Ala Lys Asn Gly Asn Tyr Tyr Gly Ile Met His Gln Lys Val Ala
          115         120         125
Ile Ile Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys
          130         135         140
Asn Ala Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr
          145         150         155         160
Glu Thr Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser
          165         170         175
Cys Val Gly Phe
          180

```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...590
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

TTGGTTGGTT GTTTTTATCA TAGAGTGTA TTTAAATAA GGATCATTTG ATG TTA	56
Met Leu	
1	
AAC AAG TTT AAA AAA ATC GTT GGC GTT AGT GTG TTA GTG GGC TGT TTA	104
Asn Lys Phe Lys Lys Ile Val Gly Val Ser Val Leu Val Gly Cys Leu	
5 10 15	
GGG GTT TTG CAA GCT AAA AAC AGC TTA TTT GTC TTA CCT TAT GAG CAA	152
Gly Val Leu Gln Ala Lys Asn Ser Leu Phe Val Leu Pro Tyr Glu Gln	
20 25 30	
AAA GAC GCT CTC AAT TCT TTA GTT TCT GGC ATT AGT AAC GCC AGA GAG	200
Lys Asp Ala Leu Asn Ser Leu Val Ser Gly Ile Ser Asn Ala Arg Glu	
35 40 45 50	
AGC GTG AAA ATC GCT ATC TAT AGT TTC ACG CAC AGA GAT ATT GCA AGA	248
Ser Val Lys Ile Ala Ile Tyr Ser Phe Thr His Arg Asp Ile Ala Arg	
55 60 65	
GCG ATT AAA AGC GTA GCG AGT AGG GGG ATT AAG GTG CAA ATC ATT TAT	296
Ala Ile Lys Ser Val Ala Ser Arg Gly Ile Lys Val Gln Ile Ile Tyr	
70 75 80	
GAT TAT GAA AGC AAT CAT CAT AAC AAG CAA TCC ACT ATT GGC TAT CTG	344
Asp Tyr Glu Ser Asn His His Asn Lys Gln Ser Thr Ile Gly Tyr Leu	
85 90 95	
GAC AAA TAC CCT AAC ACG AAA GTG TGC TTA TTG AAA GGG CTT AAG GCT	392
Asp Lys Tyr Pro Asn Thr Lys Val Cys Leu Leu Lys Gly Leu Lys Ala	
100 105 110	
AAA AAC GGG AAT TAT TAC GGC ATC ATG CAC CAA AAA GTA GCG ATC ATT	440
Lys Asn Gly Asn Tyr Tyr Gly Ile Met His Gln Lys Val Ala Ile Ile	
115 120 125 130	

	Val	Asn	
	1		
TTT TTG AAA AAG CCA AAG TAT TAT AAA TTC ATA GAG GGG GCG AAT TAT			104
Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu Gly Ala Asn Tyr			
5 10 15			
TTG AGC TTG GGG CTT TCT ATG GTG GTA GCG ATC CTT ATG GGC GTG GCT			152
Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu Met Gly Val Ala			
20 25 30			
ATA GGC TAT GGG CTT AAA AAA CTC ACT CAT ATT TCG TGG CTT TTT TGG			200
Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser Trp Leu Phe Trp			
35 40 45 50			
CTT GGG GTT ATT TGG GGC GTC TTA GCG AGC TTT CTC AAT GTC TAT AAA			248
Leu Gly Val Ile Trp Gly Val Leu Ala Ser Phe Leu Asn Val Tyr Lys			
55 60 65			
GCT TAT AAA AAC ATG CAA AAA GAC TAT GAA GAA CTA GCC AAA GAC CCT			296
Ala Tyr Lys Asn Met Gln Lys Asp Tyr Glu Glu Leu Ala Lys Asp Pro			
70 75 80			
AAA TAC ACA CAA AAT AAA ACA AAA TAAATCCAAT CAAATCCCAT GTGCCAAATC			350
Lys Tyr Thr Gln Asn Lys Thr Lys			
85 90			
CAATGCTTGC TTATTTTACT TTC			373

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Val	Asn	Phe	Leu	Lys	Lys	Pro	Lys	Tyr	Tyr	Lys	Phe	Ile	Glu	Gly	Ala
1				5				10					15		
Asn	Tyr	Leu	Ser	Leu	Gly	Leu	Ser	Met	Val	Val	Ala	Ile	Leu	Met	Gly
		20					25					30			
Val	Ala	Ile	Gly	Tyr	Gly	Leu	Lys	Lys	Leu	Thr	His	Ile	Ser	Trp	Leu
	35				40						45				
Phe	Trp	Leu	Gly	Val	Ile	Trp	Gly	Val	Leu	Ala	Ser	Phe	Leu	Asn	Val
	50				55			60							
Tyr	Lys	Ala	Tyr	Lys	Asn	Met	Gln	Lys	Asp	Tyr	Glu	Glu	Leu	Ala	Lys
65				70				75					80		
Asp	Pro	Lys	Tyr	Thr	Gln	Asn	Lys	Thr	Lys						
				85				90							

Arg	Glu	Pro	Asp	Lys	Cys	Thr	Lys	Ser	Phe	Lys	Lys	Ser	Ala	Leu	Met
65					70					75					80
Ser	Tyr	Asp	Leu	Ala	Leu	Gly	Tyr	Leu	Val	Ser	Lys	Asn	Lys	Gln	Tyr
			85						90					95	
Gly	Leu	Lys	Ala	Ile	Glu	Ile	Leu	Asn	Ala	Trp	Ala	Lys	Glu	Leu	Gln
			100					105					110		
Ser	Val	Asp	Thr	Tyr	Gln	Ser	Glu	Asp	Asn	Ile	Asn	Phe	Tyr	Met	Pro
		115					120					125			
Tyr	Met	Asn	Met	Ala	Tyr	Trp	Phe	Val	Lys	Lys	Ala	Phe	Pro	Ser	Pro
	130					135					140				
Glu	Tyr	Glu	Asp	Phe	Ile	Lys	Arg	Met	Arg	Gln	Tyr	Ser	Gln	Ser	Ala
145					150					155					160
Leu	Asn	Thr	Asn	His	Gly	Ala	Trp	Gly	Ile	Leu	Phe	Asp	Val	Ser	Ser
			165					170						175	
Ala	Leu	Ala	Leu	Asp	Asp	Asn	Ala	Leu	Leu	His	Asn	Ser	Ala	Asn	Arg
			180					185					190		
Trp	Gln	Glu	Trp	Val	Phe	Lys	Ala	Ile	Asp	Glu	Asn	Gly	Val	Ile	Xaa
		195					200					205			
Ser	Ala	Ile	Thr	Arg	Ser	Asp	Thr	Ser	Asp	Tyr	His	Gly	Gly	Pro	Thr
	210					215					220				
Lys	Gly	Ile	Lys	Gly	Ile	Ala	Tyr	Thr	Asn	Phe	Ala	Leu	Leu	Ala	Leu
225					230					235					240
Thr	Ile	Ser	Gly	Glu	Leu	Leu	Phe	Glu	Asn	Gly	Tyr	Asp	Leu	Trp	Gly
			245					250						255	
Ser	Gly	Ala	Gly	Lys	Arg	Leu	Ser	Val	Ala	Tyr	Asn	Lys	Val	Ala	Thr
			260					265					270		
Trp	Ile	Leu	Asn	Pro	Glu	Thr	Phe	Pro	Tyr	Phe	Gln	Pro	Asn	Leu	Ile
		275					280					285			
Gly	Val	His	Asn	Asn	Ala	Tyr	Phe	Ile	Ile	Leu	Ala	Lys	His	Tyr	Ser
	290					295					300				
Ser	Pro	Ser	Ala	Asn	Glu	Leu	Leu	Lys	Gln	Gly	Asp	Leu	His	Glu	Asp
305				310						315					320
Gly	Phe	Arg	Leu	Lys	Leu	Arg	Ser	Pro							
				325											

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...320
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

TTAACGATCG CAAAAGCCGA TGAAAGTTTT GATGAAATCA TAAAAGGTGT GTG AAT

56

ATC ACT AGG AGC GAT ACG AGC GAT TAT CAT GGC GGC CCT ACA AAG GGC	728
Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr Lys Gly	
215 220 225	
ATT AAG GGG ATA GCT TAT ACC AAT TTC GCG CTT CTT GCG CTA ACC ATA	776
Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu Thr Ile	
230 235 240	
TCA GGC GAA TTG CTT TTT GAG AAC GGG TAT GAT TTG TGG GGT AGT GGA	824
Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly Ser Gly	
245 250 255	
GCT GGG AAA AGG CTC TCT GTG GCG TAT AAC AAA GTT GCA ACA TGG ATT	872
Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr Trp Ile	
260 265 270	
TTA AAC CCT GAA ACT TTC CCT TAT TTC CAG CCT AAC CTT ATC GGG GTG	920
Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile Gly Val	
275 280 285 290	
CAT AAC AAC GCC TAT TTC ATT ATT TTA GCC AAG CAT TAT TCT AGC CCT	968
His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser Ser Pro	
295 300 305	
AGT GCA AAT GAG CTT TTA AAG CAA GGC GAT TTA CAC GAA GAT GGT TTC	1016
Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp Gly Phe	
310 315 320	
AGG CTG AAA CTC CGA TCG CCA TGAATTTTTC TGTATCCAAG GTTAGCCTTA AGGA	1071
Arg Leu Lys Leu Arg Ser Pro	
325	
TGGCCATGCG CTTTAACCT	1090

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Met Lys Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln	
1 5 10 15	
Ala Tyr Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp	
20 25 30	
Leu Pro Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln	
35 40 45	
Pro Cys Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val	
50 55 60	

TTACCCTAAA ACGCTATTTT TAAAATAATC CATTAAAATA AAGGCGAGGA ATG AAA	56
Met Lys	
1	
AGA TTT GTT TTG TTT TTA TTG TTC ATG TGC GTT TGC GTT CAA GCT TAC	104
Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln Ala Tyr	
5 10 15	
GCC GAG CAA GAT TAC TTT TTT AGG GAT TTT AAA TCT AGA GAT TTG CCC	152
Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp Leu Pro	
20 25 30	
CAA AAA CTC CAT CTT GAT AAA AAG CTC TCC CAA ACA ATA CAG CCA TGC	200
Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln Pro Cys	
35 40 45 50	
ATG CAA CTT AAC GCA TCA AAA CAC TAC ACT TCT ACC GGG GTT AGA GAG	248
Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val Arg Glu	
55 60 65	
CCT GAT AAA TGC ACA AAG AGT TTT AAA AAA TCC GCT CTC ATG TCC TAT	296
Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met Ser Tyr	
70 75 80	
GAC TTA GCG CTA GGT TAT TTG GTG AGT AAG AAT AAG CAA TAC GGC TTA	344
Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr Gly Leu	
85 90 95	
AAG GCT ATA GAA ATT TTA AAC GCT TGG GCT AAA GAG CTT CAA AGC GTG	392
Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln Ser Val	
100 105 110	
GAT ACT TAT CAG AGC GAG GAT AAT ATC AAT TTT TAC ATG CCT TAT ATG	440
Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro Tyr Met	
115 120 125 130	
AAC ATG GCT TAT TGG TTT GTC AAA AAG GCG TTT CCT AGC CCA GAA TAT	488
Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro Glu Tyr	
135 140 145	
GAA GAT TTC ATT AAG CGG ATG CGC CAG TAT TCT CAA TCA GCT CTT AAC	536
Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala Leu Asn	
150 155 160	
ACT AAC CAT GGG GCG TGG GGC ATT CTT TTT GAT GTG AGT TCT GCG CTA	584
Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser Ala Leu	
165 170 175	
GCG TTA GAC GAT AAT GCC CTT TTG CAC AAT AGC GCT AAT CGG TGG CAG	632
Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg Trp Gln	
180 185 190	
GAG TGG GTG TTT AAA GCC ATA GAT GAG AAT GGG GTT ATT GNT AGC GCG	680
Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Xaa Ser Ala	
195 200 205 210	

```

His Asp Glu Asp Ser Leu Glu Lys Leu Ile Thr Ile Tyr Phe Leu Gln
      165                      170                      175
Asn Arg Lys Lys Glu Gly Leu Asp Leu Leu Gln Ser His Ile Asp Arg
      180                      185                      190
Tyr Gly Cys Ser Glu Gln Leu Cys Gln Lys Ala Leu Asn Thr Phe Thr
      195                      200                      205
Gln Phe Asn Glu Leu Asp Leu Ala Lys Thr Thr Phe Ala Arg Leu Tyr
      210                      215                      220
Glu Lys Asn Pro Ile Val Gln Asn Ala Gln Phe Tyr Ile Gly Val Leu
      225                      230                      235                      240
Ile Leu Leu Lys Glu Phe Asp Lys Ala Gln Lys Ile Ala Glu Leu Phe
      245                      250                      255
Pro Phe Asp Arg Arg Leu Leu Leu Asp Leu Tyr Thr Ala Gln Lys Lys
      260                      265                      270
Phe Asp Gln Ala Ser Lys Gln Ala Ser Leu Ile Tyr Gln Glu Lys Lys
      275                      280                      285
Asp Pro Lys Phe Leu Gly Leu Glu Ala Ile Tyr His Tyr Glu Ser Leu
      290                      295                      300
Ser Ala Asn Lys Lys Lys Leu Thr Lys Glu Glu Met Leu Pro Ile Ile
      305                      310                      315                      320
Gln Lys Leu Glu Gln Ala Thr Lys Glu Arg Gln Ala Trp Leu Ala Lys
      325                      330                      335
Thr Lys Asp Lys Glu Asp Ala Gln Asp Ala Phe Phe Tyr Asn Phe Leu
      340                      345                      350
Gly Tyr Ser Leu Ile Asp Tyr Asp Met Asp Ile Lys Arg Gly Met Asp
      355                      360                      365
Phe Val Arg Lys Ala Leu Ala Leu Asp Ser Gly Ser Val Leu Tyr Leu
      370                      375                      380
Asp Ser Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala
      385                      390                      395                      400
Lys Lys Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro
      405                      410                      415
Glu Leu Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys
      420                      425                      430

```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1037
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```

TCC TTA ATA GAT TAT GAC ATG GAT ATT AAA AGG GGC ATG GAT TTT GTG      1160
Ser Leu Ile Asp Tyr Asp Met Asp Ile Lys Arg Gly Met Asp Phe Val
355                               360                               365                               370

AGG AAA GCC TTA GCG TTG GAT TCT GGA TCA GTG CTT TAT TTG GAT TCT      1208
Arg Lys Ala Leu Ala Leu Asp Ser Gly Ser Val Leu Tyr Leu Asp Ser
                               375                               380                               385

TTA GCA TGG GGT TAT TAC AAA TTA GGG AAT TGT TTG GAA GCT AAA AAA      1256
Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala Lys Lys
                               390                               395                               400

ATC TTT TCT AGC ATC GCT AAA GAG TCT ATC CAA GCC GAA CCT GAA TTG      1304
Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro Glu Leu
                               405                               410                               415

AAA GAA CAC AAT AAA ATC ATT CAA GAA TGC AAG AAA TAGGGATTTT AGAAAA      1356
Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys
                               420                               425                               430

TTTACAAAAA AGCTTAGCCT TAAAAGAGGG CATGCTT                               1393

```

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Met Asn Ile Gln Ile Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe
 1                               5                               10                               15
Ser Leu Phe Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln Ile
                               20                               25                               30
Leu Leu Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Ala Ala Gln
                               35                               40                               45
Lys Gly Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr Ala
                               50                               55                               60
Lys Glu Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr Ala
65                               70                               75                               80
Met His Leu Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn Asp
                               85                               90                               95
Val Ser Ile Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly Gln
                               100                              105                              110
Ile Asp Lys Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu Lys
                               115                              120                              125
Thr Ile Ala Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln Lys
                               130                              135                              140
Arg Leu Asp Lys Ala Phe Pro Leu Leu Asn Lys Phe Tyr Asn Gln Val
145                              150                              155                              160

```

GCC ACA GAC AAT GTG TTA GGG ACT TTG TAT TTG ACT CAA AAG CGT TTG	488
Ala Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln Lys Arg Leu	
135 140 145	
GAT AAG GCT TTC CCA TTG TTG AAT AAG TTT TAT AAC CAA GTG CAT GAT	536
Asp Lys Ala Phe Pro Leu Leu Asn Lys Phe Tyr Asn Gln Val His Asp	
150 155 160	
GAA GAC AGC CTA GAA AAA CTC ATT ACG ATC TAT TTT TTG CAA AAT CGT	584
Glu Asp Ser Leu Glu Lys Leu Ile Thr Ile Tyr Phe Leu Gln Asn Arg	
165 170 175	
AAA AAA GAG GGC TTG GAT TTG TTG CAA TCT CAT ATA GAC AGG TAT GGT	632
Lys Lys Glu Gly Leu Asp Leu Leu Gln Ser His Ile Asp Arg Tyr Gly	
180 185 190	
TGC TCA GAG CAA TTG TGC CAA AAA GCG CTC AAC ACT TTC ACG CAA TTT	680
Cys Ser Glu Gln Leu Cys Gln Lys Ala Leu Asn Thr Phe Thr Gln Phe	
195 200 205 210	
AAC GAG CTT GAT TTG GCT AAA ACG ACT TTT GCT CGT TTG TAT GAA AAA	728
Asn Glu Leu Asp Leu Ala Lys Thr Thr Phe Ala Arg Leu Tyr Glu Lys	
215 220 225	
AAC CCT ATT GTT CAA AAT GCT CAG TTT TAC ATA GGG GTA TTA ATC TTG	776
Asn Pro Ile Val Gln Asn Ala Gln Phe Tyr Ile Gly Val Leu Ile Leu	
230 235 240	
TTA AAA GAG TTT GAT AAG GCC CAG AAA ATC GCA GAA TTA TTC CCT TTT	824
Leu Lys Glu Phe Asp Lys Ala Gln Lys Ile Ala Glu Leu Phe Pro Phe	
245 250 255	
GAC AGG CGT TTG TTG TTA GAC TTA TAC ACC GCA CAA AAA AAA TTC GAT	872
Asp Arg Arg Leu Leu Leu Asp Leu Tyr Thr Ala Gln Lys Lys Phe Asp	
260 265 270	
CAA GCT TCC AAA CAA GCT TCT TTG ATC TAT CAA GAA AAA AAA GAC CCT	920
Gln Ala Ser Lys Gln Ala Ser Leu Ile Tyr Gln Glu Lys Lys Asp Pro	
275 280 285 290	
AAA TTC TTA GGA TTA GAG GCC ATT TAT CAT TAT GAA AGC TTG AGT GCG	968
Lys Phe Leu Gly Leu Glu Ala Ile Tyr His Tyr Glu Ser Leu Ser Ala	
295 300 305	
AAT AAG AAA AAG CTC ACC AAA GAA GAG ATG TTG CCT ATC ATT CAA AAA	1016
Asn Lys Lys Lys Leu Thr Lys Glu Glu Met Leu Pro Ile Ile Gln Lys	
310 315 320	
TTA GAG CAA GCC ACC AAA GAG CGC CAA GCA TGG CTC GCT AAA ACC AAA	1064
Leu Glu Gln Ala Thr Lys Glu Arg Gln Ala Trp Leu Ala Lys Thr Lys	
325 330 335	
GAT AAA GAA GAC GCG CAA GAC GCT TTC TTT TAT AAT TTT TTA GGG TAT	1112
Asp Lys Glu Asp Ala Gln Asp Ala Phe Phe Tyr Asn Phe Leu Gly Tyr	
340 345 350	

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1340
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

CTAAAGTGCG CTAAAATTCA CTTCAGTGAT ACAAAAAAGG AAATAAAATA ATG AAT      56
                                   Met Asn
                                   1

ATT CAA ATA AAG AAA AGG TTT TTA GCA AAT TTG TTG CTT TTT AGC CTG      104
Ile Gln Ile Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe Ser Leu
      5                      10                      15

TTT TGC CTT AAG GCT GAA ACC CTT TCA GAA GAT CAT CAA ATC CTG TTG      152
Phe Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln Ile Leu Leu
      20                      25                      30

AGT TCA GAC GCT TTC CAT AGA GGG GAT TTT GCT GCC GCT CAA AAA GGC      200
Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Ala Ala Gln Lys Gly
      35                      40                      45                      50

TAT ATG AAT CTC TAT AAG CAA ACC AAT AAG GTG GTG TAT GCT AAA GAA      248
Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr Ala Lys Glu
      55                      60                      65

GCG GCC ATT TCA GCG GCG AGC TTA GGG GAT ATT AAA ACC GCT ATG CAT      296
Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr Ala Met His
      70                      75                      80

TTA GCC ATG CTC TAT CAA AAA ATC ACC AAT AAT CGT AAT GAT GTT TCT      344
Leu Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn Asp Val Ser
      85                      90                      95

ATC AAT AAG ATT TTA GTG GAT GGC TAT GCG CAA ATG GGG CAG ATT GAT      392
Ile Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly Gln Ile Asp
      100                     105                     110

AAG GCG ATT GAA TTG CTG CAC AAA ATC CGT AAA GAA GAA AAG ACC ATA      440
Lys Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu Lys Thr Ile
      115                     120                     125                     130

```



```

CAA AAA CCC CCA AAA GAA AAT AAA GAA ATC CCA AAA ACC ACA GCA CCC      632
Gln Lys Pro Pro Lys Glu Asn Lys Glu Ile Pro Lys Thr Thr Ala Pro
    180                      185                      190

ACG CCC CCT ATA GCA CCC ACG CCT TTA AAA GAG CCG ATG ATA AAA GAT      680
Thr Pro Pro Ile Ala Pro Thr Pro Leu Lys Glu Pro Met Ile Lys Asp
    195                      200                      205                      210

CCT AAC ACC AAA GAG CCT GCA GGG GTA TGATGTTTCAT TGTAGCGGTT TTGATGC      734
Pro Asn Thr Lys Glu Pro Ala Gly Val
                215

TGGCGTTTTTT AATCTTTGTC CATGAA                                          760

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

Met Arg Lys Ile Leu Leu Leu Gly Leu Ile Leu Gln Ala Leu Phe Ser
 1           5           10           15
Glu Glu Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser
    20           25           30
Lys Lys Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu
    35           40           45
Gln Ser Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu
    50           55           60
Lys Thr Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu
    65           70           75           80
Lys Asn Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu
    85           90           95
Glu Lys Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu
    100          105          110
Arg Glu Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser
    115          120          125
Lys Met Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr
    130          135          140
Gln Asn Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly
    145          150          155          160
Lys Ile Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu
    165          170          175
Leu Trp Gln Lys Pro Pro Lys Glu Asn Lys Glu Ile Pro Lys Thr Thr
    180          185          190
Ala Pro Thr Pro Pro Ile Ala Pro Thr Pro Leu Lys Glu Pro Met Ile
    195          200          205
Lys Asp Pro Asn Thr Lys Glu Pro Ala Gly Val
    210          215

```

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TCTTTTAGAC	GAAAACGCCA	TGATTTTACA	CTGGCAAAAA	GAGGGCTTGC	ATG	CGT	56
					Met	Arg	
					1		
AAA ATC TTG TTA TTG GGT CTG ATT TTA CAA GCG CTC TTC AGC GAA GAA	104						
Lys Ile Leu Leu Leu Gly Leu Ile Leu Gln Ala Leu Phe Ser Glu Glu							
5 10 15							
GCC GCG CAA GAA TTG TTG CAA TGC TCT GCG ATT TTT GAA TCT AAA AAA	152						
Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser Lys Lys							
20 25 30							
GCC GAA TTG AAA GAC GAT TTG CGC CGA TTG AGT GAA AAA GAG CAG TCT	200						
Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu Gln Ser							
35 40 45 50							
TTA AGG ATC TTG CAA ACC GAA AAC GCC CGC CTT TTA GAT GAA AAA ACC	248						
Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu Lys Thr							
55 60 65							
GAT CTG TTG AAC CAA AAA GAA AAA GAA GTG GAA GAA AAA CTG AAA AAT	296						
Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu Lys Asn							
70 75 80							
TTA GCC GCT AAA GAA GAA GCC TTT AAA ACC TTA CAA ACG GAA GAA AAA	344						
Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu Glu Lys							
85 90 95							
AAA CGC CTT AAA AAT TTG ATA GAA GAA AAC GAA GGC ATT TTA AGA GAA	392						
Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu Arg Glu							
100 105 110							
ATC AAG CAG GCT AAA GAC AGC AAG ATT GGC GAG ACT TAT TCT AAA ATG	440						
Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser Lys Met							
115 120 125 130							
AAA GAT TCT AAA TCG GCT CTG ATT TTA GAA AAT TTA CCC ACT CAA AAC	488						
Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr Gln Asn							
135 140 145							
GCA TTA GAA ATT TTA ATG GCG CTA AAA CCC CAA GAA CTC GGT AAA ATT	536						
Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly Lys Ile							
150 155 160							
TTA GCC AAA ATG GAT CCT AAA AAA GCG GCG GCT TTG ACA GAG TTG TGG	584						
Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Leu Thr Glu Leu Trp							
165 170 175							

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Met Ile Leu Arg Ala Ser Val Leu Ser Ala Leu Leu Leu Val Gly Leu
 1           5           10           15
Gly Ala Ala Pro Lys His Ser Val Ser Ala Asn Asp Lys Arg Met Gln
 20           25           30
Asp Asn Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg
 35           40           45
Ile Leu Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val
 50           55           60
Val Ile Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser
 65           70           75           80
Lys Asp Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn
 85           90           95
Lys Ser Asp Asp Val Gln Leu Val Ala Glu Thr Asn Gln Lys Val Gln
100           105           110
Ala Leu Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe
115           120           125
Asn Glu Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala
130           135           140
Ala Asn Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met Cys Pro
145           150           155           160
His Cys Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys Glu Asn
165           170           175
Thr Val Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys
180           185           190
Lys Ala Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly
195           200           205
Ala Ser Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr
210           215           220
Gln Tyr Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys
225           230           235           240
Val Glu Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly
245           250           255
Val Pro Phe Leu Tyr His Tyr Lys Ala
260           265

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 760 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...707

Gly	Asn	Leu	Ile	Ile	Gly	Leu	Ser	Asn	Ile	Phe	Phe	Ser	Asn	Lys	Ser		
	85						90					95					
GAT	GAT	GTG	CAA	TTA	GTT	GCA	GAA	ACC	AAT	CAA	AAA	GTT	CAA	GCT	CTT		392
Asp	Asp	Val	Gln	Leu	Val	Ala	Glu	Thr	Asn	Gln	Lys	Val	Gln	Ala	Leu		
	100					105					110						
AAC	GCC	ACC	CAA	CAA	AAT	AGC	GCG	AAA	TTG	AAC	GCT	ATT	TTT	AAT	GAA		440
Asn	Ala	Thr	Gln	Gln	Asn	Ser	Ala	Lys	Leu	Asn	Ala	Ile	Phe	Asn	Glu		
	115				120					125					130		
ATA	CCG	GCT	GAT	TAT	GCG	ATA	GAG	TTG	CCC	TCT	ACT	AAC	GCT	GCA	AAT		488
Ile	Pro	Ala	Asp	Tyr	Ala	Ile	Glu	Leu	Pro	Ser	Thr	Asn	Ala	Ala	Asn		
				135					140						145		
AAG	GAT	AAA	ATC	CTT	TAT	ATT	GTC	TCT	GAT	CCC	ATG	TGC	CCA	CAT	TGC		536
Lys	Asp	Lys	Ile	Leu	Tyr	Ile	Val	Ser	Asp	Pro	Met	Cys	Pro	His	Cys		
			150					155					160				
CAA	AAA	GAG	CTC	ACT	AAA	CTT	AGG	GAT	CAT	TTA	AAA	GAA	AAC	ACC	GTG		584
Gln	Lys	Glu	Leu	Thr	Lys	Leu	Arg	Asp	His	Leu	Lys	Glu	Asn	Thr	Val		
		165					170					175					
AGA	ATG	GTC	GTG	GTG	GGG	TGG	CTT	GGG	GTC	AAT	TCA	GCT	AAA	AAA	GCG		632
Arg	Met	Val	Val	Val	Gly	Trp	Leu	Gly	Val	Asn	Ser	Ala	Lys	Lys	Ala		
	180					185					190						
GCT	TTA	ATC	CAA	GAA	GAA	ATG	GCG	AAA	GCT	AGG	GCT	AGG	GGA	GCG	AGC		680
Ala	Leu	Ile	Gln	Glu	Glu	Met	Ala	Lys	Ala	Arg	Ala	Arg	Gly	Ala	Ser		
	195				200				205						210		
GTG	GAA	GAT	AAG	ATC	TCT	ATT	CTT	GAA	AAG	ATT	TAT	TCC	ACC	CAA	TAC		728
Val	Glu	Asp	Lys	Ile	Ser	Ile	Leu	Glu	Lys	Ile	Tyr	Ser	Thr	Gln	Tyr		
				215					220						225		
GAT	ATT	AAC	GCT	CAA	AAA	GAG	CCT	GAA	GAT	TTA	CGC	ACT	AAA	GTG	GAA		776
Asp	Ile	Asn	Ala	Gln	Lys	Glu	Pro	Glu	Asp	Leu	Arg	Thr	Lys	Val	Glu		
			230				235						240				
AAT	ACC	ACT	AAA	AAG	ATT	TTT	GAA	TCT	GGC	GTG	ATT	AAG	GGT	GTG	CCT		824
Asn	Thr	Thr	Lys	Lys	Ile	Phe	Glu	Ser	Gly	Val	Ile	Lys	Gly	Val	Pro		
			245				250					255					
TTC	TTA	TAC	CAT	TAT	AAG	GCA	TGATATAAGG	TTGCTCTCAT	GAAAAAACCC	TATA							879
Phe	Leu	Tyr	His	Tyr	Lys	Ala											
	260					265											
GGAAGATTTC	TGATTATGC																898

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

290		295		300
Phe Asn Asp Gly Pro Lys Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn				
305		310		315
Ser Ala Ala Leu Arg Phe Ile Pro Leu Lys Asp Met Glu Lys Glu Gly				
	325		330	335
Tyr Gly Glu Phe Ile Pro Tyr Ile Lys Lys Gly Glu Leu Lys Lys Tyr				
	340		345	350
Ile Asn Asp Lys Lys Ser His				
355				

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...845
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTATTTCTTA TTATTGTAAG GATTTAGGCT ATTGAACTTT AGGAGTTTTA ATG ATA	56
Met Ile	
1	
TTA AGA GCG AGT GTG TTG AGC GCG TTA CTT CTT GTA GGC TTA GGG GCA	104
Leu Arg Ala Ser Val Leu Ser Ala Leu Leu Leu Val Gly Leu Gly Ala	
5 10 15	
GCC CCT AAA CAT TCA GTT TCA GCT AAT GAC AAA CGG ATG CAG GAT AAT	152
Ala Pro Lys His Ser Val Ser Ala Asn Asp Lys Arg Met Gln Asp Asn	
20 25 30	
TTA GTG AGC GTG ATT GAA AAA CAG ACC AAT AAA AAG GTG CGT ATT TTA	200
Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg Ile Leu	
35 40 45 50	
GAA ATC AAA CCT TTA AAA TCT AGC CAG GAT TTA AAA ATG GTC GTT ATT	248
Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val Val Ile	
55 60 65	
GAA GAT CCG GAC ACT AAA TAC AAT ATC CCG CTT GTG GTG AGT AAG GAT	296
Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser Lys Asp	
70 75 80	
GGT AAT TTA ATC ATA GGG CTT AGC AAC ATA TTC TTT AGC AAT AAA AGC	344

Asp Lys Lys Ser His
355

GGGGTTTAAG CG

1180

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met	Lys	Val	Leu	Ser	Tyr	Leu	Lys	Asn	Phe	Tyr	Leu	Phe	Leu	Ala	Ile
1				5					10					15	
Gly	Ala	Ile	Met	Gln	Ala	Ser	Glu	Asn	Met	Gly	Ser	Gln	His	Gln	Lys
			20					25					30		
Thr	Asp	Glu	Arg	Val	Ile	Tyr	Leu	Ala	Gly	Gly	Cys	Phe	Trp	Gly	Leu
		35					40					45			
Glu	Ala	Tyr	Met	Glu	Arg	Ile	Tyr	Gly	Val	Ile	Asp	Ala	Ser	Ser	Gly
		50				55					60				
Tyr	Ala	Asn	Gly	Lys	Thr	Ser	Ser	Thr	Asn	Tyr	Glu	Lys	Leu	His	Glu
65					70					75				80	
Ser	Asp	His	Ala	Glu	Ser	Val	Lys	Val	Ile	Tyr	Asp	Pro	Lys	Lys	Ile
			85						90					95	
Ser	Leu	Asp	Lys	Leu	Leu	Arg	Tyr	Tyr	Phe	Lys	Val	Val	Asp	Pro	Val
			100					105					110		
Ser	Val	Asn	Lys	Gln	Gly	Asn	Asp	Val	Gly	Arg	Gln	Tyr	Arg	Thr	Gly
		115				120					125				
Ile	Tyr	Tyr	Val	Asn	Ser	Ala	Asp	Lys	Glu	Val	Ile	Asp	His	Ala	Leu
	130					135					140				
Lys	Ala	Leu	Gln	Lys	Glu	Val	Lys	Gly	Lys	Ile	Ala	Ile	Glu	Val	Glu
145					150					155					160
Pro	Leu	Lys	Asn	Tyr	Val	Arg	Ala	Glu	Glu	Tyr	His	Gln	Asp	Tyr	Leu
			165					170					175		
Lys	Lys	His	Pro	Ser	Gly	Tyr	Cys	His	Ile	Asp	Leu	Lys	Lys	Ala	Asp
		180					185						190		
Glu	Val	Ile	Val	Asp	Asp	Asp	Lys	Tyr	Thr	Lys	Pro	Ser	Asp	Glu	Val
		195				200					205				
Leu	Lys	Lys	Lys	Leu	Thr	Lys	Leu	Gln	Tyr	Glu	Val	Thr	Gln	Asn	Lys
	210					215					220				
His	Thr	Glu	Lys	Pro	Phe	Glu	Asn	Glu	Tyr	Tyr	Asn	Lys	Glu	Glu	Glu
225				230						235					240
Gly	Ile	Tyr	Val	Asp	Ile	Thr	Thr	Gly	Glu	Pro	Leu	Phe	Ser	Ser	Ala
			245						250					255	
Asp	Lys	Tyr	Asp	Ser	Gly	Cys	Gly	Trp	Pro	Ser	Phe	Ser	Lys	Pro	Ile
		260						265					270		
Asn	Lys	Asp	Val	Val	Lys	Tyr	Glu	Asp	Asp	Glu	Ser	Leu	Asn	Arg	Lys
		275				280						285			
Arg	Ile	Glu	Val	Leu	Ser	Arg	Ile	Gly	Lys	Ala	His	Leu	Gly	His	Val

																135																	140																	145																
TTA	CAG	AAA	GAA	GTG	AAA	GGT	AAA	ATC	GCT	ATT	GAA	GTA	GAG	CCT	TTA	536																																																		
Leu	Gln	Lys	Glu	Val	Lys	Gly	Lys	Ile	Ala	Ile	Glu	Val	Glu	Pro	Leu																																																			
			150						155			160																																																						
AAA	AAT	TAT	GTG	AGG	GCT	GAA	GAG	TAT	CAT	CAG	GAT	TAT	TTG	AAG	AAA	584																																																		
Lys	Asn	Tyr	Val	Arg	Ala	Glu	Glu	Tyr	His	Gln	Asp	Tyr	Leu	Lys	Lys																																																			
			165						170			175																																																						
CAC	CCT	AGT	GGT	TAT	TGC	CAT	ATT	GAT	TTG	AAA	AAG	GCG	GAT	GAA	GTG	632																																																		
His	Pro	Ser	Gly	Tyr	Cys	His	Ile	Asp	Leu	Lys	Lys	Ala	Asp	Glu	Val																																																			
			180						185			190																																																						
ATT	GTG	GAT	GAC	GAT	AAA	TAC	ACC	AAA	CCT	AGC	GAT	GAA	GTT	TTA	AAG	680																																																		
Ile	Val	Asp	Asp	Asp	Lys	Tyr	Thr	Lys	Pro	Ser	Asp	Glu	Val	Leu	Lys																																																			
			195						200			205			210																																																			
AAA	AAA	CTC	ACC	AAA	CTC	CAG	TAT	GAG	GTT	ACG	CAA	AAC	AAA	CAC	ACT	728																																																		
Lys	Lys	Leu	Thr	Lys	Leu	Gln	Tyr	Glu	Val	Thr	Gln	Asn	Lys	His	Thr																																																			
			215						220			225																																																						
GAG	AAA	CCC	TTT	GAA	AAC	GAG	TAT	TAC	AAC	AAA	GAA	GAA	GAG	GGC	ATT	776																																																		
Glu	Lys	Pro	Phe	Glu	Asn	Glu	Tyr	Tyr	Asn	Lys	Glu	Glu	Glu	Gly	Ile																																																			
			230						235			240																																																						
TAT	GTG	GAT	ATT	ACC	ACA	GGC	GAG	CCG	TTA	TTT	TCT	TCA	GCG	GAT	AAA	824																																																		
Tyr	Val	Asp	Ile	Thr	Thr	Gly	Glu	Pro	Leu	Phe	Ser	Ser	Ala	Asp	Lys																																																			
			245						250			255																																																						
TAC	GAC	TCC	GGT	TGC	GGG	TGG	CCA	AGC	TTT	TCT	AAG	CCT	ATC	AAT	AAA	872																																																		
Tyr	Asp	Ser	Gly	Cys	Gly	Trp	Pro	Ser	Phe	Ser	Lys	Pro	Ile	Asn	Lys																																																			
			260						265			270																																																						
GAT	GTG	GTG	AAA	TAC	GAA	GAC	GAT	GAG	AGC	CTT	AAT	AGG	AAA	CGC	ATT	920																																																		
Asp	Val	Val	Lys	Tyr	Glu	Asp	Asp	Glu	Ser	Leu	Asn	Arg	Lys	Arg	Ile																																																			
			275						280			285			290																																																			
GAA	GTG	TTG	AGC	CGT	ATT	GGT	AAG	GCG	CAT	TTA	GGG	CAT	GTG	TTT	AAC	968																																																		
Glu	Val	Leu	Ser	Arg	Ile	Gly	Lys	Ala	His	Leu	Gly	His	Val	Phe	Asn																																																			
			295						300			305																																																						
GAT	GGG	CCT	AAA	GAA	TTA	GGG	GGC	TTA	AGG	TAT	TGC	ATC	AAC	AGC	GCG	1016																																																		
Asp	Gly	Pro	Lys	Glu	Leu	Gly	Gly	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	Ala																																																			
			310						315			320																																																						
GCT	TTA	AGG	TTT	ATC	CCC	TTA	AAA	GAC	ATG	GAA	AAA	GAG	GGT	TAT	GGC	1064																																																		
Ala	Leu	Arg	Phe	Ile	Pro	Leu	Lys	Asp	Met	Glu	Lys	Glu	Gly	Tyr	Gly																																																			
			325						330			335																																																						
GAG	TTT	ATC	CCT	TAT	ATC	AAA	AAG	GGT	GAA	TTG	AAA	AAA	TAC	ATC	AAT	1112																																																		
Glu	Phe	Ile	Pro	Tyr	Ile	Lys	Lys	Gly	Glu	Leu	Lys	Lys	Tyr	Ile	Asn																																																			
			340						345			350																																																						
GAT	AAA	AAG	TCG	CAT	TAAGGGGTAA	TGACTAAGCC	CCCTAAGGGG	GGTTAAAAATG	A	1168																																																								

- (A) LENGTH: 1180 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1127
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TTTTTAGTTA TAATGGCGGA CACCATTAAA ATTAAACAA AGGTTATTCA ATG AAG	56
Met Lys	
1	
GTA TTA TCT TAT TTG AAA AAT TTT TAT CTT TTT TTA GCG ATA GGA GCA	104
Val Leu Ser Tyr Leu Lys Asn Phe Tyr Leu Phe Leu Ala Ile Gly Ala	
5 10 15	
ATT ATG CAA GCG AGT GAA AAC ATG GGA TCT CAA CAC CAA AAA ACC GAT	152
Ile Met Gln Ala Ser Glu Asn Met Gly Ser Gln His Gln Lys Thr Asp	
20 25 30	
GAA AGA GTG ATT TAC TTG GCT GGG GGG TGT TTT TGG GGG CTA GAG GCG	200
Glu Arg Val Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Leu Glu Ala	
35 40 45 50	
TAT ATG GAG AGG ATT TAT GGC GTC ATA GAC GCA AGC TCT GGT TAC GCT	248
Tyr Met Glu Arg Ile Tyr Gly Val Ile Asp Ala Ser Ser Gly Tyr Ala	
55 60 65	
AAC GGC AAG ACT TCA AGC ACG AAT TAT GAG AAA TTG CAT GAA AGT GAT	296
Asn Gly Lys Thr Ser Ser Thr Asn Tyr Glu Lys Leu His Glu Ser Asp	
70 75 80	
CAT GCT GAA AGC GTG AAA GTC ATT TAT GAT CCT AAA AAA ATC AGT TTG	344
His Ala Glu Ser Val Lys Val Ile Tyr Asp Pro Lys Lys Ile Ser Leu	
85 90 95	
GAC AAA TTG TTG CGT TAC TAT TTT AAG GTG GTT GAT CCG GTG AGC GTG	392
Asp Lys Leu Leu Arg Tyr Tyr Phe Lys Val Val Asp Pro Val Ser Val	
100 105 110	
AAC AAG CAG GGT AAT GAT GTG GGC AGG CAG TAT CGC ACG GGG ATT TAT	440
Asn Lys Gln Gly Asn Asp Val Gly Arg Gln Tyr Arg Thr Gly Ile Tyr	
115 120 125 130	
TAT GTC AAT AGC GCG GAT AAA GAA GTG ATA GAT CAT GCC TTA AAA GCG	488
Tyr Val Asn Ser Ala Asp Lys Glu Val Ile Asp His Ala Leu Lys Ala	

AAG GTT GTT TTT TTA TTG TTA GTT ATA CTA GGG GGT TTA GAA GCG CAA 104
 Lys Val Val Phe Leu Leu Leu Val Ile Leu Gly Gly Leu Glu Ala Gln
 5 10 15

AGT ACT TAT TGC AGT GAT CAT TGC GAA GGC ACG CCA GAT AGC CGT ATC 152
 Ser Thr Tyr Cys Ser Asp His Cys Glu Gly Thr Pro Asp Ser Arg Ile
 20 25 30

CCT CCT ATG GGG TTT CAT TTC AGT TTT GTG CAT TCA GTG AAA TAT TAC 200
 Pro Pro Met Gly Phe His Phe Ser Phe Val His Ser Val Lys Tyr Tyr
 35 40 45 50

TTG CAA GAT CCG CAA GAG CGC GAT CAC AAG CTT GAA AAA TGC CAT CAA 248
 Leu Gln Asp Pro Gln Glu Arg Asp His Lys Leu Glu Lys Cys His Gln
 55 60 65

GCC TTT GAT TCG ACT CTT AAG GTT AAT TTT ATT ACG AAT CTT TTA AAA 296
 Ala Phe Asp Ser Thr Leu Lys Val Asn Phe Ile Thr Asn Leu Leu Lys
 70 75 80

AGG ATT GCA AGC ATG CGC AAA TGG CTT TAGAGCAAGC CCAAAAAGGG ACTCCAT 350
 Arg Ile Ala Ser Met Arg Lys Trp Leu
 85 90

AAAAGGGGTT TCTTTAGGGA TTTTAT 376

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met Lys Lys Val Val Phe Leu Leu Leu Val Ile Leu Gly Gly Leu Glu
 1 5 10 15
 Ala Gln Ser Thr Tyr Cys Ser Asp His Cys Glu Gly Thr Pro Asp Ser
 20 25 30
 Arg Ile Pro Pro Met Gly Phe His Phe Ser Phe Val His Ser Val Lys
 35 40 45
 Tyr Tyr Leu Gln Asp Pro Gln Glu Arg Asp His Lys Leu Glu Lys Cys
 50 55 60
 His Gln Ala Phe Asp Ser Thr Leu Lys Val Asn Phe Ile Thr Asn Leu
 65 70 75 80
 Leu Lys Arg Ile Ala Ser Met Arg Lys Trp Leu
 85 90

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

```

Asn Pro Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala
65          70          75          80
Leu Ile Asp Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys
          85          90          95
Thr Glu Lys Leu Asp Ser Thr Pro Glu Phe Lys Ala Met Met Glu Ala
          100         105         110
Val Lys Lys Gln Ala Leu Val Glu Phe Trp Ala Lys Lys Gln Ala Glu
          115         120         125
Glu Val Lys Lys Val Gln Ile Pro Glu Lys Glu Met Gln Asp Phe Tyr
          130         135         140
Asn Ala Asn Lys Asp Gln Leu Phe Val Lys Gln Glu Ala His Ala Arg
145          150          155          160
His Ile Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu
          165          170          175
Ile Asp Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu
          180         185         190
Ala Asn Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly
          195         200         205
Gly Asp Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser
          210         215         220
Lys Ala Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val
225          230          235          240
Lys Thr Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser
          245         250         255
Pro Val Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met
          260         265         270
Leu Gln Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu
          275         280         285
Leu Arg Lys His Ala Lys Ile Val Ile Asn Lys
          290         295

```

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...323
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

CAGCGTTGGT GTATTTTGGG GGAAGTTAGG AAAATATTGA AGGAGTATTG ATG AAA
Met Lys
1

```

56

```

AAA CAG CCA AAG GCT AAA AAA GAA GCT AAA TTC ATT GAG TTA GCC AAT      632
Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu Ala Asn
    180                      185                      190

CGG GAT ACG ATT GAT CCT AAC AGC AAG AAC GCG CAA AAT GGC GGT GAT      680
Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly Gly Asp
    195                      200                      205                      210

TTG GGG AAA TTC CAA AAG AAC CAA ATG GCT CCG GAT TTT TCT AAA GCC      728
Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser Lys Ala
                      215                      220                      225

GCT TTC GCT TTA ACT CCT GGG GAT TAC ACT AAA ACC CCT GTT AAA ACA      776
Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val Lys Thr
                      230                      235                      240

GAG TTT GGT TAT CAT ATT ATC TAT TTG ATT TCT AAA GAT AGC CCT GTA      824
Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser Pro Val
                      245                      250                      255

ACT TAT ACT TAT GAA CAG GCT AAA CCT ACC ATT AAG GGG ATG TTA CAA      872
Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met Leu Gln
    260                      265                      270

GAA AAG CTT TTC CAA GAA CGC ATG AAT CAA CGC ATT GAG GAA CTA AGA      920
Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu Leu Arg
    275                      280                      285                      290

AAG CAC GCT AAA ATT GTT ATC AAC AAG TAATTGATGA GGTGTTATCA TGTTAGT      974
Lys His Ala Lys Ile Val Ile Asn Lys
                      295

TAAAGGCAAT GAAATTTTAT TGAAAG      1000

```

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```

Met Lys Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Thr
 1           5           10           15
Ser Phe Leu Met Ala Lys Pro Ala His Asn Ala Asn Asn Ala Thr His
    20           25           30
Asn Thr Lys Lys Thr Thr Asp Ser Ser Ala Gly Val Leu Ala Thr Val
    35           40           45
Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg
    50           55           60

```

(B) LOCATION: 51...947

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CTATAATGTG AATTTAATGA TGAAAATTAG TTTAGAGTGG AGAACACACA ATG AAA	56
Met Lys	
1	
AAA AAT ATC TTA AAT TTA GCG TTA GTG GGT GCG TTG AGC ACG TCG TTT	104
Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Thr Ser Phe	
5 10 15	
TTG ATG GCT AAG CCG GCT CAT AAC GCA AAT AAC GCT ACG CAT AAC ACG	152
Leu Met Ala Lys Pro Ala His Asn Ala Asn Asn Ala Thr His Asn Thr	
20 25 30	
AAA AAA ACG ACT GAT TCT TCA GCA GGC GTG TTA GCG ACA GTG GAT GGC	200
Lys Lys Thr Thr Asp Ser Ser Ala Gly Val Leu Ala Thr Val Asp Gly	
35 40 45 50	
AGA CCT ATC ACT AAA AGC GAT TTT GAC ATG ATT AAG CAA CGA AAT CCT	248
Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg Asn Pro	
55 60 65	
AAT TTT GAT TTT GAC AAG CTT AAA GAG AAA GAA AAA GAA GCC TTG ATT	296
Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala Leu Ile	
70 75 80	
GAT CAA GCT ATT CGC ACC GCC CTT GTA GAA AAT GAA GCT AAA ACC GAG	344
Asp Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys Thr Glu	
85 90 95	
AAA TTG GAC AGC ACT CCA GAA TTT AAA GCG ATG ATG GAA GCG GTT AAA	392
Lys Leu Asp Ser Thr Pro Glu Phe Lys Ala Met Met Glu Ala Val Lys	
100 105 110	
AAA CAG GCT TTA GTG GAA TTT TGG GCT AAA AAA CAG GCT GAA GAA GTG	440
Lys Gln Ala Leu Val Glu Phe Trp Ala Lys Lys Gln Ala Glu Glu Val	
115 120 125 130	
AAA AAA GTC CAA ATC CCA GAA AAA GAA ATG CAA GAT TTT TAC AAC GCT	488
Lys Lys Val Gln Ile Pro Glu Lys Glu Met Gln Asp Phe Tyr Asn Ala	
135 140 145	
AAC AAA GAT CAG CTT TTT GTC AAG CAA GAA GCC CAT GCT AGG CAT ATT	536
Asn Lys Asp Gln Leu Phe Val Lys Gln Glu Ala His Ala Arg His Ile	
150 155 160	
TTA GTG AAA ACC GAA GAT GAG GCT AAA CGG ATT ATT TCT GAG ATT GAC	584
Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu Ile Asp	
165 170 175	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```

Met Ile Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met
 1           5           10           15
Ala Ser Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe
          20           25           30
Lys Met Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val
          35           40           45
Ala Phe Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr
          50           55           60
Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile
65           70           75           80
Thr Lys Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His
          85           90           95
Leu Ala Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val
          100          105          110
Gln Lys Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His
          115          120          125
Leu Lys Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn
          130          135          140
Gly Thr Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys
          145          150          155          160
Tyr Ala Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr
          165          170          175
Met Tyr Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu
          180          185          190
Ala Asn Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val
          195          200          205
Ser Leu Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly
          210          215          220
Glu Gln Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly
          225          230          235          240
Ser Gly Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val
          245          250          255
Pro Lys Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr
          260          265          270
Leu Gly Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys
          275          280          285
Lys Ser Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp
          290          295          300
Met Gln
305

```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr	
135 140 145	
GGC GTT AAG CAA AAT TAT GCC AAA GCC CTT TTT CTT TCT AAA TAC GCT	536
Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys Tyr Ala	
150 155 160	
TGC AGT TTG AAT TAC GGC ATT AGT TGT AAC TTT GTA GGG TAT ATG TAT	584
Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr	
165 170 175	
AGG AAC GCC AAA GGC GTA CAG AAG GAT TTG AAA AAA GCC CTT GCG AAT	632
Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn	
180 185 190	
TTT AAA AGA GGG TGC CAT TTG AAA GAC GGA GCG AGT TGT GTG AGC TTG	680
Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu	
195 200 205 210	
GGA TAC ATG TAT GAA GTC GGT ATG GAT GTC AAA CAA AAT GGA GAG CAA	728
Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln	
215 220 225	
GCC TTG AAT CTT TAT AAA AAG GGT TGT TAT TTA AAA AGG GGG AGC GGT	776
Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly	
230 235 240	
TGT CAT AAT GTG GCG GTG ATG TAT TAC ACC GGT AAG GGC GTT CCA AAG	824
Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys	
245 250 255	
GAT TTA GAT AAA GCC ATT TCG TAT TAT AAG AAA GGT TGC ACT CTA GGC	872
Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly	
260 265 270	
TTT AGT GGT AGC TGT AAA GTG TTA GAA GAA GTG ATT GGC AAG AAG TCT	920
Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser	
275 280 285 290	
GAT GAT TTG CAA GAT GAC GCG CAA AAC GAC ACG CAA GAT GAT ATG CAA T	969
Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln	
295 300 305	
AAGTTAAAGC TTATGGACTA ATGATTAAAA CTCATCTTAT AGAAATCTTT CT	1021

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...968
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TTACTGATTT TTCTTTGTGT GAGCTTTGGC TTAGTTTTGT AAGGAATGAG ATG ATA	56
Met Ile	
1	
AAG AGT TGG ACT AAA AAG TGG TTT TTG ATT TTA TTT TTA ATG GCA AGT	104
Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser	
5 10 15	
TGT TCC AGT TAT TTG GTG GCT ACA ACC GGT GAG AAA TAT TTT AAA ATG	152
Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met	
20 25 30	
GCT ACT CAA GCC TTT AAG AGA GGG GAC TAC CAT AAA GCG GTG GCT TTT	200
Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val Ala Phe	
35 40 45 50	
TAT AAG AGG AGC TGT AAT TTA AGG GTG GGG GTT GGT TGC ACG AGT TTA	248
Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr Ser Leu	
55 60 65	
GGC TCT ATG TAT GAA GAT GGC GAT GGC GTG GAT CAG AAT ATT ACA AAA	296
Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile Thr Lys	
70 75 80	
GCC GTT TTT TAT TAC AGA AGA GGG TGT AAT TTA AGG AAT CAT CTC GCT	344
Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His Leu Ala	
85 90 95	
TGC GCG AGT CTA GGC TCT ATG TAT GAA GAT GGC GAT GGT GTG CAA AAA	392
Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys	
100 105 110	
AAC CTT CCA AAG GCT ATC TAT TAT TAC AGG AGA GGG TGC CAC TTA AAG	440
Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys	
115 120 125 130	
GGT GGG GTG AGC TGT GGG AGT TTA GGT TTT ATG TAT TTT AAT GGC ACG	488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

CTTGGGTAAT TCCAGGATCA ACGCCAATCA AAACGCTAAA TAAGGGGTGA ATG ATG      56
                                     Met Met
                                     1

GAT TTA GAA AGT TTG AGA GGT TTT GCG TAT GCG TTT TTT ACC ATT CTT      104
Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr Ile Leu
      5              10              15

TTT ACG CTC TTT TTG TAT GCC TAT ATT TTT AGC ATG TAT AGA AAG CAA      152
Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg Lys Gln
      20              25              30

AAA AAA GGC ATT ATG GAT TAT GAG CGA TAC GGA TAC TTA GCG TTA AAT      200
Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala Leu Asn
      35              40              45              50

GAT GCT TTA GAA GAC GAG TTG ATT GAA CCA CGC CAT AAA AAA GTT CAT      248
Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys Val His
      55              60              65

GAT AAT GGC ATA AAG GAA AGT TGAAATGGAT TTTTAAACG ACCATATAAA TGTT      303
Asp Asn Gly Ile Lys Glu Ser
      70

TTTGGCTTGA TTGCAGCGC      322

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

Met Met Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr
  1              5              10              15
Ile Leu Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg
      20              25              30
Lys Gln Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala
      35              40              45
Leu Asn Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys
      50              55              60
Val His Asp Asn Gly Ile Lys Glu Ser
      65              70

```

(2) INFORMATION FOR SEQ ID NO:241:

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

```

Met Phe Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe
 1           5           10           15
Ile Phe Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe
 20           25           30
Phe Lys Ser Ala Arg Pro Ile Glu Gly Leu Arg Pro Tyr Thr Val Leu
 35           40           45
Glu Thr Ala Gly Arg Gln Ile Tyr Ile Gln Glu Gly Cys Tyr His Cys
 50           55           60
His Ser Gln Leu Ile Arg Pro Phe Gln Ala Glu Val Asp Arg Tyr Gly
 65           70           75           80
Ala Tyr Ser Leu Ser Gly Glu Tyr Ala Tyr Asp Arg Pro Phe Leu Trp
 85           90           95
Gly Ser Lys Arg Ile Gly Pro Asp Leu His Arg Val Gly Asp Tyr Arg
 100          105          110
Thr Thr Asp Trp His Glu Lys His Met Phe Asp Pro Lys Ser Val Val
 115          120          125
Pro His Ser Ile Met Pro Ala Tyr Lys His Leu Phe Thr Lys Lys Ser
 130          135          140
Asp Phe Asp Thr Ala Tyr Ala Glu Ala Leu Thr Gln Lys Lys Val Phe
 145          150          155          160
Gly Val Pro Tyr Asp Thr Glu Asn Gly Val Lys Leu Gly Ser Val Glu
 165          170          175
Glu Ala Lys Lys Ala Tyr Leu Glu Glu Ala Lys Lys Ile Thr Ala Asp
 180          185          190
Met Lys Asp Lys Arg Val Leu Glu Ala Ile Glu Arg Gly Glu Val Leu
 195          200          205
Glu Ile Val Ala Leu Ile Ala Tyr Leu Asn Ser Leu Gly Asn Ser Arg
 210          215          220
Ile Asn Ala Asn Gln Asn Ala Lys
 225          230

```

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 51...269
 - (D) OTHER INFORMATION:

GCG GGG AGG CAA ATT TAT ATC CAA GAA GGT TGC TAT CAT TGC CAT TCC	248
Ala Gly Arg Gln Ile Tyr Ile Gln Glu Gly Cys Tyr His Cys His Ser	
55 60 65	
CAG CTT ATT CGC CCT TTC CAA GCT GAG GTG GAT CGA TAT GGC GCG TAT	296
Gln Leu Ile Arg Pro Phe Gln Ala Glu Val Asp Arg Tyr Gly Ala Tyr	
70 75 80	
AGT TTG AGT GGG GAA TAC GCG TAT GAC AGG CCA TTT TTG TGG GGT TCT	344
Ser Leu Ser Gly Glu Tyr Ala Tyr Asp Arg Pro Phe Leu Trp Gly Ser	
85 90 95	
AAA AGG ATT GGC CCT GAT TTG CAC AGG GTA GGG GAT TAT CGC ACA ACC	392
Lys Arg Ile Gly Pro Asp Leu His Arg Val Gly Asp Tyr Arg Thr Thr	
100 105 110	
GAT TGG CAT GAA AAG CAC ATG TTT GAT CCT AAA AGC GTT GTG CCG CAC	440
Asp Trp His Glu Lys His Met Phe Asp Pro Lys Ser Val Val Pro His	
115 120 125 130	
AGC ATC ATG CCC GCC TAT AAG CAT TTA TTT ACA AAA AAG AGC GAT TTT	488
Ser Ile Met Pro Ala Tyr Lys His Leu Phe Thr Lys Lys Ser Asp Phe	
135 140 145	
GAC ACC GCT TAT GCA GAA GCT TTG ACG CAA AAA AAG GTT TTT GGC GTG	536
Asp Thr Ala Tyr Ala Glu Ala Leu Thr Gln Lys Lys Val Phe Gly Val	
150 155 160	
CCT TAT GAC ACA GAA AAC GGC GTG AAA TTA GGG AGC GTA GAA GAA GCG	584
Pro Tyr Asp Thr Glu Asn Gly Val Lys Leu Gly Ser Val Glu Glu Ala	
165 170 175	
AAA AAA GCC TAT TTA GAA GAA GCT AAA AAA ATC ACA GCC GAT ATG AAA	632
Lys Lys Ala Tyr Leu Glu Glu Ala Lys Lys Ile Thr Ala Asp Met Lys	
180 185 190	
GAC AAG AGG GTG CTA GAA GCG ATT GAG AGA GGT GAA GTG TTA GAA ATT	680
Asp Lys Arg Val Leu Glu Ala Ile Glu Arg Gly Glu Val Leu Glu Ile	
195 200 205 210	
GTG GCT TTG ATC GCT TAT TTG AAT AGC TTG GGT AAT TCC AGG ATC AAC	728
Val Ala Leu Ile Ala Tyr Leu Asn Ser Leu Gly Asn Ser Arg Ile Asn	
215 220 225	
GCC AAT CAA AAC GCT AAA TAAGGGGTGA ATGATGGATT TAGAAAGTTT GAGAGGTT	784
Ala Asn Gln Asn Ala Lys	
230	
TTGCGTATGC GTTTT	799

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

Met Lys Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala
 1           5           10           15
Asn Pro Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala
 20           25           30
Gln Phe Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Arg Ala
 35           40           45
Tyr Arg Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp
 50           55           60
Leu Glu Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn
 65           70           75           80
Ala Glu Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn
 85           90           95
Ala Ser Ser Arg Thr Val Leu Asp Ser Ala Ala Gln
 100          105

```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...746
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

AGCGTGAGCC CAATTACGCC ACGCCTATGT CTAGATAGGG GAGGTTGGAA ATG TTT      56
                                     Met Phe
                                     1

AGT TTT TTA GAA AAA AAC CCG TTC TTT TTC ACT CTT GCG TTT ATT TTT      104
Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe Ile Phe
 5           10           15

GTG TTT GCG ATC GCG GGC TTG GTG GAG ATT TTG CCC AAC TTC TTC AAA      152
Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe Phe Lys
 20           25           30

TCC GCT CGC CCG ATT GAA GGC TTA CGG CCT TAT ACG GTT TTA GAG ACA      200
Ser Ala Arg Pro Ile Glu Gly Leu Arg Pro Tyr Thr Val Leu Glu Thr
 35           40           45           50

```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...374

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

GTTAGAGATT TCTCCCAATT CTCAAGTGGG AGCGAGCGTG AAAATCCGCT ATG AAA      56
                                   Met Lys
                                   1

GCA ATC TTT AGC CTC TTT TTC CTT CTT ATT GTT TTA AAA GCA AAC CCC      104
Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala Asn Pro
      5                      10                      15

ATA AAC CCT TTA TTA GAG CCG TTA TAT TTC CCC AGT TAC GCG CAA TTT      152
Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala Gln Phe
      20                      25                      30

TTA AAC TTA GCA CCT CAC TTT GTC ATT AAA AAA AAG CGC GCT TAT AGA      200
Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Lys Arg Ala Tyr Arg
      35                      40                      45                      50

CCC TTT CAA TGG GGG AAT ACC ATT ATC ATC AAA CGC CAT GAT TTA GAA      248
Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp Leu Glu
      55                      60                      65

GAA CGC CAA AGC AAC CAG CCA AGC GAT ATT TTC CGC CAA AAC GCT GAA      296
Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn Ala Glu
      70                      75                      80

ATC AAT GTG TCT TCT CAA ACT TTT TTA AAA GGA ATG AGC AAC GCT TCT      344
Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn Ala Ser
      85                      90                      95

TCA CGA ACA GTG CTT GAT TCA GCC GCT CAG TAAAATGCTA AAACCTTTTTT TAA      397
Ser Arg Thr Val Leu Asp Ser Ala Ala Gln
      100                      105

TCACATTTTTT CTTGGTATTT TCTTAATCC      426

```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met 1	Lys	Lys	Ser	Ile 5	Leu	Leu	Gly	Val	Cys 10	Leu	Ala	Phe	Ser	Cys 15	Ala
His	Ala	Leu	Asn 20	Asp	Leu	Glu	Leu	Ile 25	Lys	Lys	Ala	Arg	Glu 30	Ser	Gln
Leu	Glu	Pro 35	Met	Pro	Met	Gly	Lys 40	Ala	Leu	Lys	Glu	Tyr 45	Gln	Ile	Lys
Lys 50	Thr	Arg	Asp	Val	Gly	Ile 55	Gly	Thr	Lys	Asn 60	Ser	Glu	Ile	Met	Thr
Ser 65	Ala	Gln	Val	Glu	Leu 70	Gly	Lys	Met	Leu 75	Tyr	Phe	Asp	Pro	Arg	Ile
Ser	Thr	Ser	Tyr 85	Leu	Val	Ser	Cys	Asn 90	Thr	Cys	His	Asn	Leu 95	Gly	Leu
Gly	Gly	Val 100	Asp	Leu	Val	Pro	Ser 105	Ala	Ile	Gly	Ser	Gln 110	Trp	Lys	Lys
Asn	Pro	His 115	Leu	Leu	Ser	Ser	Pro 120	Thr	Val	Tyr	Asn 125	Ser	Val	Phe	Asn
Asp 130	Val	Gln	Phe	Trp	Asp	Gly 135	Arg	Val	Thr	His 140	Leu	Asn	Glu	Gln	Ala
Gln 145	Gly	Pro	Ile	Gln	Ser 150	Ser	Phe	Glu	Met	Gly 155	Ala	Asp	Pro	Lys	Val
Val	Val	Glu	Lys 165	Ile	Asn	Ser	Met	Pro	Gly 170	Tyr	Val	Lys	Leu 175	Phe	Arg
Lys	Ala	Tyr 180	Gly	Ser	Lys	Val	Lys 185	Ile	Asp	Phe	Lys	Leu 190	Ile	Ala	Asp
Ser	Ile	Ala 195	Met	Phe	Glu	Ala	Thr 200	Leu	Ile	Thr	Pro	Ser 205	Arg	Tyr	Asp
Asp 210	Phe	Leu	Arg	Gly	Asn	Pro	Lys 215	Ala	Leu	Ser	Lys 220	Ala	Glu	Lys	Glu
Gly 225	Leu	Asn	Leu	Phe	Ile 230	Ser	Lys	Gly	Cys	Val 235	Ala	Cys	His	Asn	Gly
Ile	Asn	Leu	Gly 245	Gly	Thr	Met	Gln	Pro	Phe 250	Gly	Val	Val 255	Lys	Pro	Tyr
Lys	Phe	Ala 260	Asn	Val	Gly	Asp	Phe 265	Lys	Gly	Asp	Lys	Asn 270	Gly	Leu	Val
Lys	Val	Pro 275	Thr	Leu	Arg	Asn	Ile 280	Thr	Glu	Thr	Met 285	Pro	Tyr	Phe	His
Asn 290	Gly	Gln	Phe	Trp	Asp	Val 295	Lys	Asp	Ala	Ile 300	Lys	Glu	Met	Gly	Ser
Ile 305	Gln	Leu	Gly	Ile	Glu 310	Ile	Ser	Asp	Glu	Glu 315	Ala	Lys	Lys	Ile	Glu
Thr	Phe	Phe	Gly 325	Ala	Leu	Arg	Gly	Lys	Lys 330	Pro	Lys	Ile 335	Ile	Tyr	Pro
Glu	Leu	Pro 340	Ile	Met	Thr	Asp	Lys 345	Thr	Pro	Lys	Pro	Ser 350	Phe		

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

TAT GGC TCT AAA GTC AAA ATT GAT TTT AAA TTG ATC GCT GAT AGT ATC	632
Tyr Gly Ser Lys Val Lys Ile Asp Phe Lys Leu Ile Ala Asp Ser Ile	
180 185 190	
GCT ATG TTT GAA GCC ACG CTT ATT ACC CCA AGC CGT TAC GAC GAT TTT	680
Ala Met Phe Glu Ala Thr Leu Ile Thr Pro Ser Arg Tyr Asp Asp Phe	
195 200 205 210	
TTA AGA GGC AAT CCT AAA GCG CTC AGC AAA GCC GAA AAA GAG GGG CTG	728
Leu Arg Gly Asn Pro Lys Ala Leu Ser Lys Ala Glu Lys Glu Gly Leu	
215 220 225	
AAT TTA TTC ATT TCT AAA GGC TGT GTG GCT TGC CAT AAC GGC ATT AAT	776
Asn Leu Phe Ile Ser Lys Gly Cys Val Ala Cys His Asn Gly Ile Asn	
230 235 240	
CTT GGG GGA ACG ATG CAG CCT TTT GGG GTG GTC AAA CCT TAT AAA TTC	824
Leu Gly Gly Thr Met Gln Pro Phe Gly Val Val Lys Pro Tyr Lys Phe	
245 250 255	
GCT AAT GTG GGC GAT TTC AAA GGC GAT AAA AAC GGG CTT GTG AAA GTG	872
Ala Asn Val Gly Asp Phe Lys Gly Asp Lys Asn Gly Leu Val Lys Val	
260 265 270	
CCT ACT TTA AGG AAT ATC ACC GAA ACG ATG CCC TAT TTC CAT AAC GGG	920
Pro Thr Leu Arg Asn Ile Thr Glu Thr Met Pro Tyr Phe His Asn Gly	
275 280 285 290	
CAA TTC TGG GAT GTT AAG GAT GCG ATT AAA GAA ATG GGC TCT ATC CAG	968
Gln Phe Trp Asp Val Lys Asp Ala Ile Lys Glu Met Gly Ser Ile Gln	
295 300 305	
TTA GGC ATT GAA ATC AGC GAT GAA GAA GCG AAA AAA ATT GAA ACT TTC	1016
Leu Gly Ile Glu Ile Ser Asp Glu Glu Ala Lys Lys Ile Glu Thr Phe	
310 315 320	
TTT GGA GCC TTA AGG GGT AAA AAA CCT AAA ATA ATC TAC CCA GAA CTC	1064
Phe Gly Ala Leu Arg Gly Lys Lys Pro Lys Ile Ile Tyr Pro Glu Leu	
325 330 335	
CCC ATA ATG ACA GAC AAA ACC CCT AAA CCC TCT TTT TGATTTAAAA AAGTCC	1116
Pro Ile Met Thr Asp Lys Thr Pro Lys Pro Ser Phe	
340 345 350	
TTTTAGGGGT CTTTGCGCT AAATCTAAAA AATACTC	1153

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...1100

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TTATAATAAG AAAGTTTTTA TTATTTTAA TGCTATTTTA GGAGTTCATC	ATG AAA	56
	Met Lys	
	1	
AAA TCC ATT TTA TTG GGC GTT TGC TTG GCT TTT TCT TGC GCT CAT GCC		104
Lys Ser Ile Leu Leu Gly Val Cys Leu Ala Phe Ser Cys Ala His Ala		
5 10 15		
CTA AAC GAT TTA GAA TTG ATC AAA AAA GCG AGG GAA AGC CAG CTA GAA		152
Leu Asn Asp Leu Glu Leu Ile Lys Lys Ala Arg Glu Ser Gln Leu Glu		
20 25 30		
CCC ATG CCT ATG GGC AAA GCG CTC AAA GAA TAC CAG ATT AAA AAG ACC		200
Pro Met Pro Met Gly Lys Ala Leu Lys Glu Tyr Gln Ile Lys Lys Thr		
35 40 45 50		
AGA GAT GTG GGT ATT GGC ACC AAA AAC AGC GAA ATC ATG ACC TCC GCT		248
Arg Asp Val Gly Ile Gly Thr Lys Asn Ser Glu Ile Met Thr Ser Ala		
55 60 65		
CAA GTG GAA TTA GGC AAA ATG CTC TAT TTT GAC CCT AGG ATT TCC ACT		296
Gln Val Glu Leu Gly Lys Met Leu Tyr Phe Asp Pro Arg Ile Ser Thr		
70 75 80		
TCC TAC CTC GTG TCT TGC AAC ACA TGC CAT AAT CTG GGC TTA GGC GGG		344
Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu Gly Gly		
85 90 95		
GTG GAT TTA GTC CCA AGC GCC ATA GGC TCT CAA TGG AAG AAA AAC CCC		392
Val Asp Leu Val Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys Asn Pro		
100 105 110		
CAC CTT TTA AGC TCC CCA ACG GTG TAT AAC TCT GTG TTT AAC GAT GTG		440
His Leu Leu Ser Ser Pro Thr Val Tyr Asn Ser Val Phe Asn Asp Val		
115 120 125 130		
CAG TTT TGG GAT GGC AGG GTT ACG CAT TTA AAC GAA CAG GCG CAA GGG		488
Gln Phe Trp Asp Gly Arg Val Thr His Leu Asn Glu Gln Ala Gln Gly		
135 140 145		
CCC ATC CAG TCT TCT TTT GAA ATG GGG GCT GAT CCC AAA GTG GTG GTA		536
Pro Ile Gln Ser Ser Phe Glu Met Gly Ala Asp Pro Lys Val Val Val		
150 155 160		
GAA AAA ATC AAT TCC ATG CCA GGC TAT GTC AAG CTC TTT AGA AAA GCC		584
Glu Lys Ile Asn Ser Met Pro Gly Tyr Val Lys Leu Phe Arg Lys Ala		
165 170 175		

CCA AGC CTG ATC CAA TCT CAT AAA GAT TCT AAT CGC AAT TTT AAA ACC 344
 Pro Ser Leu Ile Gln Ser His Lys Asp Ser Asn Arg Asn Phe Lys Thr
 85 90 95

ATC ACT TTT TGG CTC GTT CCC ACA AAA AGC CAC GCA ACT TAC TAC ATC 392
 Ile Thr Phe Trp Leu Val Pro Thr Lys Ser His Ala Thr Tyr Tyr Ile
 100 105 110

ATT AAG GTT TAATCACAAT GGATAAAAAC AACAATAATC TCCGCTTGAT TTTAGCGAT 450
 Ile Lys Val
 115

CGCT 454

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Met Arg Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser
 1 5 10 15
 Ile Arg Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys
 20 25 30
 Arg Phe Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe
 35 40 45
 Glu Ser Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser
 50 55 60
 Cys Asn Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu
 65 70 75 80
 Lys Arg Pro Ser Leu Ile Gln Ser His Lys Asp Ser Asn Arg Asn Phe
 85 90 95
 Lys Thr Ile Thr Phe Trp Leu Val Pro Thr Lys Ser His Ala Thr Tyr
 100 105 110
 Tyr Ile Ile Lys Val
 115

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:


```

Asp Ser Gln Pro Phe Lys Ala Ile Gly Val Lys Glu Ser Val Leu Phe
145                      150                      155                      160
Leu Glu Lys Arg Leu Thr Leu Lys Glu Leu Glu Glu Ala Ile Thr Ser
                      165                      170                      175
Asn Thr Met Lys Leu Ala Lys Arg Gln Asn Thr Phe Asn Lys Thr Gln
                      180                      185                      190
Phe Asn Asn Leu Tyr Val Gly Ser Ala Glu Glu Val Arg His Ala Ile
                      195                      200                      205
Leu Lys His Ser Lys Ser Gly Ile Lys Gly
210                      215

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...401
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

CTATATGAAC AAAGCCTTAA AAGACTTGAA AAAAGGAATA ACTCATACT ATG CGA      56
                                         Met Arg
                                         1

AAC AAT AAA ACG CCT TTT TTG AGC GCG ATT TTT ACG GCA TCA ATT AGG      104
Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser Ile Arg
      5                      10                      15

GGT TAC CAA CGC TTT TTT TCG GCT TTC ACC CCT TCA AGC TGC CGG TTT      152
Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys Arg Phe
      20                      25                      30

TAC CCC ACT TGT TCC AAC TAC GCT CTG TGG TTG CTC TGT TTT GAA AGC      200
Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe Glu Ser
      35                      40                      45                      50

CCT TTG AGC GCT ATG GGT AAG ATC GCT ATA AGG ATA CTC TCA TGC AAC      248
Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser Cys Asn
      55                      60                      65

CCT TTT TGC TCT GGG GGC ATT GCT TAC CCT ACT ACT CGC TTG AAA CGC      296
Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu Lys Arg
      70                      75                      80

```

	135	140	145	
CAG CCT TTT AAA GCC ATA GGC GTT AAA GAG AGC GTT CTT TTT TTA GAA				536
Gln Pro Phe Lys Ala Ile Gly Val Lys Glu Ser Val Leu Phe Leu Glu				
	150	155	160	
AAA CGA CTC ACT TTA AAG GAG CTA GAA GAA GCG ATT ACC TCT AAC ACC				584
Lys Arg Leu Thr Leu Lys Glu Leu Glu Glu Ala Ile Thr Ser Asn Thr				
	165	170	175	
ATG AAA TTA GCC AAG CGC CAA AAC ACT TTC AAT AAA ACC CAA TTC AAT				632
Met Lys Leu Ala Lys Arg Gln Asn Thr Phe Asn Lys Thr Gln Phe Asn				
	180	185	190	
AAC CTT TAT GTG GGG AGC GCT GAA GAA GTT AGG CAT GCG ATT TTA AAA				680
Asn Leu Tyr Val Gly Ser Ala Glu Glu Val Arg His Ala Ile Leu Lys				
	195	200	205	210
CAC TCA AAA AGC GGC ATT AAA GGA TAATCTAATG GATACACAAA ACTTACCCGA				734
His Ser Lys Ser Gly Ile Lys Gly				
	215			
TCAAATTATC CCTATTTTGA TGA				757

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met	Arg	Val	Ser	Ser	Lys	Glu	Ile	Leu	Leu	Ile	Val	Gly	Gly	Ser	Ser
1				5				10						15	
Phe	Tyr	Leu	Lys	Ser	Ile	Leu	Glu	Gly	Leu	Ser	Arg	Met	Pro	Lys	Leu
			20					25					30		
Ser	Gly	Glu	Glu	Val	Val	Lys	Ile	Glu	Arg	Glu	Ile	Ala	Thr	Leu	Ser
			35					40				45			
Asn	Pro	Tyr	Ile	Phe	Leu	Lys	Ser	Ile	Asp	Pro	Asn	Met	Ala	Phe	Lys
			50				55				60				
Ile	His	Pro	Asn	Asp	Thr	Tyr	Arg	Thr	His	Lys	Ala	Leu	Glu	Ile	Phe
65					70				75					80	
Tyr	Ala	Thr	Cys	Thr	Pro	Pro	Ser	Glu	Tyr	Phe	Lys	Ala	Asn	Pro	Lys
				85				90					95		
Lys	Pro	Phe	Glu	His	Ala	Ile	Ser	Leu	Phe	Ala	Leu	Ser	Ile	Glu	Lys
			100					105					110		
Ser	Ala	Leu	His	Asn	Asn	Ile	Lys	Arg	Arg	Thr	Lys	Asn	Met	Leu	His
			115				120					125			
Ser	Gly	Leu	Val	Glu	Glu	Ile	Lys	Ala	Leu	Tyr	Thr	Gln	Tyr	Pro	Lys
			130				135					140			

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...704
- (D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

TTGATGAAAA AAATAACGCT CCTCTTTTAA AAACCTCTTTT AGAGGATGCC ATG AGA	56
Met Arg	
1	
GTG TCT TCT AAA GAG ATT TTA CTC ATT GTG GGG GGG AGC AGT TTT TAC	104
Val Ser Ser Lys Glu Ile Leu Leu Ile Val Gly Gly Ser Ser Phe Tyr	
5 10 15	
CTC AAA TCC ATT TTA GAA GGT TTG AGC CGC ATG CCA AAA CTG AGC GGT	152
Leu Lys Ser Ile Leu Glu Gly Leu Ser Arg Met Pro Lys Leu Ser Gly	
20 25 30	
GAG GAG GTT GTA AAA ATA GAG CGA GAA ATT GCC ACT CTT TCT AAC CCT	200
Glu Glu Val Val Lys Ile Glu Arg Glu Ile Ala Thr Leu Ser Asn Pro	
35 40 45 50	
TAT ATA TTT TTA AAA TCC ATT GAC CCT AAC ATG GCT TTT AAA ATC CAT	248
Tyr Ile Phe Leu Lys Ser Ile Asp Pro Asn Met Ala Phe Lys Ile His	
55 60 65	
CCA AAC GAC ACT TAC CGC ACC CAT AAG GCT TTA GAA ATC TTT TAT GCC	296
Pro Asn Asp Thr Tyr Arg Thr His Lys Ala Leu Glu Ile Phe Tyr Ala	
70 75 80	
ACC TGC ACG CCC CCA AGC GAG TAT TTT AAG GCC AAC CCT AAA AAA CCC	344
Thr Cys Thr Pro Pro Ser Glu Tyr Phe Lys Ala Asn Pro Lys Lys Pro	
85 90 95	
TTT GAG CAT GCT ATC TCC TTA TTC GCT CTG TCT ATT GAA AAA AGC GCG	392
Phe Glu His Ala Ile Ser Leu Phe Ala Leu Ser Ile Glu Lys Ser Ala	
100 105 110	
CTC CAT AAC AAT ATC AAA CGG CGC ACC AAA AAC ATG CTC CAT TCA GGG	440
Leu His Asn Asn Ile Lys Arg Arg Thr Lys Asn Met Leu His Ser Gly	
115 120 125 130	
CTT GTT GAA GAA ATC AAA GCC CTC TAT ACT CAA TAC CCT AAA GAT TCG	488
Leu Val Glu Glu Ile Lys Ala Leu Tyr Thr Gln Tyr Pro Lys Asp Ser	

GGCGATTCAA GCCTTAAAAG CCGGGTCAAA ATC

958

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Met Lys Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser
 1           5           10           15
Val Ser Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr
          20           25           30
Phe Leu Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr
          35           40           45
Thr Lys Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr
          50           55           60
Lys Thr Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys
65           70           75           80
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr
          85           90           95
Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro
          100          105          110
Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro
          115          120          125
Lys Val Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys
          130          135          140
Glu Glu Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val
145          150          155          160
Thr Thr Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn
          165          170          175
Lys Thr Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly
          180          185          190
Val Ser Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys
          195          200          205
Asn Arg Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val
          210          215          220
Leu Val Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys
225          230          235          240
Val Val Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu
          245          250          255
Ala Ile Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val
          260          265          270
His Leu Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp
          275          280          285

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

AAT GCT GAG TCG GCT AAA CCC AAA GAA GAG CCT AAA GAA AAA CCC AAG	296
Asn Ala Glu Ser Ala Lys Pro Lys Glu Glu Pro Lys Glu Lys Pro Lys	
70 75 80	
AAA GAA GAG CCA AAA AAA GAA GAA CCC AAA AAG GAG GTT ACA AAG CCT	344
Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Val Thr Lys Pro	
85 90 95	
AAA CCT AAG CCT AAA CCC AAG CCA AAG CCA AAA CCA AAA CCT AAG CCT	392
Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro Lys Pro	
100 105 110	
GAA CCC AAA CCT GAA CCA AAA CCC GAG CCT AAG CCT GAG CCT AAA GTT	440
Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Pro Glu Pro Lys Val	
115 120 125 130	
GAA GAG GTT AAA AAA GAA GAG CCT AAA GAA GAG CCC AAA AAA GAA GAA	488
Glu Glu Val Lys Lys Glu Glu Pro Lys Glu Glu Pro Lys Lys Glu Glu	
135 140 145	
GCT AAA GAG GAA GCT AAA GAA AAA AGC GCT CCT AAA CAA GTA ACA ACT	536
Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val Thr Thr	
150 155 160	
AAG GAT ATA GTC AAA GAA AAA GAC AAG CAA GAA GAA TCC AAC AAA ACC	584
Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn Lys Thr	
165 170 175	
TCT GAG GGG GCC ACT TCT GAA GCT CAA GCT TAT AAC CCA GGG GTG AGC	632
Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly Val Ser	
180 185 190	
AAC GAA TTT TTA ATG AAG ATC CAA ACC GCT ATT TCT TCT AAA AAC CGC	680
Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys Asn Arg	
195 200 205 210	
TAC CCT AAA ATG GCG CAG ATT AGG GGT ATT GAG GGC GAA GTG TTG GTG	728
Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val Leu Val	
215 220 225	
AGC TTT ACG ATC AAT GCT GAT GGG AGC GTT ACG GAC ATT AAA GTG GTC	776
Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys Val Val	
230 235 240	
AAA AGC AAC ACC ACA GAT ATT TTA AAC CAT GCG GCT TTA GAA GCC ATT	824
Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu Ala Ile	
245 250 255	
AAA AGC GCG GCA CAT CTA TTC CCT AAA CCA GAA GAA ACC GTG CAT CTA	872
Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val His Leu	
260 265 270	
AAA ATC CCT ATC GCT TAT AGC TTG AAA GAA GAC TGATTAGTCT TTCTTTTAGG	925
Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp	
275 280 285	

```

Ile Ala Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala
    35              40              45
Glu Lys Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp
    50              55              60
Glu His Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala
    65              70              75              80
Leu Ser Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu
              85              90              95
Lys Ser Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp
              100              105              110
Ile Leu Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala
              115              120              125
Gln

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...905
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

TCGTTTTGAA ACTTTTATCA GCATTATGGA TATTTTAAAA GAGCATAATC ATG AAA      56
                                Met Lys
                                1

ATT TCT CCA TCT CCA CGC AAG CTC AGT AAA GTT TCA ACG AGT GTT AGC      104
Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser Val Ser
    5              10              15

TTT TTA ATC TCT TTT GCC CTA TAC GCT ATA GGG TTT GGC TAT TTT TTA      152
Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr Phe Leu
    20              25              30

CTG CGC GAA GAC GCC CCA GAG CCT TTA GCG CAA GCC GGG ACC ACT AAG      200
Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr Thr Lys
    35              40              45              50

GTT ACC ATG AGT TTA GCC AGC ATC AAC ACT AAT TCC AAT ACA AAG ACT      248
Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr Lys Thr
              55              60              65

```

TTGTTGAGAA AATCCGATGT TTTGAGCGAA AAATTCAGGA TCATGAAAAA ATG AAA 56
Met Lys
1

AGC ATC AGA AGA GGC GAT GGG CTG AAT GTT GTC CCT TTC ATT GAT ATT 104
Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile Asp Ile
5 10 15

ATG CTC GTT TTG CTA GCG ATT GTG TTG AGC ATT TCT ACT TTT ATT GCA 152
Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe Ile Ala
20 25 30

CAA GGT AAG ATT AAG GTC AGT CTC CCT AAC GCT AAA AAT GCG GAA AAA 200
Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala Glu Lys
35 40 45 50

TCC CAG CCA AAC GAT CAA AAA GTG GTG GTC ATC TCT GTA GAT GAG CAT 248
Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp Glu His
55 60 65

GAC AAT ATT TTC GTA GAT GAC AAA CCG ATG AAT TTA GAA GCT TTG AGC 296
Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala Leu Ser
70 75 80

GCT GTA GTC AAA CAA ACA GAC CCT AAA ACC CTT ATA GAC TTA AAA AGC 344
Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser
85 90 95

GAC AAA AGC TCT CGT TTT GAA ACT TTT ATC AGC ATT ATG GAT ATT TTA 392
Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu
100 105 110

AAA GAG CAT AAT CAT GAA AAT TTC TCC ATC TCC ACG CAA GCT CAG TAAAG 442
Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln
115 120 125

TTTCAACGAG TGTTAGCTTT TTAATCTCTT TTGCCCTATA CGCTATAG 490

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Lys Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile
1 5 10 15
Asp Ile Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe
20 25 30

			100					105				110					
Gly	Met	Glu	Gln	Glu	Arg	Leu	Ile	Glu	Glu	Ser	Gln	Thr	Leu	Phe	Leu		
		115						120				125					
Gln	Glu	His	Cys	Pro	Tyr	Leu	Ser	Gly	Val	Lys	Asn	Leu	Glu	Glu	Ala		
		130						135				140					
Ser	Asn	Ala	Leu	Glu	Val	Gln	Glu	Gln	Asn	Asn	Ala	Leu	Phe	Leu	Leu		
145					150					155					160		
Lys	Glu	Pro	Lys	Leu	Ala	Arg	Leu	Leu	Ser	Arg	Leu	Asp	Leu	Met	Ser		
				165					170					175			
Ala	Leu	Asn	Ala	Leu	Cys	Asp	Gln	Val	Leu	Glu	Asn	Gln	Ala	His	Asn		
		180						185					190				
Gln	Gln	Ser	His	Asn	Lys	Ile	Leu	Glu	Tyr	Asn	Ala	Leu	Lys	Asn	His		
		195					200					205					
Asp	Phe	Gln	Ala	Tyr	Lys	Ala	Met	Arg	Leu	Lys	Lys	Phe	Lys	Asn	Lys		
	210					215					220						
Leu	Gln	Ser	Gln	Ile	Gln	Ala	Gln	Glu	Asp	Ala	Leu	Lys	Thr	Phe	Leu		
225				230					235						240		
Pro	Leu	Glu	Lys	Arg	Leu	Glu	Thr	Leu	Lys	Thr	His	Phe	Leu	Cys	Asp		
				245					250					255			
Lys	Glu	Asn	Leu	Lys	Ser	Cys	Ala	Lys	Glu	Leu	His	Gln	Arg	Tyr	Gln		
		260					265						270				
Asn	Ala	Leu	Ile	Glu	Arg	Asp	Lys	Glu	Leu	Lys	Asn	Ala	Lys	Asn	Asn		
	275					280					285						
Lys	Glu	Lys	His	Ala	Leu	Ile	Leu	Ala	Asn	Tyr	Glu	His	Thr	Leu	Lys		
	290				295					300							
Thr	Leu	Asn	Ile	Glu	Phe	Leu	Ser	Glu	Leu	Asn	Lys	Gln	Met	Ala	Phe		
305				310					315					320			
Leu	Asn	Glu	Thr	Met	Ala	Leu	Asn	Ala	Arg	Val	Leu	Ala	Leu	Leu	Ala		
			325						330				335				
Lys	Gln	His	Ala	Lys	Thr	Pro	Lys	Pro	Phe	Asn	Leu	Ser	Gly	Gly	Leu		
	340						345					350					
Ser	Gly	Asp	Leu	Ser	Gly	Gly	Lys	Ala	Leu	Ile	Lys	Asn	Ile	Arg	Leu		
	355					360					365						
Asp	Pro	His	Gly	Phe	Pro	Ser	Phe	Lys	Asn	Phe	Lys	Gln	Glu				
	370				375						380						

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...437
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:


```

Leu Ile Glu Arg Asp Lys Glu Leu Lys Asn Ala Lys Asn Asn Lys Glu
275                      280                      285                      290

AAG CAT GCT CTA ATC TTA GCC AAT TAC GAG CAT ACT TTA AAA ACC TTG      968
Lys His Ala Leu Ile Leu Ala Asn Tyr Glu His Thr Leu Lys Thr Leu
                      295                      300                      305

AAT ATA GAA TTT TTA AGC GAA TTA AAT AAG CAA ATG GCG TTT TTG AAT      1016
Asn Ile Glu Phe Leu Ser Glu Leu Asn Lys Gln Met Ala Phe Leu Asn
                      310                      315                      320

GAA ACC ATG GCG TTA AAC GCC CGA GTT TTA GCC CTT TTA GCC AAA CAG      1064
Glu Thr Met Ala Leu Asn Ala Arg Val Leu Ala Leu Leu Ala Lys Gln
                      325                      330                      335

CAT GCC AAA ACG CCA AAG CCT TTC AAT TTG AGC GGT GGT TTA AGC GGT      1112
His Ala Lys Thr Pro Lys Pro Phe Asn Leu Ser Gly Gly Leu Ser Gly
                      340                      345                      350

GAT TTG AGC GGT GGG AAA GCT CTT ATT AAA AAT ATC CGC TTA GAT CCG      1160
Asp Leu Ser Gly Gly Lys Ala Leu Ile Lys Asn Ile Arg Leu Asp Pro
355                      360                      365                      370

CAT GGA TTC CCT AGC TTT AAA AAT TTT AAG CAA GAG TAGGACAATA TTTGAC 1212
His Gly Phe Pro Ser Phe Lys Asn Phe Lys Gln Glu
                      375                      380

AAGCAAAAAC AATTATAGTA AAATAAGAGC ATAACCTT      1249

```

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Met Arg Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala
 1                      5                      10                      15
Gln Ile Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg
                      20                      25                      30
Ser Asn Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu
                      35                      40                      45
Arg Ile Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu
50                      55                      60
Ile Lys Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn
65                      70                      75                      80
Ala Ser Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser
                      85                      90                      95
Ala Leu Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys

```

- 409 -

Glu	Asn	Ile	Asn	Pro	Ile	Ile	Asn	Lys	Glu	Asp	Lys	Met	Leu	Glu	Ala
225					230					235					240
Arg	Phe	Asn	Val	Pro	Asn	Val	Lys	Gln	Ile	Tyr	Tyr	Pro	Asn	Met	Phe
				245					250					255	
Ala	Gln	Val	Glu	Ile	Phe	Gln	Lys	Pro	Gln	Lys	Met	Lys	Ile	Leu	Pro
			260					265					270		
Lys	Glu	Ala	Val	Leu	Ile	Lys	Gly	Gly	Lys	Ala	Ile	Val	Phe	Lys	Lys
		275					280					285			
Asp	Asp	Phe	Gly	Leu	Ser	Pro	Leu	Glu	Ile	Lys	Ala	Val	Arg	Leu	Ser
	290					295					300				
Asp	Gly	Ser	Tyr	Glu	Ile	Leu	Glu	Gly	Leu	Lys	Ala	Gly	Glu	Glu	Val
305					310					315					320
Ala	Asn	Asn	Ala	Leu	Phe	Val	Leu	Asp	Ala	Asp	Ala	Gln	Asn	Asn	Gly
				325					330					335	

Asp Tyr

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1196
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACTTAGA TAAAATAACA CGATAAAACC ATAGTAATAA AGATAACCCC ATG AGA	56
Met Arg	
1	
TTT TTT TGC TTT TTC TTA TTT TTT CTA ACC TTT TCA AAC GCA CAG ATA	104
Phe Phe Cys Phe Phe Leu Phe Phe Leu Thr Phe Ser Asn Ala Gln Ile	
5 10 15	
ATG ATG ACT TTT GAT TCT CAA ACT AAC GCC AAA CTC TCG CGC TCT AAC	152
Met Met Thr Phe Asp Ser Gln Thr Asn Ala Lys Leu Ser Arg Ser Asn	
20 25 30	
GAA CAG CTT TCA GAC ATG CTC TAT AAA CTC AAT GAA AGT TTA AGA ATC	200
Glu Gln Leu Ser Asp Met Leu Tyr Lys Leu Asn Glu Ser Leu Arg Ile	
35 40 45 50	
TAT CAA AGC GTG CTT TCC AAT AAC CAA GAT CAA CTC AAA GAA ATC AAA	248
Tyr Gln Ser Val Leu Ser Asn Asn Gln Asp Gln Leu Lys Glu Ile Lys	

```

TTT GGC TTA AGC CCG TTA GAA ATT AAA GCC GTC CGC TTG AGC GAT GGG      968
Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val Arg Leu Ser Asp Gly
                295                      300                      305

AGT TAT GAG ATT TTA GAG GGT TTA AAG GCG GGC GAA GAA GTC GCT AAT      1016
Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly Glu Glu Val Ala Asn
                310                      315                      320

AAC GCT TTA TTC GTG CTA GAC GCT GAC GCT CAA AAC AAT GGG GAT TAT T      1065
Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln Asn Asn Gly Asp Tyr
                325                      330                      335

GAATGATAGA AAAGATCATT GATTTAAGCG TTAAAAACAA ACTCCTTACC AC      1117

```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

Met Lys Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu
 1           5           10           15
Phe Ala Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala
 20           25           30
Lys Ser Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys
 35           40           45
Glu Phe Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu
 50           55           60
Ala Leu Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys
 65           70           75           80
Leu Tyr Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu
 85           90           95
Leu Ser Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu
100          105          110
Ser Ser Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu
115          120          125
Lys Leu Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser
130          135          140
His Lys Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile
145          150          155          160
Ile Phe Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys
165          170          175
Gly Gln Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu
180          185          190
Val Lys Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys
195          200          205
Ala Ile Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu
210          215          220

```

ATT TTT TCT CAA ACC CTG CGT TTT GAT GGC TAT GTG GAA AAG CTT TAT	296
Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys Leu Tyr	
70 75 80	
GCG AAT AAA ACC TAT ACC CCC ATT AAA AAG GGC GAC AGG TTA TTG AGC	344
Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu Leu Ser	
85 90 95	
GTG TAT TCC CCT GAA TTA GTG AGC GCT CAA AGC GAA TTG CTA TCA TCA	392
Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu Ser Ser	
100 105 110	
TTG AAA TTC AAC CAA CAA GTG GGA GCG ATT AAA GAA AAA TTA AAA CTA	440
Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu Lys Leu	
115 120 125 130	
TTA GGG TTA GAA AAC TCT AGC ATT GAA AAA ATC ATT AGC AGC CAT AAA	488
Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser His Lys	
135 140 145	
GTC CAA AAT GAA ATG ACT ATT TAC TCT CAC TTC AAC GGC ATT ATT TTT	536
Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile Ile Phe	
150 155 160	
AAA AAA AGC CCG GAT CTC AAT GAG GGG AGC TTC ATT AAA AAA GGG CAA	584
Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys Gly Gln	
165 170 175	
GAG TTG TTT CAA ATC ATA GAT TTA AGC CAA TTG TGG GCG CTG GTT AAA	632
Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu Val Lys	
180 185 190	
GTC AAT CAA GAG GAT TTA GAA TTT TTA AAA AAC ACG CAT AAA GCG ATC	680
Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys Ala Ile	
195 200 205 210	
TTG TTT GTA GAA GGG ATT AAA GGC GAG CAA GAA ATC ACG CTT GAA AAT	728
Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu Glu Asn	
215 220 225	
ATC AAC CCC ATC ATC AAC AAA GAA GAT AAA ATG CTA GAA GCG CGC TTC	776
Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala Arg Phe	
230 235 240	
AAT GTG CCT AAT GTT AAA CAG ATT TAT TAC CCT AAC ATG TTC GCT CAA	824
Asn Val Pro Asn Val Lys Gln Ile Tyr Tyr Pro Asn Met Phe Ala Gln	
245 250 255	
GTA GAA ATC TTT CAA AAA CCA CAA AAA ATG AAG ATT TTG CCT AAA GAA	872
Val Glu Ile Phe Gln Lys Pro Gln Lys Met Lys Ile Leu Pro Lys Glu	
260 265 270	
GCG GTT TTG ATT AAA GGG GGG AAA GCT ATC GTG TTT AAA AAA GAC GAT	920
Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val Phe Lys Lys Asp Asp	
275 280 285 290	

```

Gly Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val
      20                      25                      30
Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile
      35                      40                      45
Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg
      50                      55                      60
Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu
      65                      70                      75                      80
Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn
      85                      90                      95
Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys
      100                     105                     110
Glu Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
      115                     120                     125

```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1064
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

AGCGCTTTAA ATAGCACTTA TTTGTCTTTA CAAAACCTTA AAGGATTAGA ATG AAA      56
                                     Met Lys
                                     1
CGG ATT TTA TGG TTA GCC TTG ATT TTA TTT TTT AGC CCC TTA TTC GCT      104
Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu Phe Ala
      5                      10                      15
AAC GCT CAA AAA ACT CAA GAA ATT AAA AAA ACT AAA GAA GCT AAA AGC      152
Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala Lys Ser
      20                      25                      30
CAA ACC CGT TTT AAT ATT TCC ACC ACT AAG GTC ATA GAA AAA GAA TTT      200
Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys Glu Phe
      35                      40                      45                      50
TCT CAA AGC CGG CGC TAT TAC GCG CTT TTA GAG CCC AAT GAA GCG CTG      248
Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Leu Glu Pro Asn Glu Ala Leu
      55                      60                      65

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```

TCCGTTTCGCA ACAAGAATTT TCTTGTTATC TTAATGTAAA GGTCAAAACG ATG AAA      56
                                     Met Lys
                                     1

AAG TTA GCC GCT TTA TTT TTA GTA AGC GTG TTG GGG GTT ATG GGT TTA      104
Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met Gly Leu
      5                      10                      15

AAC GCA TGG GAG CAA ACC CTA AAA GCT AAT GAC TTG GAA GTG AAA ATC      152
Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys Ile
      20                      25                      30

AAA TCC GTG GGT AAC CCC ATT AAA GGC GAT AAC ACT TTC ATT CTC AGC      200
Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile Leu Ser
      35                      40                      45                      50

CCC ACT TTA AAA GGT AAG GCT TTA GAA AAA GCT ATC GTT AGG GTG CAG      248
Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val Gln
      55                      60                      65

TTT ATG ATG CCT GAA ATG CCC GGC ATG CCA GCG ATG AAA GAA ATG GCG      296
Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met Ala
      70                      75                      80

CAA GTG AGT GAA AAA AAC GGC CTT TAT GAA GCT AAA ACC AAT CTT TCT      344
Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu Ser
      85                      90                      95

ATG AAC GGG ACA TGG CAG GTT AGG GTG GAT ATT AAA TCT AAA GAG GGT      392
Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu Gly
      100                      105                      110

CAG GTT TAT CGC GCT AAA ACA AGC CTG GAT TTA TAAGAGCATG CTATCTTTTA      445
Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
      115                      120                      125

TAAGCGCGTT TGATAAAAGG GGC GTTTCAA TAC      478

```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

Met Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met
  1                      5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```

Met Lys Lys Ala Leu Ile Ser Thr Leu Phe Gly Val Ser Leu Ala Phe
 1             5             10             15
Ala Lys Pro Tyr Thr Ile Asp Lys Ala Asn Ser Ser Val Trp Phe Glu
      20             25             30
Val Lys His Phe Thr Phe Asn Glu Thr Arg Gly Ala Phe Asp Asn Phe
      35             40             45
Asp Gly Lys Ile Asp Leu Glu Pro Asn Thr Lys Met Leu Ser Val Phe
      50             55             60
Glu Gly Asn Ile Asp Val Lys Ser Val Asn Thr Arg Asp Arg Lys Arg
      65             70             75             80
Asp Asn His Leu Lys Thr Ala Asp Phe Phe Asp Val Val Lys Tyr Pro
      85             90             95
Lys Gly Ser Phe Lys Met Thr Lys Tyr Glu Asp Gly Lys Ile Tyr Gly
      100            105            110
Asp Leu Thr Leu Arg Gly Val Thr Lys Pro Val Val Leu Glu Ala Lys
      115            120            125
Ile Gln Ala Pro Leu Gln Asn Pro Met Asn Lys Lys Glu Phe Met Val
      130            135            140
Leu Gln Ala Glu Gly Lys Ile Asn Arg Lys Asp Phe Gly Ile Gly Lys
      145            150            155            160
Thr Phe Ser Asp Ala Val Val Gly Asp Glu Val Lys Ile Glu Leu Lys
      165            170            175
Leu Glu Ala Tyr Ala Gln
      180

```

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...425
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CGAATTGCTG TATAGTTAGC GTTTTAAATT CAAAATGAAG TGAGGAAACA ATG AAA	56
Met Lys	
1	
AAA GCG TTA ATA TCC ACC CTT TTT GGT GTT AGT TTG GCG TTT GCA AAA	104
Lys Ala Leu Ile Ser Thr Leu Phe Gly Val Ser Leu Ala Phe Ala Lys	
5 10 15	
CCT TAT ACG ATT GAT AAG GCA AAC TCT AGC GTG TGG TTT GAG GTC AAA	152
Pro Tyr Thr Ile Asp Lys Ala Asn Ser Ser Val Trp Phe Glu Val Lys	
20 25 30	
CAC TTC ACG TTC AAT GAA ACA AGA GGC GCG TTT GAT AAT TTT GAT GGC	200
His Phe Thr Phe Asn Glu Thr Arg Gly Ala Phe Asp Asn Phe Asp Gly	
35 40 45 50	
AAA ATT GAT CTA GAG CCC AAC ACT AAA ATG CTC AGC GTT TTT GAA GGC	248
Lys Ile Asp Leu Glu Pro Asn Thr Lys Met Leu Ser Val Phe Glu Gly	
55 60 65	
AAT ATT GAT GTG AAA AGC GTC AAT ACT AGG GAT AGA AAA AGA GAT AAC	296
Asn Ile Asp Val Lys Ser Val Asn Thr Arg Asp Arg Lys Arg Asp Asn	
70 75 80	
CAC TTG AAA ACA GCG GAC TTT TTT GAT GTG GTA AAA TAC CCC AAA GGG	344
His Leu Lys Thr Ala Asp Phe Phe Asp Val Val Lys Tyr Pro Lys Gly	
85 90 95	
AGC TTT AAA ATG ACC AAA TAC GAA GAT GGT AAA ATC TAT GGG GAT TTG	392
Ser Phe Lys Met Thr Lys Tyr Glu Asp Gly Lys Ile Tyr Gly Asp Leu	
100 105 110	
ACT CTT CGT GGC GTA ACC AAG CCT GTC GTA TTG GAA GCC AAA ATC CAA	440
Thr Leu Arg Gly Val Thr Lys Pro Val Val Leu Glu Ala Lys Ile Gln	
115 120 125 130	
GCC CCC TTA CAA AAC CCC ATG AAT AAA AAA GAA TTC ATG GTG TTA CAA	488
Ala Pro Leu Gln Asn Pro Met Asn Lys Lys Glu Phe Met Val Leu Gln	
135 140 145	
GCT GAA GGC AAA ATC AAC CGC AAG GAT TTT GGT ATC GGT AAA ACC TTT	536
Ala Glu Gly Lys Ile Asn Arg Lys Asp Phe Gly Ile Gly Lys Thr Phe	
150 155 160	
AGC GAT GCT GTC GTT GGA GAT GAG GTA AAG ATT GAG CTC AAA CTA GAA	584
Ser Asp Ala Val Val Gly Asp Glu Val Lys Ile Glu Leu Lys Leu Glu	
165 170 175	
GCT TAC GCC CAA TAATCGTTTT GCAAGAGATA GATATCTTCT TCTCTGCGT TTTTC	641
Ala Tyr Ala Gln	
180	
TAACAGCA	649

Val Lys Leu Ile His Lys Ala Leu Glu Leu Gly Ile Asn Phe Phe Asp
 35 40 45 50

ACT GCA GAG GCT TAT GGG GAA GAT AAT GAA AAG CTT TTA GGC GAA CGA 248
 Thr Ala Glu Ala Tyr Gly Glu Asp Asn Glu Lys Leu Leu Gly Glu Arg
 55 60 65

TCA AGC CTT TTA AAG ACA AGG TTG TGG TAGCGAGCAA GTTTGGGATT TACTACG 302
 Ser Ser Leu Leu Lys Thr Arg Leu Trp
 70 75

CAGATCCTAA TGACAAATAC GCAACC 328

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met Gln Gln Arg His Leu Gly Pro Leu Lys Val Gly Ala Leu Ala Leu
 1 5 10 15
 Gly Cys Met Gly Met Thr Tyr Gly Tyr Gly Glu Val His Asp Lys Lys
 20 25 30
 Gln Met Val Lys Leu Ile His Lys Ala Leu Glu Leu Gly Ile Asn Phe
 35 40 45
 Phe Asp Thr Ala Glu Ala Tyr Gly Glu Asp Asn Glu Lys Leu Leu Gly
 50 55 60
 Glu Arg Ser Ser Leu Leu Lys Thr Arg Leu Trp
 65 70 75

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...596
- (D) OTHER INFORMATION:

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

Met Met Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu
 1             5             10             15
Asn Ala Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg
      20             25             30
Val Ser Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe
      35             40             45
Tyr

```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...275
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

TTAAGATTGC GGT TATACTG AAAAAAACA TATGAAATCA AGGAGCTTGT ATG CAA      56
                                     Met Gln
                                     1

CAG CGT CAT TTA GGC CCT TTA AAA GTG GGT GCA TTA GCT CTA GGG TGC      104
Gln Arg His Leu Gly Pro Leu Lys Val Gly Ala Leu Ala Leu Gly Cys
      5             10             15

ATG GGC ATG ACT TAT GGG TAT GGG GAA GTC CAT GAT AAA AAG CAG ATG      152
Met Gly Met Thr Tyr Gly Tyr Gly Glu Val His Asp Lys Lys Gln Met
      20             25             30

GTT AAA CTT ATC CAT AAG GCT TTG GAA TTG GGT ATT AAC TTT TTT GAC      200

```

```

Ser Gln Ala Phe Ser His Asn Met Gln Leu Gln Asp Glu Ser Val Phe
                325                330                335
Leu Phe Ile Ala Gly Gly Asn Pro Asn Val Lys Ala Glu Ala Leu Gln
                340                345                350
Lys Glu Ile Val Ala Leu Leu Glu Lys Leu Lys Lys Gly Glu Ile Thr
                355                360                365
Gln Ala Glu Leu Asp Lys Leu Lys Ile Asn Gln Lys Ala Asp Phe Ile
                370                375                380
Ser Asn Leu Glu Ser Ser Ser Asp Val Ala Gly Leu Phe Ala Asp Tyr
385                390                395                400
Leu Val Gln Asn Asp Ile Gln Gly Leu Thr Asp Tyr Gln Arg Gln Phe
                405                410                415
Leu Asp Leu Lys Val Ser Asp Leu Val Arg Val Ala Asn Glu Tyr Phe
                420                425                430
Lys Asp Thr Gln Ser Thr Thr Val Phe Leu Lys Pro
                435                440

```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...197
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

ATATAATCTT TTCTTAATTT TGAAGTTTAG CAAATTTTAA GGAAGTAACC ATG ATG      56
                                   Met Met
                                   1

AAA AAA ACC CTT TTT ATC TCT TTG GCT TTA GCG TTA AGC TTG AAT GCG      104
Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu Asn Ala
    5                10                15

GGC AAT ATC CAA ATC CAG AGC ATG CCC AAA GTT AAA GAG CGA GTG AGT      152
Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg Val Ser
    20                25                30

GTC CCC TCT AAA GAC GAT ACG GAT CTA TTC TTA CCA CGA TTC TAT TAAGG      202
Val Pro Ser Lys Asp Thr Asp Leu Phe Leu Pro Arg Phe Tyr
    35                40                45

ACTCTATTAA GGCGGTGGTG AATATCTCCA CTGAAAAGAA GATTAAAA      250

```

TTTCATTCAT CTAGCGCGTT GATTACGCCT

1435

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met	Lys	His	Phe	Ser	Val	Lys	Arg	Leu	Leu	Gly	Leu	Ser	Ser	Val	Leu
1				5				10						15	
Leu	Val	Thr	Leu	Gly	Ala	Ser	Met	His	Ala	Gln	Ser	Tyr	Leu	Pro	Lys
			20					25					30		
His	Glu	Ser	Val	Thr	Leu	Lys	Asn	Gly	Leu	Gln	Val	Val	Ser	Val	Pro
			35				40					45			
Leu	Glu	Asn	Lys	Thr	Gly	Val	Ile	Glu	Val	Asp	Val	Leu	Tyr	Lys	Val
			50			55				60					
Gly	Ser	Arg	Asn	Glu	Thr	Met	Gly	Lys	Ser	Gly	Ile	Ala	His	Met	Leu
65				70				75						80	
Glu	His	Leu	Asn	Phe	Lys	Ser	Thr	Lys	Asn	Leu	Lys	Ala	Gly	Glu	Phe
			85					90					95		
Asp	Lys	Ile	Val	Lys	Arg	Phe	Gly	Gly	Val	Ser	Asn	Ala	Ser	Thr	Ser
			100					105					110		
Phe	Asp	Ile	Thr	Arg	Tyr	Phe	Ile	Lys	Thr	Ser	Gln	Ala	Asn	Leu	Asp
			115				120					125			
Lys	Ser	Leu	Glu	Leu	Phe	Ala	Glu	Thr	Met	Gly	Ser	Leu	Asn	Leu	Lys
			130			135					140				
Glu	Asp	Glu	Phe	Leu	Pro	Glu	Arg	Gln	Val	Val	Ala	Glu	Glu	Arg	Arg
145				150						155				160	
Trp	Arg	Thr	Asp	Asn	Ser	Pro	Ile	Gly	Met	Leu	Tyr	Phe	Arg	Phe	Phe
			165					170						175	
Asn	Thr	Ala	Tyr	Val	Tyr	His	Pro	Tyr	His	Trp	Thr	Pro	Ile	Gly	Phe
			180					185					190		
Met	Asp	Asp	Ile	Gln	Asn	Trp	Thr	Leu	Lys	Asp	Ile	Lys	Lys	Phe	His
			195				200					205			
Ser	Leu	Tyr	Tyr	Gln	Pro	Lys	Asn	Ala	Ile	Val	Leu	Val	Val	Gly	Asp
			210			215					220				
Val	Asn	Ser	Gln	Lys	Val	Phe	Glu	Leu	Ser	Lys	Lys	His	Phe	Glu	Ser
225				230						235				240	
Leu	Lys	Asn	Leu	Asp	Glu	Lys	Ala	Ile	Pro	Thr	Pro	Tyr	Met	Lys	Glu
			245					250					255		
Pro	Lys	Gln	Asp	Gly	Ala	Arg	Thr	Ala	Val	Val	His	Lys	Asp	Gly	Val
			260					265					270		
His	Leu	Glu	Trp	Val	Ala	Leu	Gly	Tyr	Lys	Val	Pro	Ala	Phe	Lys	His
			275				280					285			
Lys	Asp	Gln	Val	Ala	Leu	Asp	Ala	Leu	Ser	Arg	Leu	Leu	Gly	Glu	Gly
			290			295					300				
Lys	Ser	Ser	Trp	Leu	Gln	Ser	Glu	Leu	Val	Asp	Lys	Lys	Arg	Leu	Ala
305				310						315				320	

TCC CAA AAG GTT TTT GAA TTG AGT AAA AAG CAT TTT GAA TCC TTA AAA	776
Ser Gln Lys Val Phe Glu Leu Ser Lys Lys His Phe Glu Ser Leu Lys	
230 235 240	
AAC CTT GAT GAA AAA GCT ATC CCC ACC CCT TAC ATG AAA GAG CCT AAG	824
Asn Leu Asp Glu Lys Ala Ile Pro Thr Pro Tyr Met Lys Glu Pro Lys	
245 250 255	
CAA GAT GGA GCC AGA ACG GCA GTC GTG CAT AAA GAT GGG GTC CAT TTA	872
Gln Asp Gly Ala Arg Thr Ala Val Val His Lys Asp Gly Val His Leu	
260 265 270	
GAA TGG GTG GCC CTT GGG TAT AAA GTG CCT GCT TTC AAG CAT AAA GAT	920
Glu Trp Val Ala Leu Gly Tyr Lys Val Pro Ala Phe Lys His Lys Asp	
275 280 285 290	
CAA GTC GCC TTA GAC GCA CTA AGT AGG CTT TTA GGC GAA GGC AAA AGC	968
Gln Val Ala Leu Asp Ala Leu Ser Arg Leu Leu Gly Glu Gly Lys Ser	
295 300 305	
TCG TGG TTG CAA AGC GAA TTA GTG GAT AAA AAA CGC TTG GCT TCT CAA	1016
Ser Trp Leu Gln Ser Glu Leu Val Asp Lys Lys Arg Leu Ala Ser Gln	
310 315 320	
GCT TTC TCG CAC AAC ATG CAA TTA CAA GAT GAA AGC GTG TTT TTA TTC	1064
Ala Phe Ser His Asn Met Gln Leu Gln Asp Glu Ser Val Phe Leu Phe	
325 330 335	
ATT GCG GGG GGT AAT CCT AAT GTC AAA GCC GAA GCC TTA CAA AAA GAA	1112
Ile Ala Gly Gly Asn Pro Asn Val Lys Ala Glu Ala Leu Gln Lys Glu	
340 345 350	
ATC GTA GCG CTT TTA GAA AAG CTG AAA AAA GGC GAA ATC ACT CAA GCG	1160
Ile Val Ala Leu Leu Glu Lys Leu Lys Lys Gly Glu Ile Thr Gln Ala	
355 360 365 370	
GAA TTA GAC AAG CTC AAA ATC AAT CAA AAA GCT GAC TTT ATT TCT AAT	1208
Glu Leu Asp Lys Leu Lys Ile Asn Gln Lys Ala Asp Phe Ile Ser Asn	
375 380 385	
TTA GAA AGT TCT AGC GAT GTT GCG GGG CTT TTT GCG GAC TAT TTA GTG	1256
Leu Glu Ser Ser Ser Asp Val Ala Gly Leu Phe Ala Asp Tyr Leu Val	
390 395 400	
CAA AAC GAT ATT CAA GGC TTG ACG GAT TAC CAG CGA CAA TTT TTG GAT	1304
Gln Asn Asp Ile Gln Gly Leu Thr Asp Tyr Gln Arg Gln Phe Leu Asp	
405 410 415	
TTA AAA GTG AGC GAT TTG GTG CGT GTG GCC AAT GAA TAT TTT AAA GAC	1352
Leu Lys Val Ser Asp Leu Val Arg Val Ala Asn Glu Tyr Phe Lys Asp	
420 425 430	
ACC CAA TCA ACC ACC GTG TTT TTG AAA CCT TAAAAGAGCC TTATAACATG CAA	1405
Thr Gln Ser Thr Thr Val Phe Leu Lys Pro	
435 440	

CAT	TTT	TCT	GTT	AAA	AGA	CTT	TTA	GGG	CTT	AGT	TCT	GTC	TTG	TTA	GTC	104
His	Phe	Ser	Val	Lys	Arg	Leu	Leu	Gly	Leu	Ser	Ser	Val	Leu	Leu	Val	
		5					10					15				
ACT	TTA	GGA	GCG	AGC	ATG	CAC	GCA	CAA	TCT	TAC	TTA	CCC	AAA	CAT	GAG	152
Thr	Leu	Gly	Ala	Ser	Met	His	Ala	Gln	Ser	Tyr	Leu	Pro	Lys	His	Glu	
	20					25				30						
AGC	GTT	ACC	TTA	AAA	AAC	GGG	TTG	CAA	GTC	GTG	AGC	GTC	CCC	CTA	GAA	200
Ser	Val	Thr	Leu	Lys	Asn	Gly	Leu	Gln	Val	Val	Ser	Val	Pro	Leu	Glu	
35					40				45					50		
AAT	AAA	ACC	GGG	GTT	ATA	GAA	GTG	GAT	GTG	CTT	TAT	AAA	GTC	GGC	TCT	248
Asn	Lys	Thr	Gly	Val	Ile	Glu	Val	Asp	Val	Leu	Tyr	Lys	Val	Gly	Ser	
			55					60					65			
AGA	AAC	GAA	ACC	ATG	GGA	AAG	AGC	GGG	ATC	GCT	CAC	ATG	TTA	GAG	CAT	296
Arg	Asn	Glu	Thr	Met	Gly	Lys	Ser	Gly	Ile	Ala	His	Met	Leu	Glu	His	
		70					75					80				
TTG	AAT	TTT	AAA	AGC	ACC	AAA	AAC	CTT	AAA	GCC	GGC	GAA	TTT	GAT	AAA	344
Leu	Asn	Phe	Lys	Ser	Thr	Lys	Asn	Leu	Lys	Ala	Gly	Glu	Phe	Asp	Lys	
	85					90					95					
ATC	GTT	AAG	CGT	TTT	GGG	GGC	GTG	AGT	AAC	GCT	TCT	ACG	AGT	TTT	GAT	392
Ile	Val	Lys	Arg	Phe	Gly	Gly	Val	Ser	Asn	Ala	Ser	Thr	Ser	Phe	Asp	
	100					105					110					
ATT	ACG	CGC	TAC	TTC	ATT	AAA	ACC	AGT	CAG	GCT	AAC	TTG	GAT	AAG	TCT	440
Ile	Thr	Arg	Tyr	Phe	Ile	Lys	Thr	Ser	Gln	Ala	Asn	Leu	Asp	Lys	Ser	
115					120				125					130		
TTA	GAA	TTG	TTC	GCT	GAA	ACC	ATG	GGT	TCA	TTG	AAT	TTA	AAA	GAA	GAT	488
Leu	Glu	Leu	Phe	Ala	Glu	Thr	Met	Gly	Ser	Leu	Asn	Leu	Lys	Glu	Asp	
			135					140					145			
GAG	TTT	TTG	CCT	GAG	CGT	CAA	GTG	GTC	GCT	GAA	GAA	AGG	CGA	TGG	CGC	536
Glu	Phe	Leu	Pro	Glu	Arg	Gln	Val	Val	Ala	Glu	Glu	Arg	Arg	Trp	Arg	
		150					155					160				
ACT	GAT	AAT	TCC	CCT	ATC	GGC	ATG	CTT	TAT	TTC	CGC	TTT	TTT	AAC	ACC	584
Thr	Asp	Asn	Ser	Pro	Ile	Gly	Met	Leu	Tyr	Phe	Arg	Phe	Phe	Asn	Thr	
	165					170					175					
GCT	TAT	GTC	TAT	CAC	CCC	TAC	CAT	TGG	ACG	CCC	ATT	GGT	TTT	ATG	GAT	632
Ala	Tyr	Val	Tyr	His	Pro	Tyr	His	Trp	Thr	Pro	Ile	Gly	Phe	Met	Asp	
	180					185				190						
GAT	ATT	CAA	AAT	TGG	ACT	TTA	AAA	GAC	ATT	AAA	AAA	TTC	CAT	TCG	CTC	680
Asp	Ile	Gln	Asn	Trp	Thr	Leu	Lys	Asp	Ile	Lys	Lys	Phe	His	Ser	Leu	
195					200				205					210		
TAT	TAT	CAG	CCT	AAA	AAC	GCT	ATC	GTT	TTG	GTG	GTA	GGC	GAT	GTC	AAT	728
Tyr	Tyr	Gln	Pro	Lys	Asn	Ala	Ile	Val	Leu	Val	Val	Gly	Asp	Val	Asn	
			215					220					225			

```

Tyr Leu Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu
      260                      265                      270
Gln Val Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu
      275                      280                      285
Arg Ser Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr
      290                      295                      300
Gln Asp Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln
      305                      310                      315                      320
Lys Leu Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe
      325                      330                      335
Lys Asp Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu
      340                      345                      350
Leu Gln Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr
      355                      360                      365
Gln Glu Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu
      370                      375                      380
Lys Asp Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly
      385                      390                      395                      400
Gly Thr Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn
      405                      410                      415
Ala Leu Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn
      420                      425                      430
Lys Val Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe
      435                      440                      445
Ser Ala Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys
      450                      455                      460
Thr Asp Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr
      465                      470                      475                      480
Lys Ile Val Lys Tyr Ile Gln
      485

```

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1382
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

CAAAAAGATG GATTTTGTAG CGTCAAAGAG GCTATAGGAG CGGATTTAAG ATG AAA
                                     Met Lys
                                     1

```

56

TTT TTT GAT AAA GCG TTG ATA GAA GAA TTG AAA AAA CGC TAT AAG ATA 1496
 Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys Ile
 470 475 480

GTC AAA TAC ATT CAA TAAATGCAAG GGGAAATCAT GGAACATAAA GAAATCGTTA T 1552
 Val Lys Tyr Ile Gln
 485

AGGGGTTGAT CT 1564

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met	Ile	Glu	Trp	Met	Gln	Asn	His	Arg	Lys	Tyr	Leu	Val	Val	Thr	Ile
1				5					10					15	
Trp	Ile	Ser	Thr	Ile	Ala	Phe	Ile	Ala	Ala	Gly	Met	Ile	Gly	Trp	Gly
			20					25					30		
Gln	Tyr	Ser	Phe	Ser	Leu	Asp	Ser	Asp	Ser	Ala	Ala	Lys	Val	Gly	Gln
		35					40					45			
Ile	Lys	Ile	Ser	Gln	Glu	Glu	Leu	Ala	Gln	Glu	Tyr	Arg	Arg	Leu	Lys
	50				55					60					
Asp	Ala	Tyr	Ala	Glu	Ser	Ile	Pro	Asp	Phe	Lys	Glu	Leu	Thr	Lys	Asp
65				70						75				80	
Gln	Ile	Lys	Ala	Met	His	Leu	Glu	Lys	Ser	Ala	Leu	Asp	Ser	Leu	Ile
			85					90						95	
Asn	Gln	Ala	Leu	Leu	Arg	Asn	Leu	Ala	Leu	Asp	Leu	Gly	Leu	Gly	Ala
		100						105					110		
Thr	Lys	Gln	Glu	Val	Ala	Lys	Glu	Ile	Arg	Lys	Thr	Ser	Val	Phe	Gln
		115					120					125			
Lys	Asp	Gly	Val	Phe	Asp	Glu	Glu	Leu	Tyr	Lys	Asn	Ile	Leu	Lys	Gln
	130					135				140					
Ser	His	Tyr	Arg	Pro	Lys	His	Phe	Glu	Glu	Ser	Val	Glu	Arg	Leu	Leu
145					150					155				160	
Ile	Leu	Gln	Lys	Ile	Ser	Thr	Leu	Phe	Pro	Lys	Thr	Thr	Thr	Pro	Leu
			165					170						175	
Glu	Gln	Ser	Ser	Leu	Ser	Leu	Trp	Ala	Lys	Leu	Gln	Asp	Lys	Leu	Asp
		180					185					190			
Ile	Leu	Ile	Leu	Asn	Pro	Ser	Asp	Val	Lys	Ile	Ser	Leu	Asn	Glu	Glu
	195					200						205			
Glu	Met	Lys	Lys	Tyr	Tyr	Glu	Ser	His	Lys	Lys	Asp	Phe	Lys	Lys	Pro
	210					215					220				
Thr	Ser	Phe	Lys	Thr	Arg	Ser	Leu	Tyr	Phe	Asp	Ala	Ser	Leu	Glu	Lys
225				230						235				240	
Pro	Asp	Leu	Lys	Glu	Leu	Glu	Glu	Tyr	Tyr	His	Lys	Asn	Lys	Val	Ser
			245					250						255	

TTG AAG GAG TTG GAG GAA TAC TAC CAT AAA AAC AAG GTG TCT TAT TTG	824
Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu	
245 250 255	
GAC AAA GAG GGG AAA TTG CAG GAT TTT AAA AGC GTT CAA GAG CAA GTC	872
Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu Gln Val	
260 265 270	
AAG CAT GAT TTA AGC ATG CAA AAA GCG AAT GAA AAA GCC TTA AGG AGC	920
Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu Arg Ser	
275 280 285 290	
TAT ATC GCT CTA AAA AAA GCG AAC GCG CAA AAC TAC ACC ACA CAA GAT	968
Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr Gln Asp	
295 300 305	
TTT GAA GAG AAC AAC TCC CCC TAT ACT GCT GAA ATC ACG CAA AAA CTC	1016
Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys Leu	
310 315 320	
ACC GCT CTC AAA CCC CTT GAA ATC CTA AAG CCA GAG CCT TTT AAA GAT	1064
Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe Lys Asp	
325 330 335	
GGT TTT ATT GTG GTG CAA CTC ATC TCT CAA ATT AAA GAC GAA TTG CAA	1112
Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu Leu Gln	
340 345 350	
AAT TTT AAT GAA GCT AAA AGC GCT CTT AAA ACC CGC CTA ACT CAA GAA	1160
Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln Glu	
355 360 365 370	
AAA ACC CTT ATG GCG TTG CAA ACT TTA GCC AAA GAA AAG CTT AAG GAT	1208
Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys Asp	
375 380 385	
TTT AAG GGC AAA AGC GTG GGC TAT GTA AGC CCT AAT TTT GGA GGC ACT	1256
Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly Thr	
390 395 400	
ATT AGT GAG CTT AAC CAA GAA GAA AGT GCT AAG TTT ATC AAC GCT CTT	1304
Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Ala Leu	
405 410 415	
TTT AAC CGC CAG GAA AAA AAG GGG TTT ATC GCT ATT AAT AAT AAA GTG	1352
Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn Lys Val	
420 425 430	
GTG CTC TAT CAA ATC ACA GAA CAA AAT TTC AAC CAC TCA TTT AGT GCA	1400
Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe Ser Ala	
435 440 445 450	
GAA GAA AGC CAG TAT ATG CAG CGT TTA GTC AAT AAC ACT AAA ACG GAT	1448
Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr Asp	
455 460 465	

AGC	ACG	ATC	GCT	TTT	ATT	GCC	GCT	GGG	ATG	ATA	GGC	TGG	GGG	CAA	TAC	152
Ser	Thr	Ile	Ala	Phe	Ile	Ala	Ala	Gly	Met	Ile	Gly	Trp	Gly	Gln	Tyr	
20						25					30					
AGC	TTT	TCT	TTA	GAT	AGC	GAT	AGC	GCT	GCC	AAA	GTG	GGA	CAG	ATT	AAG	200
Ser	Phe	Ser	Leu	Asp	Ser	Asp	Ser	Ala	Ala	Lys	Val	Gly	Gln	Ile	Lys	
35					40					45					50	
ATT	TCT	CAA	GAA	GAA	TTA	GCC	CAA	GAA	TAC	CGC	CGC	CTT	AAA	GAC	GCA	248
Ile	Ser	Gln	Glu	Glu	Leu	Ala	Gln	Glu	Tyr	Arg	Arg	Leu	Lys	Asp	Ala	
			55					60						65		
TAT	GCT	GAG	TCT	ATC	CCT	GAT	TTT	AAA	GAA	CTC	ACC	AAA	GAT	CAA	ATC	296
Tyr	Ala	Glu	Ser	Ile	Pro	Asp	Phe	Lys	Glu	Leu	Thr	Lys	Asp	Gln	Ile	
			70					75					80			
AAA	GCC	ATG	CAT	TTA	GAA	AAA	AGC	GCT	TTA	GAT	TCG	CTC	ATC	AAT	CAA	344
Lys	Ala	Met	His	Leu	Glu	Lys	Ser	Ala	Leu	Asp	Ser	Leu	Ile	Asn	Gln	
	85						90					95				
GCC	TTA	TTG	AGA	AAT	CTC	GCT	TTA	GAT	TTA	GGG	CTT	GGC	GCT	ACA	AAG	392
Ala	Leu	Leu	Arg	Asn	Leu	Ala	Leu	Asp	Leu	Gly	Leu	Gly	Ala	Thr	Lys	
100						105					110					
CAA	GAA	GTG	GCG	AAA	GAG	ATC	AGA	AAA	ACG	AGC	GTT	TTC	CAA	AAA	GAT	440
Gln	Glu	Val	Ala	Lys	Glu	Ile	Arg	Lys	Thr	Ser	Val	Phe	Gln	Lys	Asp	
115					120					125					130	
GGC	GTT	TTT	GAT	GAA	GAA	TTG	TAT	AAA	AAT	ATC	TTA	AAG	CAA	AGC	CAT	488
Gly	Val	Phe	Asp	Glu	Glu	Leu	Tyr	Lys	Asn	Ile	Leu	Lys	Gln	Ser	His	
				135					140					145		
TAC	CGC	CCC	AAA	CAT	TTT	GAA	GAA	AGC	GTT	GAA	AGG	CTT	TTA	ATC	CTT	536
Tyr	Arg	Pro	Lys	His	Phe	Glu	Glu	Ser	Val	Glu	Arg	Leu	Leu	Ile	Leu	
			150					155					160			
CAA	AAA	ATC	AGC	ACT	CTA	TTC	CCC	AAA	ACC	ACT	ACC	CCT	TTG	GAG	CAA	584
Gln	Lys	Ile	Ser	Thr	Leu	Phe	Pro	Lys	Thr	Thr	Thr	Pro	Leu	Glu	Gln	
	165						170					175				
TCC	AGC	CTA	TCG	CTT	TGG	GCA	AAA	TTG	CAA	GAC	AAA	TTA	GAC	ATT	CTT	632
Ser	Ser	Leu	Ser	Leu	Trp	Ala	Lys	Leu	Gln	Asp	Lys	Leu	Asp	Ile	Leu	
180						185					190					
ATC	CTA	AAC	CCT	AGT	GAT	GTT	AAA	ATC	TCT	CTT	AAT	GAA	GAA	GAG	ATG	680
Ile	Leu	Asn	Pro	Ser	Asp	Val	Lys	Ile	Ser	Leu	Asn	Glu	Glu	Glu	Met	
195					200					205					210	
AAA	AAA	TAT	TAC	GAG	TCC	CAT	AAA	AAG	GAT	TTT	AAA	AAG	CCC	ACG	AGC	728
Lys	Lys	Tyr	Tyr	Glu	Ser	His	Lys	Lys	Asp	Phe	Lys	Lys	Pro	Thr	Ser	
				215					220					225		
TTT	AAA	ACA	CGC	TCT	TTA	TAT	TTT	GAC	GCT	AGT	TTG	GAA	AAA	CCT	GAT	776
Phe	Lys	Thr	Arg	Ser	Leu	Tyr	Phe	Asp	Ala	Ser	Leu	Glu	Lys	Pro	Asp	
			230					235						240		

CTCTAGGC

361

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```

Met Ser Gly Cys Ala Ser Ser Ser Pro Thr Gly Thr Leu Ile Thr Met
 1             5             10             15
Val Thr Met Pro Val Ser Gly Asn Asp Ala Gln Tyr Ser Lys Glu Gly
      20             25             30
Arg Ala Ser Cys Trp Ser Val Phe Ser Leu Val Ala Ala Gly Asn Cys
      35             40             45
Ser Val Glu Lys Ala Ala Lys Ser Gly Gly Val Thr Lys Ile Lys Met
      50             55             60
Val Ser Arg Glu Thr Asn Asn Phe Leu Gly Ile Val Gly Lys Tyr Thr
      65             70             75             80
Thr Ile Val Gln Gly Asp
              85

```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1511
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```

TTTAAACCTG AATTCATAT TTTTGATTTT TTAAAGGGAT TAGAGTTCTT ATG ATT      56
                                     Met Ile
                                     1

GAA TGG ATG CAA AAT CAT AGA AAA TAT TTA GTG GTT ACA ATA TGG ATA      104
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
      5             10             15

```

Gln	Leu	Asp	Lys	Ile	Ala	Pro	Thr	Ile	Lys	Ser	Gly	Met	Arg	Ile	Gln
		355					360					365			
Lys	Gly	Tyr	Val	Leu	Gly	Arg	Ile	Asp	Gln	Arg	Leu	Gly	Phe	Glu	Val
	370					375					380				
Thr	Met	Arg	Glu	Lys	His	Ile	Asn	Pro	Leu	Glu	Leu	Ile	Ala	Arg	Asn
385					390					395					400

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...308
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

AGGATTTAAG ATTGCGTTTG AAGTTAGCTA GCGTATGCTT GGGCGTTTTG ATG AGT	56
Met Ser	
1	
GGT TGT GCG TCT TCT TCG CCA ACT GGC ACT CTT ATC ACT ATG GTA ACG	104
Gly Cys Ala Ser Ser Ser Pro Thr Gly Thr Leu Ile Thr Met Val Thr	
5 10 15	
ATG CCA GTT TCT GGG AAT GAT GCA CAA TAC TCC AAA GAA GGG CGT GCG	152
Met Pro Val Ser Gly Asn Asp Ala Gln Tyr Ser Lys Glu Gly Arg Ala	
20 25 30	
AGT TGT TGG AGT GTT TTT AGT CTT GTG GCT GCC GGT AAT TGT TCG GTA	200
Ser Cys Trp Ser Val Phe Ser Leu Val Ala Ala Gly Asn Cys Ser Val	
35 40 45 50	
GAA AAA GCG GCT AAA AGT GGC GGT GTT ACC AAG ATT AAA ATG GTG AGC	248
Glu Lys Ala Ala Lys Ser Gly Gly Val Thr Lys Ile Lys Met Val Ser	
55 60 65	
CGT GAG ACA AAC AAC TTT TTA GGT ATT GTT GGC AAA TAC ACC ACG ATC	296
Arg Glu Thr Asn Asn Phe Leu Gly Ile Val Gly Lys Tyr Thr Thr Ile	
70 75 80	
GTT CAA GGC GAC TAGTTTTAAT ATTTAGAGAG CGTAGTTGAA TCGTCTTTCG TTCCA	353
Val Gln Gly Asp	
85	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```

Met Tyr Lys Leu Gly Val Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn
 1           5           10           15
Thr Gln Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr
 20           25           30
Leu Leu Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu
 35           40           45
Ser Ser Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Ala Glu
 50           55           60
Met Glu Arg Gln Met Ile Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg
 65           70           75           80
Asn Glu Ser Leu Ala Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser
 85           90           95
Leu Asp His Leu Gln Lys Lys Arg Ser Phe Leu Gln Lys Arg Val Phe
100           105           110
Asp Thr Leu Leu Gln Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln
115           120           125
Asn Leu Ala Ser Ser Asn Asp Val Val Leu Gln Val Ala Phe Glu Asn
130           135           140
Leu His Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu
145           150           155           160
Lys Glu Leu Asn Thr Gln Ala Leu Lys Val Lys Asn Ser Ile Gln Lys
165           170           175
Ile Ser Ser Ile Ile Asp Glu Gln Lys Thr Arg Glu Val Thr Leu Lys
180           185           190
Ser Leu Lys Thr Glu Gln Asp Lys Leu Ile Leu Ser Met Gln Lys Asp
195           200           205
Tyr Ala Ile Tyr Asn Gln Arg Leu Thr Leu Leu Glu Lys Glu Arg Gln
210           215           220
Asn Leu Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg
225           230           235           240
Glu Asn Glu Glu Lys Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu
245           250           255
Val Lys Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr
260           265           270
Asn Gly Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln
275           280           285
Lys Phe Gly Pro Tyr Ile Asp Pro Val Tyr Asn Leu Lys Ile Phe Ser
290           295           300
Glu Ser Ile Thr Leu Val Ser Lys Thr Pro Asn Ala Leu Val Arg Asn
305           310           315           320
Val Leu Asp Gly Lys Ile Val Phe Ala Lys Glu Ile Asn Met Leu Lys
325           330           335
Lys Val Val Ile Ile Glu His Lys Asn Gly Ile Arg Thr Ile Tyr Ser
340           345           350

```

Lys Thr Glu Gln Asp	Lys Leu Ile Leu Ser Met Gln Lys Asp Tyr Ala	
195	200 205 210	
ATC TAC AAC CAA CGC CTA ACC CTT TTA GAA AAA GAG CGC CAG AAT TTA		728
Ile Tyr Asn Gln Arg Leu Thr Leu Leu Glu Lys Glu Arg Gln Asn Leu	215 220 225	
AAC GCT CTT TTA AAA CGC TTG AAT ATC ATC AAA CAA AAC AGA GAA AAT		776
Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg Glu Asn	230 235 240	
GAA GAA AAA GTC AGT TTG AAA AAA TCT TCT CAA GCC TTA GAA GTC AAA		824
Glu Glu Lys Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu Val Lys	245 250 255	
CAA GTG GCT AGC TCT TAT CAA AAT ATC AAC ACC ACG AGC TAT AAC GGA		872
Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr Asn Gly	260 265 270	
CCA AAA ACG ATC GCT CCC TTG AAC GAT TAT GAA GTG GTG CAA AAA TTT		920
Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln Lys Phe	275 280 285 290	
GGC CCC TAT ATT GAC CCG GTT TAT AAT TTA AAA ATT TTT AGC GAG TCT		968
Gly Pro Tyr Ile Asp Pro Val Tyr Asn Leu Lys Ile Phe Ser Glu Ser	295 300 305	
ATT ACG CTC GTG TCA AAA ACC CCA AAC GCT TTG GTG CGT AAT GTT TTA		1016
Ile Thr Leu Val Ser Lys Thr Pro Asn Ala Leu Val Arg Asn Val Leu	310 315 320	
GAC GGG AAA ATC GTG TTC GCT AAA GAA ATC AAC ATG CTT AAA AAA GTC		1064
Asp Gly Lys Ile Val Phe Ala Lys Glu Ile Asn Met Leu Lys Lys Val	325 330 335	
GTT ATC ATT GAG CAT AAA AAT GGG ATC CGC ACG ATT TAT TCT CAA TTG		1112
Val Ile Ile Glu His Lys Asn Gly Ile Arg Thr Ile Tyr Ser Gln Leu	340 345 350	
GAT AAA ATC GCT CCC ACC ATT AAA AGC GGC ATG CGG ATC CAA AAA GGC		1160
Asp Lys Ile Ala Pro Thr Ile Lys Ser Gly Met Arg Ile Gln Lys Gly	355 360 365 370	
TAT GTT TTA GGG CGC ATT GAT CAA CGC TTG GGC TTT GAA GTT ACC ATG		1208
Tyr Val Leu Gly Arg Ile Asp Gln Arg Leu Gly Phe Glu Val Thr Met	375 380 385	
AGA GAA AAA CAC ATC AAC CCC TTA GAA CTC ATC GCA CGC AAT TAAACAAAT		1259
Arg Glu Lys His Ile Asn Pro Leu Glu Leu Ile Ala Arg Asn	390 395 400	
CGTTTTTTATT GCCGATATTG GCTAAAGAAT TTATGCAAAC AAAT		1303

(2) INFORMATION FOR SEQ ID NO:206:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

CCTTGTGGTC TCATTTGTTT CTGTTTACT TGTAGCTTGG AGGACTAGGC ATG TAT	56
Met Tyr	
1	
AAA TTA GGG GTG TTT TTG TTA GCC ACC TTA CTA TCA GCT AAC ACG CAA	104
Lys Leu Gly Val Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn Thr Gln	
5 10 15	
AAA GTG AGC GAT ATT GCT AAA GAT ATC CAA CAT AAA GAA ACC CTT TTG	152
Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr Leu Leu	
20 25 30	
AAA AAA ACC CAT GAA GAA AAA AAC CAA CTA AAC AGC CGT TTG AGT TCT	200
Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu Ser Ser	
35 40 45 50	
TTA GGC GAA GCG ATC CGC TCT AAA GAG CTT CAA AAG GCT GAG ATG GAG	248
Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Ala Glu Met Glu	
55 60 65	
CGC CAA ATG ATC GCT TTA AAA AAG AGT CTT GAA AAA AAT CGT AAC GAA	296
Arg Gln Met Ile Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg Asn Glu	
70 75 80	
AGT TTG GCG CAA GAA AAA GTC CTA ACC AAC TAC CGC AAG TCT TTA GAT	344
Ser Leu Ala Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser Leu Asp	
85 90 95	
CAT TTG CAA AAA AAG CGA TCA TTT TTA CAA AAG AGG GTG TTT GAT ACG	392
His Leu Gln Lys Lys Arg Ser Phe Leu Gln Lys Arg Val Phe Asp Thr	
100 105 110	
CTT TTA CAG GAT TTC CTT TTT TCA CAA GCC CTA AAG GGG CAG AAT TTA	440
Leu Leu Gln Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln Asn Leu	
115 120 125 130	
GCC TCT TCT AAT GAT GTT GTT TTG CAA GTG GCG TTT GAA AAC TTG CAC	488
Ala Ser Ser Asn Asp Val Val Leu Gln Val Ala Phe Glu Asn Leu His	
135 140 145	
CAA AGC ACT CTG TCT AAA ATG TCG CAA CTG AGC CAA GAA GAA AAG GAA	536
Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu Lys Glu	
150 155 160	
CTC AAT ACG CAA GCT TTA AAA GTC AAA AAC AGC ATT CAA AAA ATC TCA	584
Leu Asn Thr Gln Ala Leu Lys Val Lys Asn Ser Ile Gln Lys Ile Ser	
165 170 175	
TCC ATC ATA GAT GAG CAA AAA ACT CGT GAA GTA ACC TTA AAA TCC TTG	632
Ser Ile Ile Asp Glu Gln Lys Thr Arg Glu Val Thr Leu Lys Ser Leu	
180 185 190	
AAA ACC GAA CAA GAT AAG CTC ATT TTG AGC ATG CAA AAA GAT TAT GCG	680


```

Arg Ser Glu Ile Tyr Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp
      100                      105                      110
Ile Lys Glu Ile Thr Cys Leu Ile Glu Pro His Leu Val Val Val Ala
      115                      120                      125
Glu Val Gly Glu Gln His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile
      130                      135                      140
Cys Glu Thr Lys Ala Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala
      145                      150                      155                      160
Phe Cys Tyr Ser Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser
      165                      170                      175
Pro Leu Ile Asp Tyr Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu
      180                      185                      190
Lys Gly Thr Ser Phe Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe
      195                      200                      205
Glu Thr Lys Val Leu Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala
      210                      215                      220
Ile Leu Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg
      225                      230                      235                      240
Leu Val Leu Glu Leu Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu
      245                      250                      255
Val Asn Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys
      260                      265                      270
Gly Met Leu Glu Gly Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys
      275                      280                      285
Val Ile Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu
      290                      295                      300
Ala Leu Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr
      305                      310                      315                      320
Gly Glu Leu Asn Ser Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln
      325                      330                      335
Lys Ile Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala
      340                      345                      350
Thr Thr Ile Gln Gly Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn
      355                      360                      365
Tyr Ile
      370

```

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1250
- (D) OTHER INFORMATION:

CAA AAA ATC ATC ATA GAC GAT AGC TTT AAT GGG AAT TTA AAG GGC ATG	872
Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met	
260 265 270	
TTA GAG GGC ATT CGT TTA GCG AGT TTG CAC AAA GGG CGT AAA GTC ATT	920
Leu Glu Gly Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys Val Ile	
275 280 285 290	
GTA ACA CCG GGC TTA GTG GAA AGC AAT ACA GAA AGT AAT GAG GCT TTA	968
Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu	
295 300 305	
GCG CAA AAA ATA GAC GGG GTT TTT GAT GTC GCT ATC ATC ACA GGG GAG	1016
Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu	
310 315 320	
TTG AAT TCC AAA ACG ATT GCT TCA CAA TTG AAA ACC CCC CAA AAA ATC	1064
Leu Asn Ser Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln Lys Ile	
325 330 335	
TTA CTC AAG GAT AAG GCG CAA TTG GAA AAT ATC TTA CAA GCC ACC ACG	1112
Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr	
340 345 350	
ATT CAA GGC GAT TTG ATT TTA TTC GCT AAT GAC GCC CCT AAT TAC ATT T	1161
Ile Gln Gly Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn Tyr Ile	
355 360 365 370	
AGGAAATGAA CATGCAACAT TTATACGCTC CTTGGCGCGA AAGTTATTTG AA	1213

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Met Gly Phe Xaa Leu Ala Leu Gly Tyr Leu Cys Leu Phe Ile Phe Val	
1 5 10 15	
Leu Ser Ala Ser Leu Ile Ser Glu Lys Ala Leu Ser Lys Gln Tyr Leu	
20 25 30	
Gln Thr Ala Lys Asp Lys Ile Thr Ser Leu Lys Asn Leu Lys Val Ile	
35 40 45	
Ala Ile Thr Gly Ser Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu Leu	
50 55 60	
Gln Ile Leu Gln Thr Thr Phe Asn Ala His Ala Ser Pro Lys Ser Val	
65 70 75 80	
Asn Thr Leu Leu Gly Leu Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp	
85 90 95	

GCT AAA GAT AAA ATC ACC TCT TTA AAG AAT TTA AAA GTC ATC GCC ATT	200
Ala Lys Asp Lys Ile Thr Ser Leu Lys Asn Leu Lys Val Ile Ala Ile	
35 40 45 50	
ACC GGA AGC TTT GGG AAA ACC AGC ACC AAA AAT TTC TTG CTT CAA ATC	248
Thr Gly Ser Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu Leu Gln Ile	
55 60 65	
TTA CAA ACC ACA TTC AAC GCG CAT GCA AGC CCC AAA AGC GTC AAT ACC	296
Leu Gln Thr Thr Phe Asn Ala His Ala Ser Pro Lys Ser Val Asn Thr	
70 75 80	
CTT TTA GGG CTT GCG AAT GAT ATT AAT CAG AAT TTA GAC GAT AGG AGT	344
Leu Leu Gly Leu Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp Arg Ser	
85 90 95	
GAA ATC TAT ATC GCT GAA GCC GGG GCA AGG AAT AAG GGC GAT ATT AAA	392
Glu Ile Tyr Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp Ile Lys	
100 105 110	
GAA ATC ACC TGT CTC ATT GAA CCG CAC CTT GTT GTG GTT GCA GAA GTG	440
Glu Ile Thr Cys Leu Ile Glu Pro His Leu Val Val Val Ala Glu Val	
115 120 125 130	
GGC GAA CAG CAT TTA GAA TAC TTT AAA ACT TTA GAA AAT ATT TGC GAG	488
Gly Glu Gln His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile Cys Glu	
135 140 145	
ACT AAA GCG GAA TTA TTG GAT TCC AAA CGC TTA GAA AAA GCC TTT TGT	536
Thr Lys Ala Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala Phe Cys	
150 155 160	
TAC TCG GTG GAA AAG ATC AAG CCC TAT GCC CCT AAA GAT AGC CCT TTA	584
Tyr Ser Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu	
165 170 175	
ATA GAC TAT TCT AGC CTG GTT AAA AAC ATC CAA TCC ACT TTA AAA GGC	632
Ile Asp Tyr Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu Lys Gly	
180 185 190	
ACT TCT TTT GAA ATG CTT ATA GGT AGC GTT TGG GAA AGA TTT GAA ACA	680
Thr Ser Phe Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe Glu Thr	
195 200 205 210	
AAG GTT CTA GGG GAG TTT AGC GCT TAT AAT ATC GCT TCA GCC ATT TTA	728
Lys Val Leu Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala Ile Leu	
215 220 225	
ATC GCT AAG CAT TTA GGC TTA GAG ACC GAA AGG ATC AAA CGG CTT GTT	776
Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val	
230 235 240	
TTA GAA CTC AAC CCT ATT GCT CAT CGT TTG CAA CTT TTG GAA GTG AAT	824
Leu Glu Leu Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu Val Asn	
245 250 255	

```

Asp Ser Val Arg Glu Ile Asp Glu Lys Ala Asn Arg Leu Lys Gly Ser
 130                      135                      140
Glu Lys Ser Tyr Thr Phe His Gly Arg Asp Val Tyr Ala Tyr Thr Gly
145                      150                      155                      160
Ala Arg Leu Ala Ser Gly Ala Ile Thr Phe Glu Gln Val Gly Pro Glu
                      165                      170                      175
Leu Pro Pro Lys Val Val Glu Ile Pro Tyr Gln Lys Ala Lys Ala Thr
                      180                      185                      190
Lys Gly Glu Val Lys Gly Asn Ile Pro Ile Leu Asp Ile Gln Tyr Gly
                      195                      200                      205
Asn Val Trp Ser Asn Ile Ser Asp Lys Leu Leu Asn Gln Ala Lys Ile
                      210                      215                      220
Lys Leu Asn Asp Thr Leu Cys Val Thr Ile Phe Lys Gly Ser Lys Lys
225                      230                      235                      240
Gln Tyr Glu Gly Lys Met Pro Tyr Val Ala Ser Phe Gly Asp Val Pro
                      245                      250                      255
Glu Gly Gln Pro Leu Val Tyr Leu Asn Ser Leu Leu Asn Val Ser Val
                      260                      265                      270
Ala Leu Asn Arg Asp Asn Phe Ala Gln Lys Tyr Gln Ile Lys Ser Gly
                      275                      280                      285
Ala Asp Trp Asn Ile Asp Ile Lys Lys Cys Ala Lys
                      290                      295                      300

```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1160
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

ATTATTTTTA ATCTTGCATG AAATCTTAAA TATAGAATTA GTCCCTTTGG ATG GGA      56
                                     Met Gly
                                     1

TTT TCN CTC GCG CTA GGC TAT TTG TGT TTG TTT ATA TTC GTT TTA AGC      104
Phe Xaa Leu Ala Leu Gly Tyr Leu Cys Leu Phe Ile Phe Val Leu Ser
      5                      10                      15

GCT TCT TTA ATC TCT GAA AAA GCC TTA TCC AAG CAG TAT TTG CAA ACC      152
Ala Ser Leu Ile Ser Glu Lys Ala Leu Ser Lys Gln Tyr Leu Gln Thr
      20                      25                      30

```

TGG AGC AAC ATC AGC GAT AAA TTA CTC AAT CAA GCA AAA ATC AAA CTC 728
 Trp Ser Asn Ile Ser Asp Lys Leu Leu Asn Gln Ala Lys Ile Lys Leu
 215 220 225

AAT GAC ACG CTG TGT GTA ACG ATT TTT AAA GGT TCT AAG AAA CAA TAC 776
 Asn Asp Thr Leu Cys Val Thr Ile Phe Lys Gly Ser Lys Lys Gln Tyr
 230 235 240

GAA GGG AAA ATG CCG TAT GTC GCA AGC TTT GGC GAT GTG CCA GAA GGC 824
 Glu Gly Lys Met Pro Tyr Val Ala Ser Phe Gly Asp Val Pro Glu Gly
 245 250 255

CAG CCG TTA GTT TAT TTA AAC AGC TTG TTA AAT GTT TCC GTG GCG CTG 872
 Gln Pro Leu Val Tyr Leu Asn Ser Leu Leu Asn Val Ser Val Ala Leu
 260 265 270

AAT AGG GAT AAT TTC GCG CAA AAA TAT CAA ATC AAA TCC GGT GCT GAC 920
 Asn Arg Asp Asn Phe Ala Gln Lys Tyr Gln Ile Lys Ser Gly Ala Asp
 275 280 285 290

TGG AAT ATT GAT ATA AAG AAG TGC GCT AAG TAAAGCGCTG TTTAGAAAAT TAA 973
 Trp Asn Ile Asp Ile Lys Lys Cys Ala Lys
 295 300

GGGGCGTGAA ACGCCCTAAC CGCTAAAGAT 1003

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Met Arg Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu
 1 5 10 15
 Ser Ser Val Tyr Ala Asp Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser
 20 25 30
 Leu Lys Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val
 35 40 45
 Asp Ser His Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr
 50 55 60
 Asn Ile Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp
 65 70 75 80
 Pro Lys Gly Ser Val Phe Val Ser Val Val Asp Pro Gly Val Gly Thr
 85 90 95
 Lys Arg Lys Ser Val Val Leu Lys Thr Lys Asn Gly Gln Tyr Phe Val
 100 105 110
 Ser Pro Asp Asn Gly Thr Leu Thr Leu Val Ala Gln Thr Leu Gly Ile
 115 120 125

ATCATGAGAA AACGCTTCAC TCCACTTTTG TTATTCAGGA AATAATACAG ATG AGA	56
Met Arg	
1	
AAA ACG ATT TCA GCG TTG TTT TTA TCA GCG TGC ATA GGG TTA TCG TCT	104
Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu Ser Ser	
5 10 15	
GTT TAT GCA GAT AAC GCT TTG ATT TTG CAA ACC GAT TTT AGT CTA AAA	152
Val Tyr Ala Asp Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser Leu Lys	
20 25 30	
GAT GGG GCC GTC TCG GCG ATG AAA GGC GTC GCT TTC AGC GTT GAT TCC	200
Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val Asp Ser	
35 40 45 50	
CAT CTT AAA ATC TTT GAT TTA ACG CAC GAA ATC CCC CCG TAT AAC ATC	248
His Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr Asn Ile	
55 60 65	
TGG GAA GGC GCT TAC CGC TTG TAT CAG ACC GCC AGT TAT TGG CCA AAA	296
Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp Pro Lys	
70 75 80	
GGT TCG GTA TTT GTG AGC GTA GTT GAT CCG GGC GTA GGC ACT AAG CGT	344
Gly Ser Val Phe Val Ser Val Val Asp Pro Gly Val Gly Thr Lys Arg	
85 90 95	
AAA TCG GTG GTA CTA AAA ACT AAA AAC GGC CAG TAT TTC GTC TCG CCG	392
Lys Ser Val Val Leu Lys Thr Lys Asn Gly Gln Tyr Phe Val Ser Pro	
100 105 110	
GAT AAC GGC ACG CTG ACT TTG GTG GCA CAA ACT TTG GGG ATT GAT AGC	440
Asp Asn Gly Thr Leu Thr Leu Val Ala Gln Thr Leu Gly Ile Asp Ser	
115 120 125 130	
GTG CGT GAA ATT GAT GAA AAA GCT AAC CGC TTG AAA GGT TCT GAA AAA	488
Val Arg Glu Ile Asp Glu Lys Ala Asn Arg Leu Lys Gly Ser Glu Lys	
135 140 145	
TCC TAT ACT TTC CAT GGT CGT GAT GTG TAT GCT TAC ACC GGT GCA CGC	536
Ser Tyr Thr Phe His Gly Arg Asp Val Tyr Ala Tyr Thr Gly Ala Arg	
150 155 160	
TTG GCT TCT GGG GCG ATC ACA TTC GAG CAG GTC GGG CCA GAG CTT CCC	584
Leu Ala Ser Gly Ala Ile Thr Phe Glu Gln Val Gly Pro Glu Leu Pro	
165 170 175	
CCA AAA GTC GTT GAA ATT CCT TAC CAA AAA GCG AAA GCC ACA AAA GGG	632
Pro Lys Val Val Glu Ile Pro Tyr Gln Lys Ala Lys Ala Thr Lys Gly	
180 185 190	
GAA GTG AAA GGT AAT ATC CCG ATT TTG GAT ATT CAA TAT GGC AAT GTT	680
Glu Val Lys Gly Asn Ile Pro Ile Leu Asp Ile Gln Tyr Gly Asn Val	
195 200 205 210	

GATGATATTA ACATGCGTAA AAGCCTGGAG CTT

574

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```

Met Arg Phe Phe Ser Phe Phe Tyr Phe Leu Phe Tyr Phe Leu Gly Val
 1             5             10             15
Ser Leu Gln Ala Leu Ser Pro Leu Glu Asp Gln Glu Phe Leu Ile Ser
          20             25             30
Tyr Arg Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr Ser
          35             40             45
Val Ser Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val Leu
          50             55             60
Asp Tyr His Cys Ser Ile Ile Thr Arg Asn Leu Pro Asn Leu Lys Asn
65             70             75             80
Pro Leu Leu Pro Ile Lys Leu Glu Arg Phe Leu Leu Glu Ile Ala Leu
          85             90             95
Lys Lys Glu Lys Glu Arg Val Ile Asp Cys Ile Leu Lys Ser Gln Val
          100            105            110
Ala Ile Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr Thr
          115            120            125
Ser Ile Leu Ala Leu Lys Ala Leu Ser Val Arg Ala Ser Leu Val Gly
          130            135            140
Asp Ala Leu Phe Leu Asp Ile Phe Arg Lys Glu Glu Glu
145            150            155

```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...950
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...521

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAAGAGCCAG AAAATTTAGA AACCTCTTCG GCACAAAATT TGTTTGAGTG ATG CGT	56
Met Arg	
1	
TTC TTT TCA TTC TTT TAT TTT TTA TTT TAT TTT TTA GGG GTT TCT TTG	104
Phe Phe Ser Phe Phe Tyr Phe Leu Phe Tyr Phe Leu Gly Val Ser Leu	
5 10 15	
CAA GCT CTC AGC CCC CTA GAA GAT CAA GAA TTT TTA ATT TCG TAC CGC	152
Gln Ala Leu Ser Pro Leu Glu Asp Gln Glu Phe Leu Ile Ser Tyr Arg	
20 25 30	
TTG AAA ATC GTT GAT TCT AGA GTG ATG GGC GAA GAG TAT TCT GTC TCT	200
Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr Ser Val Ser	
35 40 45 50	
AAA CCT ATC GTT AGC CGC ATT AAA ACA GCC CCC TAT GTT TTA GAC TAT	248
Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val Leu Asp Tyr	
55 60 65	
CAT TGC TCC ATC ATC ACT CGT AAC TTA CCC AAT TTG AAA AAC CCC TTG	296
His Cys Ser Ile Ile Thr Arg Asn Leu Pro Asn Leu Lys Asn Pro Leu	
70 75 80	
CTC CCA ATA AAG TTA GAA CGC TTC CTT TTA GAA ATC GCG TTA AAA AAA	344
Leu Pro Ile Lys Leu Glu Arg Phe Leu Leu Glu Ile Ala Leu Lys Lys	
85 90 95	
GAA AAA GAG CGG GTC ATA GAC TGC ATT TTA AAA AGC CAG GTC GCT ATC	392
Glu Lys Glu Arg Val Ile Asp Cys Ile Leu Lys Ser Gln Val Ala Ile	
100 105 110	
ACG CAT TAT GAT CAT AGC TAT AAA AAC GGC ACC ACT ACC ACA AGC ATT	440
Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr Thr Ser Ile	
115 120 125 130	
CTT GCC CTC AAA GCC TTA AGC GTT AGA GCG AGT TTA GTG GGA GAT GCG	488
Leu Ala Leu Lys Ala Leu Ser Val Arg Ala Ser Leu Val Gly Asp Ala	
135 140 145	
CTG TTT TTA GAT ATT TTT AGA AAG GAA GAA GAA TGAAATCGC CATGTAGAA	541
Leu Phe Leu Asp Ile Phe Arg Lys Glu Glu Glu	
150 155	

Ala	Lys	Leu	Phe	Ala	Gln	Val	Leu	Asn	Glu	Gly	Thr	Lys	Glu	Leu	Gly	65	70	75	80
Ala	Val	Gly	Phe	Ala	Gln	Leu	Leu	Glu	Gln	Lys	Ala	Ile	Ser	Leu	Asn	85	90	95	
Val	Asp	Thr	Ser	Thr	Glu	Asp	Leu	Gln	Ile	Thr	Leu	Glu	Phe	Leu	Lys	100	105	110	
Glu	Tyr	Glu	Asp	Glu	Ala	Ile	Thr	Arg	Leu	Lys	Glu	Leu	Leu	Lys	Ser	115	120	125	
Pro	Asn	Phe	Thr	Gln	Asn	Ala	Leu	Glu	Lys	Val	Lys	Thr	Gln	Met	Leu	130	135	140	
Ala	Ala	Leu	Leu	Gln	Lys	Glu	Ser	Asp	Phe	Asp	Tyr	Leu	Ala	Lys	Leu	145	150	155	160
Thr	Leu	Lys	Gln	Glu	Leu	Phe	Ala	Asn	Thr	Pro	Leu	Ala	Asn	Ala	Ala	165	170	175	
Leu	Gly	Thr	Lys	Glu	Ser	Ile	Gln	Lys	Ile	Lys	Leu	Asp	Asp	Leu	Lys	180	185	190	
Gln	Gln	Phe	Ala	Lys	Val	Phe	Glu	Leu	Asn	Lys	Leu	Val	Val	Val	Leu	195	200	205	
Gly	Gly	Asp	Leu	Lys	Ile	Asp	Gln	Thr	Leu	Lys	Arg	Leu	Asn	Asn	Ala	210	215	220	
Leu	Asn	Phe	Leu	Pro	Gln	Gly	Lys	Ala	Tyr	Glu	Glu	Pro	Tyr	Phe	Glu	225	230	235	240
Thr	Ser	Asp	Lys	Lys	Ser	Glu	Lys	Val	Leu	Tyr	Lys	Asp	Thr	Glu	Gln	245	250	255	
Ala	Phe	Val	Tyr	Phe	Gly	Ala	Pro	Phe	Lys	Ile	Lys	Asp	Leu	Lys	Gln	260	265	270	
Asp	Leu	Ala	Lys	Ser	Lys	Val	Met	Met	Phe	Val	Leu	Gly	Gly	Gly	Phe	275	280	285	
Gly	Ser	Arg	Leu	Met	Glu	Lys	Ile	Arg	Val	Gln	Glu	Gly	Leu	Ala	Tyr	290	295	300	
Ser	Val	Tyr	Ile	Arg	Ser	Asn	Phe	Ser	Lys	Val	Ala	His	Phe	Ala	Ser	305	310	315	320
Gly	Tyr	Leu	Gln	Thr	Lys	Leu	Ser	Thr	Gln	Thr	Lys	Ser	Val	Ala	Leu	325	330	335	
Val	Lys	Lys	Ile	Val	Lys	Glu	Phe	Ile	Glu	Lys	Gly	Met	Thr	Gln	Gln	340	345	350	
Glu	Leu	Asp	Asp	Ala	Lys	Lys	Phe	Leu	Leu	Gly	Ser	Glu	Pro	Leu	Arg	355	360	365	
Asn	Glu	Thr	Ile	Ser	Ser	Arg	Leu	Asn	Thr	Thr	Tyr	Asn	Tyr	Phe	Tyr	370	375	380	
Leu	Gly	Leu	Pro	Leu	Asn	Phe	Asn	Gln	Thr	Leu	Leu	Asn	Gln	Ile	Gln	385	390	395	400
Lys	Met	Ser	Leu	Lys	Glu	Ile	Asn	Asp	Phe	Ile	Lys	Ala	His	Thr	Glu	405	410	415	
Ile	Asn	Asp	Leu	Thr	Phe	Ala	Ile	Val	Ser	Asn	Lys	Lys	Lys	Asp	Lys	420	425	430	

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

TAT ATC CGC TCC AAT TTT TCT AAA GTG GCG CAT TTT GCG AGC GGG TAT 1016
 Tyr Ile Arg Ser Asn Phe Ser Lys Val Ala His Phe Ala Ser Gly Tyr
 310 315 320

TTG CAA ACC AAG CTC AGC ACT CAA ACT AAA AGC GTT GCC TTA GTT AAA 1064
 Leu Gln Thr Lys Leu Ser Thr Gln Thr Lys Ser Val Ala Leu Val Lys
 325 330 335

AAA ATC GTT AAG GAA TTT ATA GAA AAA GGC ATG ACG CAA CAA GAA TTA 1112
 Lys Ile Val Lys Glu Phe Ile Glu Lys Gly Met Thr Gln Gln Glu Leu
 340 345 350

GAC GAC GCT AAA AAG TTT TTA CTA GGC TCT GAG CCT TTA AGG AAT GAA 1160
 Asp Asp Ala Lys Lys Phe Leu Leu Gly Ser Glu Pro Leu Arg Asn Glu
 355 360 365 370

ACG ATC TCT AGC CGC TTG AAC ACC ACT TAC AAT TAT TTT TAT TTA GGT 1208
 Thr Ile Ser Ser Arg Leu Asn Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly
 375 380 385

TTG CCT TTA AAT TTT AAC CAA ACG CTG CTC AAT CAA ATC CAA AAA ATG 1256
 Leu Pro Leu Asn Phe Asn Gln Thr Leu Leu Asn Gln Ile Gln Lys Met
 390 395 400

AGT TTG AAA GAA ATC AAT GAT TTC ATT AAA GCC CAC ACC GAA ATC AAC 1304
 Ser Leu Lys Glu Ile Asn Asp Phe Ile Lys Ala His Thr Glu Ile Asn
 405 410 415

GAC TTG ACT TTT GCT ATT GTG AGC AAT AAA AAG AAG GAC AAA TGATGCCAT 1355
 Asp Leu Thr Phe Ala Ile Val Ser Asn Lys Lys Asp Lys
 420 425 430

TTGAAGCTGT AATCGGGCTA GAAGTCCATG TCCAACCTCAA CACC 1399

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Met Lys Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu
 1 5 10 15
 Gln Ala Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro
 20 25 30
 Val Ile Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe Ile His Leu
 35 40 45
 Ala Phe Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu
 50 55 60

GGG TTT GCG CAA CTT TTA GAG CAA AAA GCG ATC AGT TTG AAT GTG GAT	344
Gly Phe Ala Gln Leu Leu Glu Gln Lys Ala Ile Ser Leu Asn Val Asp	
85 90 95	
ACC AGC ACA GAA GAT TTG CAA ATC ACT TTA GAA TTT TTA AAA GAA TAC	392
Thr Ser Thr Glu Asp Leu Gln Ile Thr Leu Glu Phe Leu Lys Glu Tyr	
100 105 110	
GAA GAT GAA GCC ATT ACG CGC TTA AAA GAG CTT TTA AAA TCC CCT AAT	440
Glu Asp Glu Ala Ile Thr Arg Leu Lys Glu Leu Lys Ser Pro Asn	
115 120 125 130	
TTC ACG CAA AAC GCT TTA GAA AAA GTC AAA ACC CAA ATG TTA GCC GCA	488
Phe Thr Gln Asn Ala Leu Glu Lys Val Lys Thr Gln Met Leu Ala Ala	
135 140 145	
CTT TTA CAA AAA GAA AGC GAT TTT GAC TAT TTG GCT AAA TTG ACT TTA	536
Leu Leu Gln Lys Glu Ser Asp Phe Asp Tyr Leu Ala Lys Leu Thr Leu	
150 155 160	
AAG CAA GAG CTT TTT GCT AAC ACC CCT TTA GCT AAC GCA GCC TTA GGC	584
Lys Gln Glu Leu Phe Ala Asn Thr Pro Leu Ala Asn Ala Ala Leu Gly	
165 170 175	
ACT AAA GAG AGC ATT CAA AAA ATC AAG CTA GAC GAT TTG AAA CAG CAA	632
Thr Lys Glu Ser Ile Gln Lys Ile Lys Leu Asp Asp Leu Lys Gln Gln	
180 185 190	
TTT GCT AAG GTC TTT GAA CTC AAT AAG CTC GTG GTG GTG CTT GGG GGC	680
Phe Ala Lys Val Phe Glu Leu Asn Lys Leu Val Val Val Leu Gly Gly	
195 200 205 210	
GAT TTG AAA ATC GAT CAA ACC CTT AAG CGT TTG AAT AAC GCC CTT AAT	728
Asp Leu Lys Ile Asp Gln Thr Leu Lys Arg Leu Asn Asn Ala Leu Asn	
215 220 225	
TTC TTG CCA CAA GGT AAA GCG TAT GAA GAG CCT TAT TTT GAA ACG AGC	776
Phe Leu Pro Gln Gly Lys Ala Tyr Glu Glu Pro Tyr Phe Glu Thr Ser	
230 235 240	
GAT AAA AAA AGC GAA AAA GTC CTC TAT AAA GAC ACT GAG CAG GCT TTC	824
Asp Lys Lys Ser Glu Lys Val Leu Tyr Lys Asp Thr Glu Gln Ala Phe	
245 250 255	
GTG TAT TTT GGT GCG CCC TTT AAA ATC AAG GAT TTA AAA CAG GAT TTA	872
Val Tyr Phe Gly Ala Pro Phe Lys Ile Lys Asp Leu Lys Gln Asp Leu	
260 265 270	
GCG AAA TCT AAA GTC ATG ATG TTT GTG CTT GGT GGG GGG TTT GGC TCT	920
Ala Lys Ser Lys Val Met Met Phe Val Leu Gly Gly Gly Phe Gly Ser	
275 280 285 290	
CGT TTA ATG GAA AAA ATC AGG GTT CAA GAG GGA TTA GCT TAT AGC GTG	968
Arg Leu Met Glu Lys Ile Arg Val Gln Glu Gly Leu Ala Tyr Ser Val	
295 300 305	

```

      290              295              300
Gly Glu Ala Lys His Ala Asp Met Ala Ile Ala Phe Gly Asn Arg Ser
305              310              315              320
Gly Leu Ile Ile Lys Glu Gly Lys Val Ile His Lys Leu Ala Glu Lys
      325              330              335
Asp Leu Phe Glu Thr Phe Val Ile Glu Val Glu Asn Leu Ala Lys Glu
      340              345              350
Arg Glu Lys Ser Leu Lys Asp
      355

```

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1346
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

GCCTATGAAA TCTTAAAGCG TTATCCGGCT AAAGCAAAGG TATAAATAAC ATG AAA      56
                                     Met Lys
                                     1

AAA TTT TTA ATC ACT TTA TTA TTA GGA GTT TTT ATG GGG TTA CAA GCG      104
Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu Gln Ala
      5              10              15

AGC GCT TTG ACA CAC CAA GAA ATC AAT CAA GCT AAA GTC CCT GTG ATT      152
Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro Val Ile
      20              25              30

TAT GAA GAA AAC CAT TTG TTG CCT ATG GGG TTT ATC CAT TTA GCC TTT      200
Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe Ile His Leu Ala Phe
      35              40              45              50

AGG GGG GGT GGG AGC TTA AGC GAT AAA AAC CAG TTG GGT TTG GCG AAA      248
Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu Ala Lys
      55              60              65

TTA TTC GCG CAA GTT TTA AAC GAA GGC ACT AAA GAG CTT GGT GCG GTG      296
Leu Phe Ala Gln Val Leu Asn Glu Gly Thr Lys Glu Leu Gly Ala Val
      70              75              80

```

Lys Ser Leu Lys Asp
355

CAGCAATCTA AC

1180

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met	Leu	Glu	Asn	Arg	Val	Lys	Thr	Lys	Gln	Ile	Phe	Ile	Gly	Gly	Val	1	5	10	15
Ala	Ile	Gly	Gly	Asp	Ala	Pro	Ile	Ser	Thr	Gln	Ser	Met	Thr	Phe	Ser	20	25	30	
Lys	Thr	Ala	Asp	Ile	Glu	Ser	Thr	Lys	Asn	Gln	Ile	Asp	Arg	Leu	Lys	35	40	45	
Leu	Ala	Gly	Ala	Asp	Leu	Val	Arg	Val	Ala	Val	Ser	Asn	Glu	Lys	Asp	50	55	60	
Ala	Leu	Ala	Leu	Lys	Glu	Leu	Lys	Lys	Val	Ser	Pro	Leu	Pro	Leu	Ile	65	70	75	80
Ala	Asp	Ile	His	Phe	His	Tyr	Lys	Phe	Ala	Leu	Ile	Ala	Ala	Gln	Ser	85	90	95	
Val	Asp	Ala	Ile	Arg	Ile	Asn	Pro	Gly	Asn	Ile	Gly	Ser	Lys	Glu	Lys	100	105	110	
Ile	Lys	Ala	Val	Val	Asp	Ala	Cys	Lys	Glu	Lys	Asn	Ile	Pro	Ile	Arg	115	120	125	
Ile	Gly	Val	Asn	Ala	Gly	Ser	Leu	Glu	Lys	Gln	Phe	Asp	Gln	Lys	Tyr	130	135	140	
Gly	Pro	Thr	Pro	Lys	Gly	Met	Val	Glu	Ser	Ala	Leu	Tyr	Asn	Ala	Lys	145	150	155	160
Leu	Leu	Glu	Asp	Leu	Asp	Phe	Thr	Asn	Phe	Lys	Ile	Ser	Leu	Lys	Ala	165	170	175	
Ser	Asp	Val	Ile	Arg	Thr	Ile	Glu	Ala	Tyr	Arg	Met	Leu	Arg	Pro	Leu	180	185	190	
Val	Ile	Tyr	Pro	Phe	His	Leu	Gly	Val	Thr	Glu	Ala	Gly	Asn	Leu	Phe	195	200	205	
Ser	Ser	Ser	Ile	Lys	Ser	Ala	Met	Ala	Leu	Gly	Gly	Leu	Leu	Met	Glu	210	215	220	
Gly	Ile	Gly	Asp	Thr	Met	Arg	Val	Ser	Ile	Thr	Gly	Glu	Leu	Glu	Asn	225	230	235	240
Glu	Ile	Lys	Val	Ala	Arg	Ala	Ile	Leu	Arg	His	Ser	Gly	Arg	Leu	Lys	245	250	255	
Glu	Gly	Ile	Asn	Trp	Ile	Ser	Cys	Pro	Thr	Cys	Gly	Arg	Ile	Glu	Ala	260	265	270	
Asn	Leu	Val	Asp	Met	Ala	Ile	Lys	Val	Glu	Lys	Arg	Leu	Ser	His	Ile	275	280	285	
Lys	Thr	Pro	Leu	Asp	Ile	Ser	Val	Met	Gly	Cys	Val	Val	Asn	Ala	Leu				

135										140										145										
ACC	CCA	AAA	GGC	ATG	GTA	GAA	AGC	GCT	TTG	TAT	AAC	GCC	AAA	CTT	TTA					536										
Thr	Pro	Lys	Gly	Met	Val	Glu	Ser	Ala	Leu	Tyr	Asn	Ala	Lys	Leu	Leu															
			150					155					160																	
GAA	GAT	TTG	GAT	TTT	ACC	AAT	TTT	AAG	ATT	TCT	TTA	AAA	GCG	AGC	GAT					584										
Glu	Asp	Leu	Asp	Phe	Thr	Asn	Phe	Lys	Ile	Ser	Leu	Lys	Ala	Ser	Asp															
		165					170					175																		
GTG	ATT	CGC	ACC	ATA	GAA	GCT	TAC	AGG	ATG	CTT	CGC	CCT	CTT	GTG	ATC					632										
Val	Ile	Arg	Thr	Ile	Glu	Ala	Tyr	Arg	Met	Leu	Arg	Pro	Leu	Val	Ile															
	180					185					190																			
TAT	CCT	TTC	CAT	TTG	GGG	GTT	ACG	GAG	GCG	GGG	AAT	CTT	TTT	AGC	TCC					680										
Tyr	Pro	Phe	His	Leu	Gly	Val	Thr	Glu	Ala	Gly	Asn	Leu	Phe	Ser	Ser															
195				200				205							210															
AGT	ATC	AAA	TCC	GCT	ATG	GCT	TTA	GGG	GGG	CTT	TTA	ATG	GAG	GGC	ATT					728										
Ser	Ile	Lys	Ser	Ala	Met	Ala	Leu	Gly	Gly	Leu	Leu	Met	Glu	Gly	Ile															
			215					220						225																
GGG	GAT	ACG	ATG	CGC	GTA	TCC	ATC	ACA	GGG	GAA	TTA	GAA	AAT	GAA	ATC					776										
Gly	Asp	Thr	Met	Arg	Val	Ser	Ile	Thr	Gly	Glu	Leu	Glu	Asn	Glu	Ile															
		230						235					240																	
AAA	GTG	GCC	AGA	GCA	ATT	TTA	CGC	CAT	AGC	GGG	CGG	TTG	AAA	GAA	GGG					824										
Lys	Val	Ala	Arg	Ala	Ile	Leu	Arg	His	Ser	Gly	Arg	Leu	Lys	Glu	Gly															
		245					250					255																		
ATT	AAT	TGG	ATT	TCT	TGC	CCC	ACT	TGC	GGG	CGC	ATT	GAA	GCC	AAT	TTA					872										
Ile	Asn	Trp	Ile	Ser	Cys	Pro	Thr	Cys	Gly	Arg	Ile	Glu	Ala	Asn	Leu															
	260					265					270																			
GTG	GAT	ATG	GCG	ATC	AAG	GTA	GAA	AAA	CGC	TTA	AGC	CAC	ATC	AAA	ACC					920										
Val	Asp	Met	Ala	Ile	Lys	Val	Glu	Lys	Arg	Leu	Ser	His	Ile	Lys	Thr															
275					280				285					290																
CCT	TTA	GAC	ATT	AGC	GTG	ATG	GGT	TGC	GTG	GTG	AAT	GCT	TTG	GGT	GAA					968										
Pro	Leu	Asp	Ile	Ser	Val	Met	Gly	Cys	Val	Val	Asn	Ala	Leu	Gly	Glu															
			295					300					305																	
GCC	AAG	CAT	GCA	GAC	ATG	GCG	ATC	GCT	TTT	GGG	AAT	CGC	AGC	GGT	TTG					1016										
Ala	Lys	His	Ala	Asp	Met	Ala	Ile	Ala	Phe	Gly	Asn	Arg	Ser	Gly	Leu															
		310					315					320																		
ATC	ATT	AAA	GAG	GGT	AAA	GTC	ATT	CAC	AAA	CTG	GCT	GAA	AAG	GAT	TTA					1064										
Ile	Ile	Lys	Glu	Gly	Lys	Val	Ile	His	Lys	Leu	Ala	Glu	Lys	Asp	Leu															
		325				330					335																			
TTT	GAA	ACT	TTT	GTG	ATA	GAA	GTG	GAA	AAT	TTA	GCT	AAA	GAA	AGA	GAA					1112										
Phe	Glu	Thr	Phe	Val	Ile	Glu	Val	Glu	Asn	Leu	Ala	Lys	Glu	Arg	Glu															
	340					345					350																			
AAA	AGT	TTA	AAG	GAT	TAGGCATGAT	CAATAAGTTT	AAAAATTTTG	TGAGCAACTA	C											1168										

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1127
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCAAGAAAGA GTATAATAGC GCATAAGAAT TTAAGTATG AAGAGGTTTA	ATG CTA	56
	Met Leu	
	1	
GAA AAT AGA GTT AAG ACC AAG CAA ATT TTT ATC GGT GGC GTG GCC ATA		104
Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val Ala Ile		
5 10 15		
GGG GGT GAT GCT CCC ATA AGC ACG CAA AGC ATG ACC TTT AGC AAA ACC		152
Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser Lys Thr		
20 25 30		
GCT GAT ATT GAA AGC ACT AAA AAT CAA ATT GAC AGA CTC AAA CTC GCC		200
Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys Leu Ala		
35 40 45 50		
GGG GCC GAT TTA GTG AGG GTG GCG GTG AGT AAT GAA AAG GAC GCT CTA		248
Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp Ala Leu		
55 60 65		
GCC TTA AAA GAA TTG AAA AAA GTG TCC CCT TTG CCT TTA ATC GCT GAT		296
Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile Ala Asp		
70 75 80		
ATT CAT TTC CAT TAT AAA TTC GCT CTC ATT GCC GCT CAA AGC GTG GAT		344
Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser Val Asp		
85 90 95		
GCG ATC AGG ATT AAC CCC GGA AAC ATC GGC TCT AAA GAG AAG ATC AAA		392
Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys Ile Lys		
100 105 110		
GCG GTG GTT GAT GCT TGT AAA GAA AAA AAC ATT CCT ATA AGA ATT GGC		440
Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg Ile Gly		
115 120 125 130		
GTG AAT GCT GGG AGT TTA GAA AAG CAG TTT GAT CAA AAA TAC GGA CCC		488
Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr Gly Pro		

TCT ATC ATT TCT TCT TGC GTG TTT TCT TGT GGG TTT TCT TCT TTT TTA	204
Ser Ile Ile Ser Ser Cys Val Phe Ser Cys Gly Phe Ser Ser Phe Leu	
35 40 45	
GGG TGG TTG GGG GTT TTT TGG TTT TCT GTT TTG TTG TCA TTT TCT ATT	252
Gly Trp Leu Gly Val Phe Trp Phe Ser Val Leu Leu Ser Phe Ser Ile	
50 55 60	
ATG GGT GCA AGT GTG GGC ATG ATA GGT TTG GGC GTG GTG GGC GTA AGA	300
Met Gly Ala Ser Val Gly Met Ile Gly Leu Gly Val Val Gly Val Arg	
65 70 75	
GTT TCT TTT GTA GGC GTG GGT TCT CTT TCT TTA GTT TCT TGT TTA ATT	348
Val Ser Phe Val Gly Val Gly Ser Leu Ser Leu Val Ser Cys Leu Ile	
80 85 90	
TCT TTT AAA GGG GGG TTA GTG GGG TTA GTC AAA TCA TCA AAT CGG TTT	396
Ser Phe Lys Gly Gly Leu Val Gly Leu Val Lys Ser Ser Asn Arg Phe	
95 100 105 110	
CTT TTA GGG TAAAT GGTGTAATGG GTAGGGGGGT GGGAGGAAAT TTGGACT	447
Leu Leu Gly	

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Val Gly Val Thr Gly Leu Lys Phe Gly Ala Phe Cys Thr Ser Phe Ser	
1 5 10 15	
Ser Phe Phe Arg Phe Ser Phe Ile Ile Ser Ser Ile Leu Pro Ser Ile	
20 25 30	
Ile Ser Ser Cys Val Phe Ser Cys Gly Phe Ser Ser Phe Leu Gly Trp	
35 40 45	
Leu Gly Val Phe Trp Phe Ser Val Leu Leu Ser Phe Ser Ile Met Gly	
50 55 60	
Ala Ser Val Gly Met Ile Gly Leu Gly Val Val Gly Val Arg Val Ser	
65 70 75 80	
Phe Val Gly Val Gly Ser Leu Ser Leu Val Ser Cys Leu Ile Ser Phe	
85 90 95	
Lys Gly Gly Leu Val Gly Leu Val Lys Ser Ser Asn Arg Phe Leu Leu	
100 105 110	
Gly	

(2) INFORMATION FOR SEQ ID NO:195:

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

Met Phe Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys
 1             5             10             15
Phe Leu Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser
             20             25             30
Leu Ser Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile
             35             40             45
Glu Asn Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro
             50             55             60
Asn Lys Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly
65             70             75             80
Cys Val Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly
             85             90             95
Ser Ile Ser Gln Trp His Thr
             100

```

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...405
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

TCCAATCCGT CTAATATCTC TTTATTTTCG CTCAATTCTT TAACCATAAC GGGTTTTTTTA      60
GCGCTT GTG GGG GTT ACT GGG CTA AAG TTT GGA GCG TTT TGC ACT TCT      108
    Val Gly Val Thr Gly Leu Lys Phe Gly Ala Phe Cys Thr Ser
      1             5             10

TTT TCT TCT TTT TTT AGA TTT TCC TTT ATC ATT TCT TCT ATC CTT CCT      156
Phe Ser Ser Phe Phe Arg Phe Ser Phe Ile Ile Ser Ser Ile Leu Pro
15             20             25             30

```

	500		505		510
Ile Thr Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe					
515		520		525	

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...359
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TTTTGTCTGA TTTGTTGCTA CCAAAACCAT TACCAACCAA AGCAGATCCC	ATG TTT	56
	Met Phe	
	1	
TTG ATA CTA TCG AAT CCA TTC TTC AAC ACT TCT GCC ATA AAA TTC TTG		104
Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys Phe Leu		
5 10 15		
ATA TTG TCC ATA GGC AAG TTG AAT TTT TTC CCT AAT ATT TCA TTA AGT		152
Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser Leu Ser		
20 25 30		
CCC ATC ATT AAC ATC AGG AAG AAC AAA AAA TTT AAT ATC ATA GAA AAC		200
Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile Glu Asn		
35 40 45 50		
AAA TCA CTG GAT AAA CCT GTA AAA AGA TTT GTT CCG CCA CCC AAC AAA		248
Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro Asn Lys		
55 60 65		
GAA GCT AAA ATT TTT CCC ATG ATC AGT CCT TTT ATT TTT GGT TGT GTA		296
Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly Cys Val		
70 75 80		
AGT TCT TGC TTG TTC GGA TCT CTA ATG CGT GTT TTA GTA GGA AGC ATT		344
Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly Ser Ile		
85 90 95		
TCA CAA TGG CAT ACC TAAAGCTACT AAGAAAATTC TTGAATCTAT TG GTAAGATT A		400
Ser Gln Trp His Thr		
100		
CTCATGAAAT CA		412

Asn	Leu	Thr	Gly	Lys	Leu	Glu	Gly	Ser	Val	His	Leu	Gly	Arg	Gly	Trp	65	70	75	80
Thr	Val	Asn	Leu	Gly	Gly	Val	Leu	Gly	Gly	Gln	Ala	Tyr	Asp	Gly	Thr	85	90	95	
Lys	Tyr	Asp	Arg	Trp	Ala	Lys	Asp	Phe	Thr	Pro	Pro	Ser	Tyr	Trp	Asp	100	105	110	
Lys	Thr	Ser	Cys	Gly	Thr	Asp	Ser	Met	Ser	Leu	Cys	Met	Asn	Ala	Thr	115	120	125	
Lys	Met	Trp	Gln	Gln	Ser	Gly	Pro	Gly	Gly	Val	Ile	Asn	Pro	Arg	Gly	130	135	140	
Ile	Gly	Trp	Glu	Tyr	Met	Gly	Glu	Trp	Asn	Gly	Leu	Phe	Pro	Asn	Tyr	145	150	155	160
Tyr	Pro	Ala	Asn	Ala	Tyr	Leu	Pro	Gly	Gly	Ser	Arg	Arg	Tyr	Gln	Val	165	170	175	
Tyr	Lys	Ala	Asn	Leu	Thr	Tyr	Asp	Ser	Asp	Arg	Val	His	Met	Val	Met	180	185	190	
Gly	Arg	Phe	Asp	Ile	Thr	Glu	Gln	Glu	Gln	Met	Asp	Trp	Ile	Tyr	Gln	195	200	205	
Leu	Phe	Gln	Gly	Phe	Tyr	Gly	Thr	Phe	Lys	Leu	Thr	Lys	Asn	Met	Lys	210	215	220	
Phe	Leu	Leu	Phe	Ser	Gly	Trp	Gly	Arg	Gly	Ile	Ala	Asp	Gly	Gln	Trp	225	230	235	240
Leu	Phe	Pro	Ile	Tyr	Arg	Glu	Lys	Pro	Trp	Gly	Val	His	Lys	Ala	Gly	245	250	255	
Ile	Ile	Tyr	Arg	Pro	Thr	Lys	Asn	Leu	Met	Ile	His	Pro	Tyr	Val	Tyr	260	265	270	
Leu	Ile	Pro	Met	Val	Gly	Thr	Leu	Pro	Gly	Ala	Lys	Ile	Glu	Tyr	Asp	275	280	285	
Thr	Asn	Pro	Glu	Phe	Ser	Gly	Arg	Gly	Ile	Arg	Asn	Arg	Thr	Thr	Phe	290	295	300	
Tyr	Ala	Leu	Tyr	Asp	Tyr	Arg	Trp	Asn	Asn	Ala	Glu	Tyr	Gly	Arg	Tyr	305	310	315	320
Ala	Pro	Ala	Arg	Tyr	Asn	Thr	Trp	Asp	Pro	Phe	Leu	Asp	Asn	Gly	Lys	325	330	335	
Trp	Arg	Gly	Leu	Gln	Gly	Pro	Gly	Gly	Ala	Thr	Leu	Leu	Leu	Arg	His	340	345	350	
His	Ile	Asp	Ile	Asn	Asn	Tyr	Phe	Val	Val	Gly	Gly	Ala	Tyr	Leu	Asn	355	360	365	
Ile	Gly	Asn	Pro	Asn	Met	Asn	Leu	Gly	Thr	Trp	Gly	Asn	Pro	Val	Ala	370	375	380	
Val	Asp	Gly	Ile	Glu	Gln	Trp	Val	Gly	Ser	Ile	Tyr	Ser	Leu	Gly	Phe	385	390	395	400
Ala	Gly	Ile	Asp	Asn	Ile	Thr	Asp	Ala	Asp	Ala	Phe	Thr	Glu	Tyr	Val	405	410	415	
Lys	Gly	Gly	Gly	Lys	His	Gly	Lys	Phe	Ser	Trp	Ser	Val	Tyr	Gln	Arg	420	425	430	
Phe	Thr	Thr	Ala	Pro	Arg	Ala	Leu	Glu	Tyr	Gly	Ile	Gly	Met	Tyr	Leu	435	440	445	
Asp	Tyr	Gln	Phe	Ser	Lys	His	Val	Lys	Ala	Gly	Leu	Lys	Leu	Val	Trp	450	455	460	
Leu	Glu	Phe	Gln	Ile	Arg	Ala	Gly	Tyr	Asn	Pro	Gly	Thr	Gly	Phe	Leu	465	470	475	480
Gly	Pro	Asn	Gly	Gln	Pro	Leu	Asn	Leu	Asn	Thr	Gly	Leu	Phe	Glu	Ser	485	490	495	
Ser	Ala	Phe	Ala	Gln	Gly	Pro	Gln	Asn	Met	Gly	Gly	Ile	Ala	Lys	Ser				

```

ATT GAC AAC ATT ACC GAT GCT GAC GCG TTC ACC GAG TAT GTT AAA GGT      1304
Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val Lys Gly
      405                      410                      415

GGA GGC AAG CAT GGT AAG TTT AGT TGG AGC GTT TAT CAG CGC TTC ACT      1352
Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr Gln Arg Phe Thr
      420                      425                      430

ACC GCT CCA AGG GCT TTG GAA TAT GGT ATC GGT ATG TAT CTA GAC TAT      1400
Thr Ala Pro Arg Ala Leu Glu Tyr Gly Ile Gly Met Tyr Leu Asp Tyr
      435                      440                      445                      450

CAG TTC AGC AAG CAT GTT AAA GCG GGT CTC AAA CTC GTA TGG TTA GAG      1448
Gln Phe Ser Lys His Val Lys Ala Gly Leu Lys Leu Val Trp Leu Glu
      455                      460                      465

TTC CAA ATT CGT GCG GGT TAC AAC CCT GGA ACC GGT TTC CTT GGG CCA      1496
Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu Gly Pro
      470                      475                      480

AAC GGT CAG CCG CTT AAC TTG AAT ACT GGT TTG TTT GAG TCT TCA GCG      1544
Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser Ser Ala
      485                      490                      495

TTC GCT CAA GGC CCT CAA AAC ATG GGC GGT ATC GCA AAA AGC ATC ACT      1592
Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser Ile Thr
      500                      505                      510

CAA GAC AGA AGC CAT TTG ATG ACA CAC ATT AGT TAT AGT TTC TAAGAGAGT 1643
Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe
      515                      520                      525

TCTCCCCCTA TCTCTTAGAT ATGCCTTTTT GTATTTTTTAT TTTA      1687

```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

Met Lys Leu Lys Lys Arg Lys Val Ala Ala Ala Leu Leu Lys Arg Phe
 1           5           10           15
Thr Leu Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr
      20           25           30
Glu Val His Gly Asp Phe Ile Asn Phe Ala Lys Val Gly Phe Asn His
      35           40           45
Ser Pro Ile Asn Pro Val Lys Gly Ile Tyr Pro Thr Glu Thr Phe Val
      50           55           60

```

GCA AAT TTG ACC TAT GAT AGC GAC AGG GTC CAT ATG GTA ATG GGG CGT	632
Ala Asn Leu Thr Tyr Asp Ser Asp Arg Val His Met Val Met Gly Arg	
180 185 190	
TTT GAC ATT ACC GAG CAG GAG CAA ATG GAT TGG ATT TAC CAA TTG TTC	680
Phe Asp Ile Thr Glu Gln Glu Gln Met Asp Trp Ile Tyr Gln Leu Phe	
195 200 205 210	
CAA GGG TTT TAT GGG ACT TTC AAG CTC ACT AAG AAT ATG AAA TTC TTG	728
Gln Gly Phe Tyr Gly Thr Phe Lys Leu Thr Lys Asn Met Lys Phe Leu	
215 220 225	
CTC TTT AGT GGT TGG GGT CGT GGT ATC GCT GAT GGT CAG TGG TTG TTC	776
Leu Phe Ser Gly Trp Gly Arg Gly Ile Ala Asp Gly Gln Trp Leu Phe	
230 235 240	
CCT ATC TAT CGT GAA AAG CCT TGG GGG GTT CAT AAA GCG GGT ATT ATT	824
Pro Ile Tyr Arg Glu Lys Pro Trp Gly Val His Lys Ala Gly Ile Ile	
245 250 255	
TAT CGC CCT ACA AAG AAT TTG ATG ATC CAC CCT TAT GTG TAT CTT ATC	872
Tyr Arg Pro Thr Lys Asn Leu Met Ile His Pro Tyr Val Tyr Leu Ile	
260 265 270	
CCA ATG GTA GGC ACA TTG CCT GGT GCT AAA ATA GAA TAC GAT ACC AAT	920
Pro Met Val Gly Thr Leu Pro Gly Ala Lys Ile Glu Tyr Asp Thr Asn	
275 280 285 290	
CCT GAA TTT AGC GGT AGG GGC ATT AGG AAC AGA ACG ACT TTC TAT GCG	968
Pro Glu Phe Ser Gly Arg Gly Ile Arg Asn Arg Thr Thr Phe Tyr Ala	
295 300 305	
TTG TAT GAC TAT CGT TGG AAT AAC GCT GAA TAC GGT CGT TAC GCG CCC	1016
Leu Tyr Asp Tyr Arg Trp Asn Asn Ala Glu Tyr Gly Arg Tyr Ala Pro	
310 315 320	
GCT CGT TAT AAC ACT TGG GAT CCG TTC TTG GAT AAT GGT AAG TGG CGT	1064
Ala Arg Tyr Asn Thr Trp Asp Pro Phe Leu Asp Asn Gly Lys Trp Arg	
325 330 335	
GGC TTG CAA GGT CCT GGT GGT GCG ACG CTC CTT TTA CGC CAC CAT ATA	1112
Gly Leu Gln Gly Pro Gly Gly Ala Thr Leu Leu Leu Arg His His Ile	
340 345 350	
GAT ATT AAC AAC TAC TTT GTG GTT GGT GGT GCT TAT CTC AAC ATT GGT	1160
Asp Ile Asn Asn Tyr Phe Val Val Gly Gly Ala Tyr Leu Asn Ile Gly	
355 360 365 370	
AAC CCT AAC ATG AAC TTA GGT ACT TGG GGT AAC CCT GTG GCT GTT GAT	1208
Asn Pro Asn Met Asn Leu Gly Thr Trp Gly Asn Pro Val Ala Val Asp	
375 380 385	
GGT ATC GAA CAA TGG GTC GGT AGT ATC TAT AGC TTA GGG TTT GCG GGG	1256
Gly Ile Glu Gln Trp Val Gly Ser Ile Tyr Ser Leu Gly Phe Ala Gly	
390 395 400	

(B) LOCATION: 51...1634

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTATTTTAC AGAGTAATTT ATCTATTCTC AGGTAAAGTA AGGAAGAGGA ATG AAA	56
Met Lys	
1	
TTA AAG AAA CGA AAA GTT GCG GCT GCA TTG CTA AAG CGT TTT ACC TTG	104
Leu Lys Lys Arg Lys Val Ala Ala Ala Leu Leu Lys Arg Phe Thr Leu	
5 10 15	
CCA CTA TTG TTC ACT ACG GGT TCA TTA GGG GCG GTT ACT TAT GAA GTG	152
Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr Glu Val	
20 25 30	
CAT GGA GAT TTT ATC AAT TTT GCT AAA GTG GGT TTT AAC CAT TCG CCC	200
His Gly Asp Phe Ile Asn Phe Ala Lys Val Gly Phe Asn His Ser Pro	
35 40 45 50	
ATT AAT CCT GTT AAA GGT ATC TAT CCC ACA GAA ACT TTT GTT AAC CTT	248
Ile Asn Pro Val Lys Gly Ile Tyr Pro Thr Glu Thr Phe Val Asn Leu	
55 60 65	
ACG GGT AAG CTA GAG GGG TCT GTG CAT TTA GGT AGG GGA TGG ACC GTG	296
Thr Gly Lys Leu Glu Gly Ser Val His Leu Gly Arg Gly Trp Thr Val	
70 75 80	
AAT TTA GGC GGT GTT TTG GGC GGA CAG GCT TAT GAT GGC ACT AAG TAT	344
Asn Leu Gly Gly Val Leu Gly Gly Gln Ala Tyr Asp Gly Thr Lys Tyr	
85 90 95	
GAT AGG TGG GCG AAG GAT TTT ACC CCC CCA AGC TAT TGG GAT AAA ACT	392
Asp Arg Trp Ala Lys Asp Phe Thr Pro Pro Ser Tyr Trp Asp Lys Thr	
100 105 110	
TCT TGC GGT ACT GAT TCT ATG AGT CTT TGT ATG AAT GCC ACT AAA ATG	440
Ser Cys Gly Thr Asp Ser Met Ser Leu Cys Met Asn Ala Thr Lys Met	
115 120 125 130	
TGG CAG CAA TCA GGG CCA GGT GGC GTC ATT AAC CCT AGA GGT ATT GGT	488
Trp Gln Gln Ser Gly Pro Gly Gly Val Ile Asn Pro Arg Gly Ile Gly	
135 140 145	
TGG GAA TAC ATG GGT GAG TGG AAC GGC TTG TTC CCT AAC TAC TAT CCG	536
Trp Glu Tyr Met Gly Glu Trp Asn Gly Leu Phe Pro Asn Tyr Tyr Pro	
150 155 160	
GCT AAC GCC TAC TTG CCT GGT GGC TCA AGG CGC TAT CAA GTC TAT AAA	584
Ala Asn Ala Tyr Leu Pro Gly Gly Ser Arg Arg Tyr Gln Val Tyr Lys	
165 170 175	

BNSDOCID: <WO 9843478A1 | >

```

GGT TTT GTG GGC AAT GGC TTT GAT GGT TTA GGC AAA ATG AAT AAC CAT      776
Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn Asn His
      230                      235                      240

CTC TAT GGG CTT GGG ATA GAC TAT CTT TAT AAT TTC ATT GAT AAT GCA      824
Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp Asn Ala
      245                      250                      255

AAA AAA CAC TCT AGC GTA GGT TTT TAT CTG GGT TTT GCT TTA GCG GGG      872
Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu Ala Gly
      260                      265                      270

AGT TCG TGG GTA GGG AGT GGT TTG AGC ATG TGG GTG AGC CAA ACG GAT      920
Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln Thr Asp
      275                      280                      285                      290

TTT ATC AAC AAT TAC TTG ACG GGC TAT CAA GCT AAA ATG CAC ACG AGT      968
Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His Thr Ser
      295                      300                      305

TTT TTC CAG ATC CCT TTG AAT TTT GGG GTT CGT GTG AAT GTC AAT AGG      1016
Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val Asn Arg
      310                      315                      320

CAT AAT GGC TTT GAA ATG GGC TTG AAA ATC CCT TTA GCG ATG AAT TCC      1064
His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Met Asn Ser
      325                      330                      335

TTT TAT GAA ACG CAT GGC AAA GGG CTA AAC ACT TCC CTC TTT TTC AAA      1112
Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Thr Ser Leu Phe Phe Lys
      340                      345                      350

CGC CTT GTC ATG TTT AAC GTG AGT TAC GTT TAT AGT TTT TAGGGGGGTA AA      1163
Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser Phe
      355                      360                      365

TGCCTTCAAAA CGCTCTTTTG ATTGAAGAAA TCACTCATTT A      1204

```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

Met Gln Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu Phe Leu
 1              5              10              15
Ser Phe Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val Gly Phe
      20                      25                      30

```


Lys	Ala	Leu	Leu	His	Ser	Ser	Phe	Phe	Leu	Pro	Leu	Phe	Leu	Ser	Phe		
		5					10					15					
TGT	ATC	GCT	GAA	GAA	AAT	GGG	GCG	TAT	GCG	AGC	GTG	GGT	TTT	GAA	TAT	152	
Cys	Ile	Ala	Glu	Glu	Asn	Gly	Ala	Tyr	Ala	Ser	Val	Gly	Phe	Glu	Tyr		
	20					25				30							
TCC	ATT	AGT	CAT	GCC	GTT	GAA	CAC	AAT	AAC	CCC	TTT	TTA	AAT	CAA	GAA	200	
Ser	Ile	Ser	His	Ala	Val	Glu	His	Asn	Asn	Pro	Phe	Leu	Asn	Gln	Glu		
	35				40				45					50			
CGC	ATC	CAA	ATC	ATT	TCT	AAC	GCT	CAA	AAT	AAA	ATC	TAT	AAA	CTC	CAT	248	
Arg	Ile	Gln	Ile	Ile	Ser	Asn	Ala	Gln	Asn	Lys	Ile	Tyr	Lys	Leu	His		
				55				60						65			
CAA	GTT	AAA	AAT	GAA	ATC	ACA	AGC	ATG	CCT	AAA	ACC	TTT	GCA	TAT	ATC	296	
Gln	Val	Lys	Asn	Glu	Ile	Thr	Ser	Met	Pro	Lys	Thr	Phe	Ala	Tyr	Ile		
			70					75					80				
AAC	AAC	GCT	TTA	AAA	AAC	AAC	TCC	AAA	TTA	ACC	CCC	ACT	GAA	ATG	CAA	344	
Asn	Asn	Ala	Leu	Lys	Asn	Asn	Ser	Lys	Leu	Thr	Pro	Thr	Glu	Met	Gln		
		85					90					95					
GCC	GAA	CAA	TAC	TAC	CTC	CAA	TCC	ACC	TTT	CAA	AAC	ATT	GAA	AAA	ATA	392	
Ala	Glu	Gln	Tyr	Tyr	Leu	Gln	Ser	Thr	Phe	Gln	Asn	Ile	Glu	Lys	Ile		
	100					105					110						
GTA	ATG	CTT	AGC	GGT	GGC	GTT	TCA	TCT	AAC	CCA	CAA	TTA	GTC	CAA	GCG	440	
Val	Met	Leu	Ser	Gly	Gly	Val	Ser	Ser	Asn	Pro	Gln	Leu	Val	Gln	Ala		
	115				120					125					130		
TTG	GAA	AAA	ATG	CAA	GAA	CCC	ATT	ACT	AAC	CCT	TTA	GAA	TTT	GAA	GAA	488	
Leu	Glu	Lys	Met	Gln	Glu	Pro	Ile	Thr	Asn	Pro	Leu	Glu	Phe	Glu	Glu		
				135				140						145			
AAC	TTA	AGA	AAT	TTA	GAA	GTG	CAA	TTT	GCT	CAA	TCT	CAA	AAC	CGC	ATG	536	
Asn	Leu	Arg	Asn	Leu	Glu	Val	Gln	Phe	Ala	Gln	Ser	Gln	Asn	Arg	Met		
			150					155					160				
CTT	TCT	TCT	TTA	TCT	TCT	CAA	ATC	GCT	GCC	ATT	TCA	AAT	TCC	TTA	AAC	584	
Leu	Ser	Ser	Leu	Ser	Ser	Gln	Ile	Ala	Ala	Ile	Ser	Asn	Ser	Leu	Asn		
		165					170					175					
GCG	CTT	GAT	CCT	AAC	TCT	TAT	TCT	AAA	AAC	ATT	TCA	AGC	ATG	TAT	GGG	632	
Ala	Leu	Asp	Pro	Asn	Ser	Tyr	Ser	Lys	Asn	Ile	Ser	Ser	Met	Tyr	Gly		
	180					185					190						
GTG	AGT	TTG	AGC	GTA	GGT	TAT	AAG	CAT	TTC	TTT	ACC	AAG	AAA	AAA	AAT	680	
Val	Ser	Leu	Ser	Val	Gly	Tyr	Lys	His	Phe	Phe	Thr	Lys	Lys	Lys	Asn		
	195				200					205					210		
CAA	GGG	TTG	CGC	TAT	TAC	TTG	TTT	TAT	GAC	TAT	GGT	TAC	ACT	AAT	TTT	728	
Gln	Gly	Leu	Arg	Tyr	Tyr	Leu	Phe	Tyr	Asp	Tyr	Gly	Tyr	Thr	Asn	Phe		
				215					220					225			

TTATCCTACA AG

412

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Met Phe Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile
 1             5             10             15
Leu Glu Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr
      20             25             30
Leu Tyr Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser
      35             40             45
Val Gly Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln
      50             55             60
Ile Met Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys
      65             70             75             80
Ile Thr Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys
      85             90             95
Lys Glu Leu Ile Met Leu Phe
      100

```

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1151
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```

TTCTATTAAA ATTAGTGTAT GATTGAGATT ATTTTGTGATT AGGATCAACC ATG CAA      56
                                     Met Gln
                                     1
AAA GCC TTA TTA CAT TCA TCA TTC TTT TTA CCT TTA TTT TTA TCT TTT      104

```

Lys Arg
385

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...359
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CATTTAATGC TAAGTCTAAT AAGATTGCCC TAGATAGACA TTACGCCAAA ATG TTT	56
Met Phe	
1	
TTG CAA GTT GTA GCA AGA ACT CTA AGA AAG AAT GTC AAT ATA TTA GAA	104
Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile Leu Glu	
5 10 15	
GAG CAA GGT TTT ATT GAA GTC ATT AAA GGA AAA CAA AGA TAC TTG TAT	152
Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr	
20 25 30	
GTG TAT CTT AAA GAT TAC AGA GAA TTA GAG GGC TAT AAC TCC GTA GGA	200
Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser Val Gly	
35 40 45 50	
GCT AAT CAA AAG AAC AAT ATC CCA TCG CCT TTT TTC TTA CAG ATT ATG	248
Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln Ile Met	
55 60 65	
CGT TTC TTA GAA AAG TTT GCC AAA GAA ATT GAG AGA GTA AAA ATA ACA	296
Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys Ile Thr	
70 75 80	
ACA AAG AAT GTG TTA TGC ATA TTC CTA GCC AAG AGC TTA TGC AAA GAG	344
Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys Lys Glu	
85 90 95	
TTA ATA ATG TTG TTT TAAAATTCAC GCCTATTTCT AATCCTAATA CCACTTACAC T	400
Leu Ile Met Leu Phe	
100	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```

Met Ala Glu Lys Leu Glu Glu Thr Asn Pro Glu Trp Phe Glu Lys Trp
 1           5           10           15
Arg Glu Lys Gln Tyr Thr Gln Thr Gly Glu Ser Lys Pro Ser Lys Arg
           20           25           30
Ile Lys Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr
           35           40           45
Ile Glu Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu
           50           55           60
Ile Cys Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr
           65           70           75           80
Pro Ser Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu
           85           90           95
Ser Lys Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu
           100          105          110
Asn Asp Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met
           115          120          125
Gln Ala Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp
           130          135          140
Ile Lys Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp
           145          150          155          160
Gly Ser Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile
           165          170          175
Tyr Phe Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg
           180          185          190
Glu Asn Ala Gln Glu Glu Lys His Tyr Lys Lys Asn Ala Glu Ile Asp
           195          200          205
Asp Arg Ser Gln Leu Ser Asn Leu Asn Ala Pro Lys Pro Leu Phe Glu
           210          215          220
Cys Phe Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys
           225          230          235          240
Glu Glu Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe
           245          250          255
Glu Ile Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe
           260          265          270
Lys Asn Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu
           275          280          285
Asp Ser Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys
           290          295          300
Asn Asp Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys
           305          310          315          320
Lys Tyr Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe
           325          330          335
Ile Ala Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys
           340          345          350
Glu Leu Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln
           355          360          365
Ala Leu Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu
           370          375          380

```

Ala	Gln	Glu	Glu	Lys	His	Tyr	Lys	Lys	Asn	Ala	Glu	Ile	Asp	Asp	Arg	
195					200					205					210	
TCC	CAG	CTA	TCA	AAC	TTA	AAC	GCA	CCC	AAA	CCC	TTA	TTT	GAA	TGT	TTT	728
Ser	Gln	Leu	Ser	Asn	Leu	Asn	Ala	Pro	Lys	Pro	Leu	Phe	Glu	Cys	Phe	
				215					220					225		
GTA	GGA	GTT	AAT	CTG	GCC	AAA	GCC	AAA	TAT	TAT	TCT	AAA	AAA	GAA	GAA	776
Val	Gly	Val	Asn	Leu	Ala	Lys	Ala	Lys	Tyr	Tyr	Ser	Lys	Lys	Glu	Glu	
			230					235						240		
AGA	GAA	AAA	GAA	AAG	ATG	ATC	TTG	AAT	TTT	TGT	AAG	ATA	TTT	GAA	ATT	824
Arg	Glu	Lys	Glu	Lys	Met	Ile	Leu	Asn	Phe	Cys	Lys	Ile	Phe	Glu	Ile	
		245					250					255				
ATT	CTT	TTT	GAA	GCT	ATC	CAA	AAA	CAA	CCA	AAG	CCT	GAT	TTT	AAA	AAT	872
Ile	Leu	Phe	Glu	Ala	Ile	Gln	Lys	Gln	Pro	Lys	Pro	Asp	Phe	Lys	Asn	
	260					265					270					
AAA	GAC	GAG	CTT	TTA	GGG	GAT	TAT	CCT	AAT	CTT	AAA	AAT	TTA	GAT	TCT	920
Lys	Asp	Glu	Leu	Leu	Gly	Asp	Tyr	Pro	Asn	Leu	Lys	Asn	Leu	Asp	Ser	
275					280					285					290	
TTA	AGA	GAA	GTG	AGG	GAA	GAC	TTT	TTG	AAA	AGA	GCG	TTT	AAG	AAT	GAT	968
Leu	Arg	Glu	Val	Arg	Glu	Asp	Phe	Leu	Lys	Arg	Ala	Phe	Lys	Asn	Asp	
			295					300						305		
GAA	GCG	AGT	TTG	GGA	GCG	TAT	GTG	TTA	GTG	TTG	CTT	AGC	TGT	AAG	TAT	1016
Glu	Ala	Ser	Leu	Gly	Ala	Tyr	Val	Leu	Val	Leu	Leu	Ser	Cys	Lys	Tyr	
		310						315					320			
TTT	GAG	AGC	GTG	TTT	GAA	AAA	GTT	CAA	GAA	TGG	CTA	GAT	TTT	ATC	GCT	1064
Phe	Glu	Ser	Val	Phe	Glu	Lys	Val	Gln	Glu	Trp	Leu	Asp	Phe	Ile	Ala	
		325					330					335				
AGG	CTT	ATT	GCT	TTG	AGA	GGC	CAT	GTG	CAC	AAG	ATA	ACT	AAA	GAA	CTT	1112
Arg	Leu	Ile	Ala	Leu	Arg	Gly	His	Val	His	Lys	Ile	Thr	Lys	Glu	Leu	
	340					345				350						
GAA	AGA	TTA	GAA	GAA	GAG	GAT	TTA	GAA	AAA	TTG	GAA	AAA	CAA	GCA	CTA	1160
Glu	Arg	Leu	Glu	Glu	Glu	Asp	Leu	Glu	Lys	Leu	Glu	Lys	Gln	Ala	Leu	
355					360					365					370	
GAA	TAT	TTT	AAT	AAA	ATA	GCA	AAT	AAA	ATA	TAT	CTA	AAG	GAG	AAA	CGA	T 1209
Glu	Tyr	Phe	Asn	Lys	Ile	Ala	Asn	Lys	Ile	Tyr	Leu	Lys	Glu	Lys	Arg	
			375					380					385			
GAGCGGGAAT	GAAGAATTGG	AGCTAAGAGC	CAGAGAAACT	GAGTTGGATA	AA											1261

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATGATAGTAA GGAAATAAGA GTGGAATGCA AGAATCACCC TATTGAAAAG ATG GCA	56
Met Ala	
1	
GAA AAA TTA GAG GAA ACT AAT CCT GAA TGG TTT GAA AAA TGG AGG GAA	104
Glu Lys Leu Glu Glu Thr Asn Pro Glu Trp Phe Glu Lys Trp Arg Glu	
5 10 15	
AAA CAA TAC ACC CAA ACT GGC GAA TCT AAG CCA TCA AAA CGA ATC AAA	152
Lys Gln Tyr Thr Gln Thr Gly Glu Ser Lys Pro Ser Lys Arg Ile Lys	
20 25 30	
GTT TTT AAA AAC TTT ACG GCA TTT GAT GAC AGA TTG TAT ACA ATT GAA	200
Val Phe Lys Asn Phe Thr Ala Phe Asp Asp Arg Leu Tyr Thr Ile Glu	
35 40 45 50	
TGT AAT TTA AAA AAT CTG GAT ACC CAT CAA AAA AAG TTT GAA ATT TGT	248
Cys Asn Leu Lys Asn Leu Asp Thr His Gln Lys Lys Phe Glu Ile Cys	
55 60 65	
GGG GCT CTG TAT GAC ATT TAT GAA CAA ATT TTT GAT GAA ACA CCA AGC	296
Gly Ala Leu Tyr Asp Ile Tyr Glu Gln Ile Phe Asp Glu Thr Pro Ser	
70 75 80	
TTG AAA GGG CGC GAT TTA GAA ACA TAC AAA GCA CAA GAT TTG TCA AAG	344
Leu Lys Gly Arg Asp Leu Glu Thr Tyr Lys Ala Gln Asp Leu Ser Lys	
85 90 95	
AAA TTC ATG CAT TTA GGT TTT GAA CAG ATC TCA AAA GAT TTA AAC GAC	392
Lys Phe Met His Leu Gly Phe Glu Gln Ile Ser Lys Asp Leu Asn Asp	
100 105 110	
TCT AGA TTG AAC GCT TTA TTG TGC TAT GAG GAA AAA GTC ATG CAA GCT	440
Ser Arg Leu Asn Ala Leu Leu Cys Tyr Glu Glu Lys Val Met Gln Ala	
115 120 125 130	
TTG GCT AAA AAA TAC CCT AGT TTT TTA CAA GAT TTG CAT GAT ATA AAA	488
Leu Ala Lys Lys Tyr Pro Ser Phe Leu Gln Asp Leu His Asp Ile Lys	
135 140 145	
AAA TAC AGG AAT AAA GAT AAA CAC GGC GAG AAA CCA CAA GAT GGG TCT	536
Lys Tyr Arg Asn Lys Asp Lys His Gly Glu Lys Pro Gln Asp Gly Ser	
150 155 160	
TCT TTA ACG AGA GTG GAA TTA GAA AGA TAC AGA GAT GGA ATT TAT TTT	584
Ser Leu Thr Arg Val Glu Leu Glu Arg Tyr Arg Asp Gly Ile Tyr Phe	
165 170 175	
CTA GTA GAA AAT CTT TTA AAA AAC CCC TTG ATT AAA GAG AGA GAA AAT	632
Leu Val Glu Asn Leu Leu Lys Asn Pro Leu Ile Lys Glu Arg Glu Asn	
180 185 190	
GCT CAA GAA GAA AAA CAT TAT AAG AAA AAT GCA GAG ATT GAC GAC CGA	680

Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met Ile Glu
 70 75 80

ATT GTG GTG TTT GAT AAA AAG CCT TTT AAA TTC AAT TTT AAA GAA GAG T 345
 Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys Glu Glu
 85 90 95

AGTTAAATGG TTATTGTTTT AGTCGTGGAT AGTTTAAAG ACACCAGTAA TG 397

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Val Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala
 1 5 10 15

Cys Asn Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val
 20 25 30

Val Ser Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu
 35 40 45

Ala Leu Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu
 50 55 60

Ile Lys Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met
 65 70 75 80

Ile Glu Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys
 85 90 95

Glu Glu

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1208
- (D) OTHER INFORMATION:

```

          595              600              605
Lys Val Phe Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu
   610              615              620
Tyr Asn Ser Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu
   625              630              635              640
Asp Ile Val Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser
          645              650              655
Val Gly Ile Ser Val Pro Leu Ile Gln Ser Gly Ile Lys Ile Ala Ser
          660              665              670
Asn Asn Gly Ile Tyr Ala Asn Ser Val Val Leu Asn Glu Gly Gly Ser
          675              680              685
His Phe Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe
   690              695              700

```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...344
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```

TCGTTTTTGGGA AAAAGATATA GCCCATGCGC GTTTC AAGGG TAATGAAAGC ATG GTG      56
                                   Met Val
                                   1

TAT GAA GAA AAT TTT GTG CAT GCC GGG TTT GTG CTT ATT GCG TGC AAT      104
Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala Cys Asn
   5              10              15

TAT GCG GCC TTG TGC GCG TTG AAT AAA AGA CAC AGC GTG GTG GTT TCT      152
Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val Val Ser
   20              25              30

AAT AAC ATC AAT TTT TAT GCC CCC CTA GAA TTG AAT CAA GAA GCA CTC      200
Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu Ala Leu
   35              40              45              50

ATT AAA GCG CAA GTG ATT CAA GAT GGC GTG AAA AAA GCT GAA ATA AAA      248
Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu Ile Lys
          55              60              65

ATA GAG GCG TTT GTG TTA GAC ATT CAG GTT TTA GAG GGA ATG ATA GAA      296

```


Glu Thr Ile Pro Lys Gln Ser Gln Ile Thr Leu Pro Ala Ser Leu Phe
 165 170 175
 Asn Asp Ser Glu Phe Glu Gln Ala Asp Ser Phe Asn Tyr Gln Gln Leu
 180 185 190
 Gln Ala Thr Ala Thr Gln Phe Ser Asp Ala Asn Thr Gln Ser Leu Phe
 195 200 205
 Gln Lys Leu Ser Lys Ile Thr Thr Asn Val Thr Met Ser Tyr Glu Asn
 210 215 220
 Ala Asp Thr Asn Asn Phe Lys Gly Asn Cys His Asp Cys Val Ser Asp
 225 230 235 240
 Phe Thr Pro Gln Thr Ala Glu Glu Leu Thr Asn Leu Met Leu Asp Met
 245 250 255
 Ile Ala Val Phe Asp Ser Lys Ser Trp Glu Glu Ala Val Leu Asn Ala
 260 265 270
 Pro Phe Gln Phe Ser Asn Ser Ser Ser Glu Cys Gly Ser Asp Phe Pro
 275 280 285
 Lys Cys Val Asn Pro Phe Asn Asn Gly Arg Val Ala Pro Ile Tyr Glu
 290 295 300
 Lys Tyr Val Leu Thr Pro Gln Ser Val Ile Asp Ala Phe Arg Arg Thr
 305 310 315 320
 Ile Asn Leu Glu Val Asn Ile Leu Lys Ser Gly Phe Val Gly Leu Gly
 325 330 335
 Tyr Glu Leu Asp Asp Asn Asp Gly Asn Leu Gly Ile Glu Ala Ser Ala
 340 345 350
 Leu Asn Pro Glu Lys Leu Phe Gly Lys Thr Leu Asn Lys Val Asp Ile
 355 360 365
 Val Glu Leu Arg Asp Ile Ile His Glu Phe Ser His Thr Lys Gly Tyr
 370 375 380
 Thr His Asn Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu
 385 390 395 400
 Asn Gly Gly Ala Ile Gln Glu Cys Glu Gly Lys Glu Glu Leu Val
 405 410 415
 Asn Gly Lys Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp
 420 425 430
 Gln Asp Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His
 435 440 445
 Gln Val Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys
 450 455 460
 Ala Gln Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln
 465 470 475 480
 Gln Leu Ile Asn Gln Asn Ala Leu Pro Ile Asn Phe Ala Asn Leu Asn
 485 490 495
 Ser Pro Thr Asn His Leu Asn Ala Gly Leu Asn Ala Gln Asn Phe Ala
 500 505 510
 Thr Ser Ile Val Ser Ala Ile Ala Gln Asn Phe Ser Thr Thr Ser Thr
 515 520 525
 Thr Thr Tyr Arg Ser Ser Ser Lys Asn Phe Arg Ser Pro Ile Leu Gly
 530 535 540
 Val Asn Val Lys Ile Gly Tyr Gln His Tyr Phe Asn Asp Tyr Ile Gly
 545 550 555 560
 Leu Ala Tyr Tyr Gly Ile Ile Lys Tyr Asn Tyr Ala Lys Thr Asn Asp
 565 570 575
 Glu Lys Ile Gln Gln Leu Ser Tyr Gly Gly Met Asp Val Leu Phe
 580 585 590
 Asp Phe Ile Thr Thr Tyr Ala Asn Lys Lys Gln Asp Asn Pro Thr Lys

AGC TAT TAT GTC TTC AAC CAA GTC AAA GGA AGC GGT AAT TTA GAT ATA 1976
 Ser Tyr Tyr Val Phe Asn Gln Val Lys Gly Ser Gly Asn Leu Asp Ile
 630 635 640

GTT ACT GGG TTT AAT TAC CGC TAC AAG CAT TCT AAA TAT TCT GTA GGC 2024
 Val Thr Gly Phe Asn Tyr Arg Tyr Lys His Ser Lys Tyr Ser Val Gly
 645 650 655

ATT AGC GTT CCT TTA ATC CAA AGC GGT ATT AAA ATC GCT TCT AAT AAT 2072
 Ile Ser Val Pro Leu Ile Gln Ser Gly Ile Lys Ile Ala Ser Asn Asn
 660 665 670

GGC ATC TAT GCG AAC TCC GTT GTT TTG AAT GAA GGG GGC AGT CAT TTT 2120
 Gly Ile Tyr Ala Asn Ser Val Val Leu Asn Glu Gly Gly Ser His Phe
 675 680 685 690

AAA GTG TTT TTT AAT TAC GGG TGG ATT TTT TAGGATTTAA AATCCCCAAT AAC 2173
 Lys Val Phe Phe Asn Tyr Gly Trp Ile Phe
 695 700

CCCCTAAACT TGTGCGATAC TCGCTACAAA 2203

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Met Leu Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu
 1 5 10 15
 Phe Asn Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe
 20 25 30
 Ile Glu Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys
 35 40 45
 Glu Glu Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His
 50 55 60
 Pro Gln Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala
 65 70 75 80
 Thr Pro Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile
 85 90 95
 Leu Lys Asn Ala Thr Ala Leu Phe Thr Thr Asp Lys Ile Glu Asn Gly
 100 105 110
 Leu Thr Phe Tyr Ser Gln Asn Pro Val Tyr Ala Asn Met Val Asn Gly
 115 120 125
 Ser Val Thr Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Val Glu
 130 135 140
 Leu Ser Phe Lys Asp Ala Gln Gly Lys Val Val Asn Leu Gly Val Ile
 145 150 155 160

GGA GCC ATA CAA GAA TGT GAG GGT GGG AAA GAA GAG TTA GTC AAT GGA	1304
Gly Ala Ile Gln Glu Cys Glu Gly Gly Lys Glu Glu Leu Val Asn Gly	
405 410 415	
AAA GAA GAA CTA AAA TTT ACA AAT GGG AAA GAA GTG AAA GAT CAG GAT	1352
Lys Glu Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp Gln Asp	
420 425 430	
GGT TAC ACC TAT GAT GTA TGT TCT TTT TAT AAG GAC AAC CAC CAA GTC	1400
Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His Gln Val	
435 440 445 450	
TAT ACA GCG AGC AAT TAC CCC AAT TCC ATT TAT ACG AAT TGC GCT CAA	1448
Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys Ala Gln	
455 460 465	
GTC CCT GCT GGG CTT ATA GGG GTT ACC ACC GCT GTC TGG CAA CAG CTC	1496
Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln Gln Leu	
470 475 480	
ATC AAT CAA AAC GCT CTG CCC ATT AAT TTC GCT AAT CTA AAT AGC CCA	1544
Ile Asn Gln Asn Ala Leu Pro Ile Asn Phe Ala Asn Leu Asn Ser Pro	
485 490 495	
ACC AAC CAC TTA AAC GCC GGG TTG AAC GCA CAA AAT TTT GCA ACC TCT	1592
Thr Asn His Leu Asn Ala Gly Leu Asn Ala Gln Asn Phe Ala Thr Ser	
500 505 510	
ATA GTC AGC GCG ATC GCG CAA AAT TTT TCC ACC ACT TCC ACC ACC ACT	1640
Ile Val Ser Ala Ile Ala Gln Asn Phe Ser Thr Thr Ser Thr Thr Thr	
515 520 525 530	
TAC CGC TCT TCA AGT AAG AAT TTT AGA AGC CCT ATT TTA GGG GTT AAT	1688
Tyr Arg Ser Ser Lys Asn Phe Arg Ser Pro Ile Leu Gly Val Asn	
535 540 545	
GTT AAA ATA GGC TAC CAA CAT TAT TTC AAT GAC TAC ATA GGG TTA GCC	1736
Val Lys Ile Gly Tyr Gln His Tyr Phe Asn Asp Tyr Ile Gly Leu Ala	
550 555 560	
TAT TAC GGC ATT ATC AAA TAC AAT TAC GCC AAA ACT AAC GAT GAA AAA	1784
Tyr Tyr Gly Ile Ile Lys Tyr Asn Tyr Ala Lys Thr Asn Asp Glu Lys	
565 570 575	
ATC CAG CAA TTA AGC TAT GGT GGG GGA ATG GAT GTG TTG TTT GAT TTC	1832
Ile Gln Gln Leu Ser Tyr Gly Gly Gly Met Asp Val Leu Phe Asp Phe	
580 585 590	
ATC ACC ACT TAC GCT AAC AAA AAG CAA GAC AAC CCA ACT AAA AAA GTT	1880
Ile Thr Thr Tyr Ala Asn Lys Lys Gln Asp Asn Pro Thr Lys Lys Val	
595 600 605 610	
TTT GCT TCC TCT TTT GGG GTG TTT GGG GGG TTA AGG GGC TTA TAC AAT	1928
Phe Ala Ser Ser Phe Gly Val Phe Gly Gly Leu Arg Gly Leu Tyr Asn	
615 620 625	

Ser	Glu	Phe	Glu	Gln	Ala	Asp	Ser	Phe	Asn	Tyr	Gln	Gln	Leu	Gln	Ala		
180						185					190						
ACT	GCC	ACA	CAA	TTT	TCT	GAC	GCT	AAC	ACG	CAA	AGT	TTG	TTT	CAA	AAG	680	
Thr	Ala	Thr	Gln	Phe	Ser	Asp	Ala	Asn	Thr	Gln	Ser	Leu	Phe	Gln	Lys		
195					200				205					210			
CTC	AGC	AAG	ATC	ACA	ACC	AAT	GTA	ACA	ATG	AGT	TAT	GAA	AAC	GCC	GAT	728	
Leu	Ser	Lys	Ile	Thr	Thr	Asn	Val	Thr	Met	Ser	Tyr	Glu	Asn	Ala	Asp		
				215					220					225			
ACC	AAC	AAT	TTT	AAA	GGT	AAT	TGC	CAT	GAT	TGT	GTG	TCA	GAT	TTC	ACC	776	
Thr	Asn	Asn	Phe	Lys	Gly	Asn	Cys	His	Asp	Cys	Val	Ser	Asp	Phe	Thr		
			230					235						240			
CCA	CAA	ACC	GCA	GAA	GAA	TTG	ACC	AAT	TTA	ATG	CTA	GAT	ATG	ATT	GCG	824	
Pro	Gln	Thr	Ala	Glu	Glu	Leu	Thr	Asn	Leu	Met	Leu	Asp	Met	Ile	Ala		
		245					250						255				
GTG	TTT	GAC	TCT	AAA	TCG	TGG	GAA	GAA	GCC	GTT	TTA	AAC	GCT	CCT	TTC	872	
Val	Phe	Asp	Ser	Lys	Ser	Trp	Glu	Glu	Ala	Val	Leu	Asn	Ala	Pro	Phe		
	260					265					270						
CAA	TTT	TCT	AAC	AGC	TCA	TCA	GAG	TGC	GGC	TCT	GAC	TTT	CCT	AAG	TGC	920	
Gln	Phe	Ser	Asn	Ser	Ser	Ser	Glu	Cys	Gly	Ser	Asp	Phe	Pro	Lys	Cys		
275					280					285					290		
GTG	AAT	CCT	TTC	AAT	AAC	GGG	CGT	GTC	GCT	CCC	ATC	TAT	GAA	AAA	TAC	968	
Val	Asn	Pro	Phe	Asn	Asn	Gly	Arg	Val	Ala	Pro	Ile	Tyr	Glu	Lys	Tyr		
				295					300					305			
GTG	CTA	ACC	CCA	CAA	TCC	GTT	ATA	GAT	GCG	TTT	AGA	AGA	ACG	ATC	AAT	1016	
Val	Leu	Thr	Pro	Gln	Ser	Val	Ile	Asp	Ala	Phe	Arg	Arg	Thr	Ile	Asn		
			310					315					320				
CTT	GAA	GTG	AAT	ATC	CTA	AAA	TCA	GGG	TTT	GTA	GGG	CTA	GGG	TAT	GAA	1064	
Leu	Glu	Val	Asn	Ile	Leu	Lys	Ser	Gly	Phe	Val	Gly	Leu	Gly	Tyr	Glu		
		325					330					335					
CTT	GAT	GAT	AAT	GAT	GGT	AAT	CTG	GGG	ATA	GAA	GCT	TCT	GCC	TTA	AAT	1112	
Leu	Asp	Asp	Asn	Asp	Gly	Asn	Leu	Gly	Ile	Glu	Ala	Ser	Ala	Leu	Asn		
	340					345					350						
CCT	GAA	AAA	TTG	TTT	GGT	AAA	ACT	TTG	AAC	AAA	GTT	GAT	ATT	GTG	GAA	1160	
Pro	Glu	Lys	Leu	Phe	Gly	Lys	Thr	Leu	Asn	Lys	Val	Asp	Ile	Val	Glu		
355					360					365				370			
TTA	AGA	GAC	ATT	ATC	CAT	GAA	TTT	AGC	CAC	ACT	AAA	GGC	TAT	ACG	CAT	1208	
Leu	Arg	Asp	Ile	Ile	His	Glu	Phe	Ser	His	Thr	Lys	Gly	Tyr	Thr	His		
				375					380					385			
AAT	GGG	AAC	ATG	ACT	TAT	CAA	AGA	GTG	CGC	TTG	TGT	CAA	GAA	AAC	GGC	1256	
Asn	Gly	Asn	Met	Thr	Tyr	Gln	Arg	Val	Arg	Leu	Cys	Gln	Glu	Asn	Gly		
			390					395					400				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAGTTACACA CTCTTTGAGA ACAAAACGCC AAACCATTTA GGAAATTACC ATG CTA	56
Met Leu	
1	
AGA TTC GTT AGT AAA ACG ATT TGC TTG TCT TTA ATC GGC TTG TTC AAC	104
Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu Phe Asn	
5 10 15	
CCT TTA GAA GCC TTT CAA AAA CAC CAA AAA GAC GGC TTT TTT ATA GAA	152
Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe Ile Glu	
20 25 30	
GCT GGG TTT GAA ACT GGG TTA TTA GAA GGA ACG CAA ACT AAA GAA GAA	200
Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys Glu Glu	
35 40 45 50	
GTC ATA ACC ACC CAA AAA ATC TAT GAA AAC CCC CTA ACC CAC CCA CAA	248
Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His Pro Gln	
55 60 65	
ACT AAA GAA CAG CCT AAA GAA CAA AAT AAA AGC GAT ACG GCC ACC CCA	296
Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala Thr Pro	
70 75 80	
CAA AGC GCT TAC GGA AAA TAC TAC ATA CCC CAA AGC ACC ATT TTA AAA	344
Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile Leu Lys	
85 90 95	
AAT GCA ACG GCT TTA TTC ACC ACG GAC AAG ATA GAA AAT GGC TTA ACT	392
Asn Ala Thr Ala Leu Phe Thr Thr Asp Lys Ile Glu Asn Gly Leu Thr	
100 105 110	
TTT TAT TCT CAA AAC CCT GTG TAT GCG AAT ATG GTT AAT GGC AGC GTA	440
Phe Tyr Ser Gln Asn Pro Val Tyr Ala Asn Met Val Asn Gly Ser Val	
115 120 125 130	
ACC ATA CAA AAC TTT CTG CCT TAT AAT TTA AAC AAT GTT GAA CTG AGT	488
Thr Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Val Glu Leu Ser	
135 140 145	
TTT AAA GAC GCT CAA GGC AAG GTG GTC AAT TTA GGC GTG ATA GAG ACC	536
Phe Lys Asp Ala Gln Gly Lys Val Val Asn Leu Gly Val Ile Glu Thr	
150 155 160	
ATC CCT AAA CAA TCT CAA ATT ACC TTG CCT GCA AGC TTG TTT AAT GAT	584
Ile Pro Lys Gln Ser Gln Ile Thr Leu Pro Ala Ser Leu Phe Asn Asp	
165 170 175	
TCA GAA TTT GAA CAA GCT GAT AGC TTT AAT TAC CAA CAA CTT CAA GCC	632

Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys Tyr Phe
 115 120 125 130

AGG AGT GAG TAT GGA AAA TGATGTTAAA GAAGATCTAG AGCAAGCAAG ACCAAAGT 496
 Arg Ser Glu Tyr Gly Lys
 135

TAGAGCCAGA AAAGC

511

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Leu	Lys	Ser	Thr	Ile	Lys	Glu	Asp	Tyr	Leu	Met	Leu	Met	Ser	Arg
1				5					10					15	
Glu	Val	Ser	Ala	Phe	Val	Gly	Thr	Leu	Phe	Phe	Ile	Gly	Leu	Ser	Cys
			20					25					30		
Tyr	Ala	Ile	Tyr	His	Gly	Asn	Met	Pro	Asp	Tyr	Leu	Arg	Pro	Ala	Leu
		35				40						45			
Ile	Asp	Thr	Ile	Lys	Ala	Ala	Ser	Asp	Ser	Ile	Tyr	Ser	Ser	Cys	Asp
	50					55					60				
Tyr	Met	Asp	Tyr	Phe	Leu	Lys	Ala	Arg	Lys	Met	Leu	Glu	Gly	Phe	Ala
65					70					75				80	
Trp	Trp	Ser	Met	Phe	Lys	Ala	Glu	Ser	Met	Gly	Leu	Asn	Lys	Gly	Phe
			85						90					95	
Met	Val	Ala	Gly	Trp	Val	Ala	Phe	Ile	Ile	Tyr	Asn	Ala	Leu	Ser	Gly
			100					105					110		
Ile	Ala	Ile	Ser	Arg	Leu	Ser	Ala	Gln	Ile	Ile	Tyr	Trp	Leu	Ser	Lys
		115				120						125			
Tyr	Phe	Arg	Ser	Glu	Tyr	Gly	Lys								
	130					135									

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...2150
- (D) OTHER INFORMATION:

130

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...458
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

TTTTTGCACT ATCGTTGTTT GCGCTGTGGT GTTTGGCACG CTTGAAAAAA ATG CTC      56
                                     Met Leu
                                     1

AAG AGT ACC ATC AAA GAA GAT TAT TTG ATG CTG ATG TCT AGA GAA GTG      104
Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg Glu Val
      5                      10                      15

AGT GCT TTT GTG GGG ACT CTT TTC TTC ATT GGC TTG AGT TGC TAT GCG      152
Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys Tyr Ala
      20                      25                      30

ATC TAT CAT GGC AAC ATG CCC GAT TAT TTG AGA CCG GCT TTG ATA GAC      200
Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu Ile Asp
      35                      40                      45                      50

ACT ATT AAG GCA GCG AGT GAT TCC ATC TAT TCC AGC TGC GAC TAC ATG      248
Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp Tyr Met
      55                      60                      65

GAT TAT TTT TTG AAG GCT AGA AAG ATG TTA GAG GGG TTT GCT TGG TGG      296
Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala Trp Trp
      70                      75                      80

AGC ATG TTC AAA GCG GAG AGC ATG GGC TTA AAT AAG GGG TTT ATG GTT      344
Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe Met Val
      85                      90                      95

GCG GGC TGG GTA GCG TTT ATC ATC TAT AAC GCT CTT AGC GGG ATA GCC      392
Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly Ile Ala
      100                      105                      110

ATC AGC AGG CTG AGC GCT CAA ATC ATT TAT TGG TTA TCA AAA TAT TTT      440

```

Val	Lys	Lys	Arg	Leu	Asp	Leu	Arg	Lys	Gln	Asn	Ser	Ile	Glu	Lys	Glu		
				55					60					65			
GAA	AAG	CAA	AAA	TTC	CAA	AAA	TTC	GCC	CTG	GGC	TTG	GAA	ATG	TCT	TTC		296
Glu	Lys	Gln	Lys	Phe	Gln	Lys	Phe	Ala	Leu	Gly	Leu	Glu	Met	Ser	Phe		
			70					75					80				
AAT	GTG	TGG	CGT	TTA	GGA	GGG	TAT	GGG	GTT	TTA	CTA	GGC	ATT	TTA	GGA		344
Asn	Val	Trp	Arg	Leu	Gly	Gly	Tyr	Gly	Val	Leu	Leu	Gly	Ile	Leu	Gly		
		85					90					95					
ACG	CTT	TTA	TTC	TTG	CAT	CTT	TTT	AAC	GGG	TTA	ATC	TTT	CTT	ATT	GGC		392
Thr	Leu	Leu	Phe	Leu	His	Leu	Phe	Asn	Gly	Leu	Ile	Phe	Leu	Ile	Gly		
	100					105				110							
GTG	TTT	GTG	AGC	TCG	CTC	TCT	AGC	GCG	TTA	TTA	CGA	TTT	TTG	AAT	AAT		440
Val	Phe	Val	Ser	Ser	Leu	Ser	Ser	Ala	Leu	Leu	Arg	Phe	Leu	Asn	Asn		
	115				120				125					130			
AAT	GGT	AAG	TTT	TGACACAAAC	TCACATGGAT	TTTAACCCCT	TTAATCCTCT	TTTAA									497
Asn	Gly	Lys	Phe														
TTTTTTAAT																	505

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Cys	Gln	Ile	Gln	Cys	Leu	Leu	Ile	Leu	Leu	Ser	Ile	Asn	Ile	Val		
1				5					10					15			
Ser	Ala	Ile	Ile	Val	Tyr	Phe	Phe	Gln	Ala	Phe	Gln	Gly	Val	Leu	Asn		
			20					25					30				
Phe	Glu	Gly	Gly	Phe	Leu	Gly	Phe	Phe	Ile	Val	Ala	Leu	Ser	Ser	Tyr		
		35					40					45					
Tyr	Gly	Val	Lys	Lys	Arg	Leu	Asp	Leu	Arg	Lys	Gln	Asn	Ser	Ile	Glu		
	50					55					60						
Lys	Glu	Glu	Lys	Gln	Lys	Phe	Gln	Lys	Phe	Ala	Leu	Gly	Leu	Glu	Met		
65				70					75					80			
Ser	Phe	Asn	Val	Trp	Arg	Leu	Gly	Gly	Tyr	Gly	Val	Leu	Leu	Gly	Ile		
			85					90					95				
Leu	Gly	Thr	Leu	Leu	Phe	Leu	His	Leu	Phe	Asn	Gly	Leu	Ile	Phe	Leu		
		100					105					110					
Ile	Gly	Val	Phe	Val	Ser	Ser	Leu	Ser	Ser	Ala	Leu	Leu	Arg	Phe	Leu		
	115					120						125					
Asn	Asn	Asn	Gly	Lys	Phe												

Gly	Val	Gly	Thr	Asp	Phe	Leu	Tyr	Asn	Val	Tyr	Glu	Arg	Ser	Arg	Arg
		355					360					365			
Arg	Glu	Arg	Thr	Thr	Ile	Gly	Leu	Phe	Phe	Gly	Ala	Gln	Ile	Ala	Gly
	370					375					380				
Gln	Thr	Trp	Ser	Thr	Asn	Val	Thr	Asn	Leu	Leu	Ser	Gly	Gln	Arg	Pro
385					390					395					400
Asp	Val	Lys	Ser	Ser	Ser	Phe	Gln	Phe	Leu	Phe	Asp	Leu	Gly	Val	Arg
			405						410					415	
Thr	Asn	Phe	Ala	Lys	Thr	Asn	Phe	Asn	Lys	His	Arg	Leu	Asp	Gln	Gly
			420					425					430		
Ile	Glu	Phe	Gly	Val	Lys	Ile	Pro	Val	Ile	Ala	His	Lys	Tyr	Phe	Ala
		435					440					445			
Thr	Gln	Gly	Ser	Ser	Ala	Ser	Tyr	Met	Arg	Asn	Phe	Ser	Phe	Tyr	Val
	450					455					460				
Gly	Tyr	Ser	Val	Gly	Phe										
465					470										

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...452
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AAGACCCTAA ATACACACAA AATAAAACAA AATAAATCCA ATCAAATCCC ATG TGC	56
Met Cys	
1	
CAA ATC CAA TGC TTG CTT ATT TTA CTT TCT ATC AAT ATA GTT AGC GCG	104
Gln Ile Gln Cys Leu Leu Ile Leu Leu Ser Ile Asn Ile Val Ser Ala	
5 10 15	
ATC ATC GTT TAT TTT TTC CAA GCA TTT CAA GGG GTT TTG AAT TTT GAA	152
Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn Phe Glu	
20 25 30	
GGG GGT TTT TTA GGG TTT TTT ATC GTG GCG TTG TCT TCG TAT TAC GGC	200
Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser Tyr Tyr Gly	
35 40 45 50	
GTT AAA AAG CGT TTG GAT TTA AGG AAA CAA AAT TCA ATA GAA AAA GAA	248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

Met Ser Leu Cys Arg Ala Glu Glu Asp Gly Ala Phe Phe Val Ile Asp
 1             5             10             15
Tyr Gln Thr Ser Leu Ala Arg Gln Glu Leu Lys Asn Pro Gly Phe Thr
             20             25             30
Gln Ala Gln Glu Leu Arg Gln Leu Ile Arg Asp Gly Ala Val Arg Leu
             35             40             45
Gln Thr Ser Ala Ile Pro Leu Ser Tyr Tyr Leu Asp Ile Leu Gly Asn
             50             55             60
Lys Thr Ala Thr Leu Leu Arg Glu Ser Leu Lys Asn Asn Ala Gln Pro
65             70             75             80
Ser Gln Pro Asn Ala Gln Pro Pro Gln Gln Asn Gly Pro Ser Asn Gln
             85             90             95
Ala Leu Ala Asn Leu Glu Gln Ser Leu Gly Ile Leu Gly Lys Leu Leu
             100            105            110
Asp Leu Ser Gln Gln Tyr Ala Ser Gln Gly Val Ile Lys Pro Leu Val
             115            120            125
Val Asp Val Gly Lys Glu Gln Ile Gly Ile Thr Asp Ser Met Leu Leu
             130            135            140
Val Ala Gln Asn Ile Val Leu Ala Leu Gly Gln Val Asp Leu Ser Lys
145            150            155            160
Ile Gln Gln Asn Asn Glu Gln Leu Tyr Glu Asn Ile Met Lys Val
             165            170            175
Met Leu Leu Gly Ala Gly Gly Thr Asn Gly Ala Tyr Asn Gly Val Ser
             180            185            190
Val Gly Asp Ile Ala Thr Gly Met Gln Asn Phe Ser Ser Gln Thr Gly
             195            200            205
Leu Ile Gly Ala Asn Ser Thr Val Ser Glu Leu Asn Ala Leu Ile Lys
             210            215            220
Ser Gly Ile Ser Leu Asp Arg Glu Thr Leu Gly Leu Gly Ser Phe Ile
225            230            235            240
Glu Lys Asn Ile Cys Ser Gly Ala Ser Ser Cys Phe Ser Gly Asn Gln
             245            250            255
Leu Ile Tyr Lys Lys Gly Leu Asp Arg Thr Ile Asn Ile Ile Asn Thr
             260            265            270
Val Leu Gly Gln Phe Glu Ser Ser Ala Ser Ser Leu Tyr Lys Ile Ser
             275            280            285
Tyr Ile Pro Asn Leu Phe Ser Leu Lys Asp Tyr Gln Ser Ala Ser Met
             290            295            300
Asn Gly Phe Gly Ala Lys Met Gly Tyr Lys Gln Phe Phe Thr His Lys
305            310            315            320
Lys Asn Val Gly Leu Arg Tyr Tyr Gly Phe Leu Asp Tyr Gly Tyr Ala
             325            330            335
Asn Phe Gly Asp Thr Asn Leu Lys Val Gly Ala Asn Leu Val Thr Tyr
             340            345            350

```

Gly	Gln	Phe	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Tyr	Lys	Ile	Ser	Tyr	Ile	
275					280					285					290	
CCT	AAC	CTC	TTT	TCG	CTC	AAG	GAT	TAC	CAG	TCA	GCG	AGC	ATG	AAC	GGC	968
Pro	Asn	Leu	Phe	Ser	Leu	Lys	Asp	Tyr	Gln	Ser	Ala	Ser	Met	Asn	Gly	
				295					300					305		
TTT	GGG	GCT	AAG	ATG	GGC	TAT	AAA	CAA	TTT	TTC	ACC	CAT	AAG	AAA	AAT	1016
Phe	Gly	Ala	Lys	Met	Gly	Tyr	Lys	Gln	Phe	Phe	Thr	His	Lys	Lys	Asn	
			310					315					320			
GTT	GGC	TTA	AGG	TAT	TAC	GGG	TTT	TTG	GAT	TAT	GGC	TAT	GCG	AAC	TTT	1064
Val	Gly	Leu	Arg	Tyr	Tyr	Gly	Phe	Leu	Asp	Tyr	Gly	Tyr	Ala	Asn	Phe	
		325					330					335				
GGC	GAT	ACG	AAT	TTA	AAA	GTG	GGG	GCG	AAT	CTT	GTT	ACT	TAT	GGG	GTA	1112
Gly	Asp	Thr	Asn	Leu	Lys	Val	Gly	Ala	Asn	Leu	Val	Thr	Tyr	Gly	Val	
	340					345				350						
GGA	ACG	GAT	TTT	TTA	TAC	AAT	GTG	TAT	GAA	CGC	TCT	AGA	AGG	AGG	GAA	1160
Gly	Thr	Asp	Phe	Leu	Tyr	Asn	Val	Tyr	Glu	Arg	Ser	Arg	Arg	Arg	Glu	
355					360				365						370	
AGG	ACT	ACG	ATC	GGT	CTT	TTC	TTT	GGC	GCT	CAA	ATT	GCA	GGG	CAA	ACT	1208
Arg	Thr	Thr	Ile	Gly	Leu	Phe	Phe	Gly	Ala	Gln	Ile	Ala	Gly	Gln	Thr	
			375					380					385			
TGG	AGC	ACT	AAT	GTA	ACG	AAC	TTA	TTG	AGC	GGG	CAA	AGG	CCT	GAT	GTC	1256
Trp	Ser	Thr	Asn	Val	Thr	Asn	Leu	Leu	Ser	Gly	Gln	Arg	Pro	Asp	Val	
			390					395					400			
AAG	TCC	AGT	TCG	TTC	CAA	TTC	TTG	TTT	GAT	TTG	GGC	GTG	CGC	ACC	AAC	1304
Lys	Ser	Ser	Ser	Phe	Gln	Phe	Leu	Phe	Asp	Leu	Gly	Val	Arg	Thr	Asn	
		405					410					415				
TTT	GCA	AAA	ACC	AAT	TTC	AAT	AAG	CAC	AGG	CTA	GAC	CAA	GGG	ATA	GAA	1352
Phe	Ala	Lys	Thr	Asn	Phe	Asn	Lys	His	Arg	Leu	Asp	Gln	Gly	Ile	Glu	
	420					425				430						
TTT	GGG	GTG	AAA	ATC	CCT	GTT	ATC	GCT	CAT	AAA	TAT	TTT	GCA	ACC	CAA	1400
Phe	Gly	Val	Lys	Ile	Pro	Val	Ile	Ala	His	Lys	Tyr	Phe	Ala	Thr	Gln	
435					440				445					450		
GGC	TCA	AGC	GCG	AGC	TAT	ATG	AGG	AAT	TTT	AGC	TTC	TAT	GTG	GGC	TAT	1448
Gly	Ser	Ser	Ala	Ser	Tyr	Met	Arg	Asn	Phe	Ser	Phe	Tyr	Val	Gly	Tyr	
				455				460					465			
TCA	GTC	GGT	TTT	TAAGGAAGGC	TCTTGATGAA	AAATACCAAT	ACAAAAGAGA	TAAAG								1505
Ser	Val	Gly	Phe													
				470												
AATACAAG																1513

(2) INFORMATION FOR SEQ ID NO:174:

- 343 -

```

Asn Met Gln Val Leu Ala Lys Ala Leu Lys Glu Lys Asn His Lys Leu
 290                      295                      300
Val Ser Gly Gly Thr Ser Asn His Leu Leu Leu Met Asp Phe Leu Asp
305                      310                      315                      320
Lys Pro Tyr Ser Gly Lys Asp Ala Asp Ile Ala Leu Gly Asn Ala Gly
                      325                      330                      335
Ile Thr Val Asn Lys Asn Thr Ile Pro Gly Glu Thr Arg Ser Pro Phe
                      340                      345                      350
Val Thr Ser Gly Ile Arg Ile Gly Ser Ala Ala Leu Ser Ala Arg Gly
                      355                      360                      365
Met Gly Ala Lys Glu Phe Glu Ile Ile Gly Asn Lys Ile Ser Asp Ile
                      370                      375                      380
Leu Asn Asp Ile Asn Asn Val Ser Leu Gln Leu His Val Lys Glu Glu
385                      390                      395                      400
Leu Lys Ala Met Val Asn Gln Phe Pro Val Tyr His Gln Pro Ile Phe
                      405                      410                      415

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1460
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

TGAAAAACCA CTCCTTTAAA AAAACGATCG CTCTTTCCTT ACTAGCGAGC ATG TCT      56
                                   Met Ser
                                   1

TTG TGC AGG GCT GAA GAA GAT GGG GCG TTT TTT GTC ATA GAT TAC CAG      104
Leu Cys Arg Ala Glu Glu Asp Gly Ala Phe Phe Val Ile Asp Tyr Gln
   5                      10                      15

ACG AGT TTG GCC AGA CAG GAA TTG AAA AAT CCA GGC TTC ACC CAA GCG      152
Thr Ser Leu Ala Arg Gln Glu Leu Lys Asn Pro Gly Phe Thr Gln Ala
  20                      25                      30

CAA GAA TTA AGG CAG TTG ATC AGA GAT GGG GCT GTG AGG TTG CAA ACT      200
Gln Glu Leu Arg Gln Leu Ile Arg Asp Gly Ala Val Arg Leu Gln Thr
  35                      40                      45                      50

TCT GCC ATT CCC TTA TCC TAC TAC TTG GAT ATT TTA GGG AAT AAA ACA      248
Ser Ala Ile Pro Leu Ser Tyr Tyr Leu Asp Ile Leu Gly Asn Lys Thr

```

GCC ATG GTC AAT CAA TTC CCT GTG TAC CAC CAA CCT ATT TTT TAAGGGAGT 1307
 Ala Met Val Asn Gln Phe Pro Val Tyr His Gln Pro Ile Phe
 405 410 415

CAAGATGACA GAAATGGAAT TAAAGCTCAT TAAGATAGAC ACAA

1351

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Ala	Tyr	Phe	Leu	Glu	Gln	Thr	Asp	Ser	Glu	Ile	Phe	Glu	Leu	Ile	1	5	10	15
Phe	Glu	Glu	Tyr	Lys	Arg	Gln	Asn	Glu	His	Leu	Glu	Met	Ile	Ala	Ser	20	25	30	
Glu	Asn	Tyr	Thr	Phe	Ala	Ser	Val	Met	Glu	Ala	Met	Gly	Ser	Val	Leu	35	40	45	
Thr	Asn	Lys	Tyr	Ala	Glu	Gly	Tyr	Pro	Asn	Lys	Arg	Tyr	Tyr	Gly	Gly	50	55	60	
Cys	Glu	Val	Val	Asp	Lys	Ile	Glu	Ser	Leu	Ala	Ile	Glu	Arg	Ala	Lys	65	70	75	80
Lys	Leu	Phe	Asn	Cys	Gln	Phe	Ala	Asn	Val	Gln	Ala	His	Ser	Gly	Ser	85	90	95	
Gln	Ala	Asn	Asn	Ala	Val	Tyr	His	Ala	Leu	Leu	Lys	Pro	Tyr	Asp	Lys	100	105	110	
Ile	Leu	Gly	Met	Asp	Leu	Ser	Cys	Gly	Gly	His	Leu	Thr	His	Gly	Ala	115	120	125	
Lys	Val	Ser	Leu	Thr	Gly	Lys	His	Tyr	Gln	Ser	Phe	Ser	Tyr	Gly	Val	130	135	140	
Asn	Leu	Asp	Gly	Tyr	Ile	Asp	Tyr	Glu	Glu	Ala	Leu	Lys	Ile	Ala	Gln	145	150	155	160
Ser	Val	Lys	Pro	Glu	Ile	Ile	Val	Cys	Gly	Phe	Ser	Ala	Tyr	Pro	Arg	165	170	175	
Glu	Ile	Asp	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Glu	Val	Gly	Ala	180	185	190	
Leu	Leu	Leu	Gly	Asp	Ile	Ala	His	Val	Ala	Gly	Leu	Val	Val	Thr	Gly	195	200	205	
Glu	His	Ala	His	Pro	Phe	Pro	His	Cys	His	Val	Val	Ser	Ser	Thr	Thr	210	215	220	
His	Lys	Thr	Leu	Arg	Gly	Pro	Arg	Gly	Gly	Ile	Ile	Leu	Thr	Asn	Asp	225	230	235	240
Glu	Glu	Ile	Ala	Ala	Lys	Ile	Asp	Lys	Ala	Ile	Phe	Pro	Gly	Thr	Gln	245	250	255	
Gly	Gly	Pro	Leu	Met	His	Val	Ile	Ala	Ala	Lys	Ala	Val	Gly	Phe	Lys	260	265	270	
Glu	Asn	Leu	Lys	Pro	Glu	Phe	Lys	Ala	Tyr	Ala	Gln	Leu	Val	Lys	Ser	275	280	285	

Asp	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Glu	Val	Gly	Ala	Leu	Leu		
180						185					190						
TTA	GGC	GAT	ATA	GCC	CAT	GTG	GCA	GGG	CTT	GTG	GTA	ACC	GGT	GAG	CAT	680	
Leu	Gly	Asp	Ile	Ala	His	Val	Ala	Gly	Leu	Val	Val	Thr	Gly	Glu	His	210	
195					200					205							
GCC	CAT	CCT	TTC	CCG	CAT	TGC	CAT	GTG	GTT	TCA	AGC	ACC	ACT	CAT	AAG	728	
Ala	His	Pro	Phe	Pro	His	Cys	His	Val	Val	Ser	Ser	Thr	Thr	His	Lys		
				215					220					225			
ACC	TTA	AGA	GGG	CCT	AGA	GGG	GGG	ATT	ATT	TTA	ACT	AAT	GAT	GAA	GAG	776	
Thr	Leu	Arg	Gly	Pro	Arg	Gly	Gly	Ile	Ile	Leu	Thr	Asn	Asp	Glu	Glu		
			230					235						240			
ATA	GCG	GCT	AAG	ATT	GAC	AAA	GCG	ATT	TTT	CCA	GGA	ACT	CAA	GGC	GGG	824	
Ile	Ala	Ala	Lys	Ile	Asp	Lys	Ala	Ile	Phe	Pro	Gly	Thr	Gln	Gly	Gly		
			245				250						255				
CCT	TTG	ATG	CAT	GTG	ATT	GCT	GCT	AAA	GCG	GTG	GGT	TTT	AAA	GAG	AAT	872	
Pro	Leu	Met	His	Val	Ile	Ala	Ala	Lys	Ala	Val	Gly	Phe	Lys	Glu	Asn		
		260				265					270						
CTA	AAA	CCA	GAA	TTT	AAA	GCT	TAT	GCA	CAA	TTA	GTG	AAA	TCT	AAC	ATG	920	
Leu	Lys	Pro	Glu	Phe	Lys	Ala	Tyr	Ala	Gln	Leu	Val	Lys	Ser	Asn	Met		
275					280					285					290		
CAA	GTT	TTG	GCT	AAA	GCG	TTA	AAA	GAA	AAA	AAC	CAT	AAG	TTA	GTG	AGT	968	
Gln	Val	Leu	Ala	Lys	Ala	Leu	Lys	Glu	Lys	Asn	His	Lys	Leu	Val	Ser		
				295					300					305			
GGT	GGC	ACT	TCT	AAC	CAT	TTG	CTT	TTA	ATG	GAT	TTT	TTA	GAT	AAG	CCT	1016	
Gly	Gly	Thr	Ser	Asn	His	Leu	Leu	Leu	Met	Asp	Phe	Leu	Asp	Lys	Pro		
			310					315					320				
TAT	AGC	GGG	AAA	GAC	GCT	GAT	ATT	GCA	TTA	GGG	AAT	GCC	GGA	ATC	ACC	1064	
Tyr	Ser	Gly	Lys	Asp	Ala	Asp	Ile	Ala	Leu	Gly	Asn	Ala	Gly	Ile	Thr		
			325				330					335					
GTG	AAT	AAA	AAC	ACC	ATT	CCT	GGT	GAA	ACG	CGC	AGC	CCT	TTT	GTA	ACG	1112	
Val	Asn	Lys	Asn	Thr	Ile	Pro	Gly	Glu	Thr	Arg	Ser	Pro	Phe	Val	Thr		
			340			345					350						
AGC	GGG	ATA	AGG	ATT	GGC	TCA	GCG	GCA	TTG	AGC	GCA	AGG	GGC	ATG	GGA	1160	
Ser	Gly	Ile	Arg	Ile	Gly	Ser	Ala	Ala	Leu	Ser	Ala	Arg	Gly	Met	Gly		
355					360					365				370			
GCT	AAG	GAA	TTT	GAA	ATC	ATA	GGG	AAT	AAA	ATA	TCA	GAT	ATT	TTG	AAT	1208	
Ala	Lys	Glu	Phe	Glu	Ile	Ile	Gly	Asn	Lys	Ile	Ser	Asp	Ile	Leu	Asn		
				375				380						385			
GAT	ATT	AAT	AAT	GTT	AGT	TTG	CAA	TTG	CAT	GTG	AAA	GAA	GAA	TTG	AAA	1256	
Asp	Ile	Asn	Asn	Val	Ser	Leu	Gln	Leu	His	Val	Lys	Glu	Glu	Leu	Lys		
			390					395						400			

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CCAGCGATGC	GTCCTGTAA	AAACGATTTT	AATGTGGAGA	GTGAAGAATA	ATG GCG	56
					Met Ala	
					1	
TAT TTT TTA GAA CAA ACG GAT AGT GAA ATT TTT GAG CTT ATC TTT GAA	104					
Tyr Phe Leu Glu Gln Thr Asp Ser Glu Ile Phe Glu Leu Ile Phe Glu						
5 10 15						
GAA TAC AAG CGG CAA AAT GAG CAT TTA GAA ATG ATA GCG AGC GAG AAT	152					
Glu Tyr Lys Arg Gln Asn Glu His Leu Glu Met Ile Ala Ser Glu Asn						
20 25 30						
TAC ACT TTT GCA AGC GTT ATG GAG GCT ATG GGG AGT GTT TTA ACG AAT	200					
Tyr Thr Phe Ala Ser Val Met Glu Ala Met Gly Ser Val Leu Thr Asn						
35 40 45 50						
AAA TAC GCT GAA GGC TAC CCT AAC AAG CGC TAT TAT GGA GGC TGT GAA	248					
Lys Tyr Ala Glu Gly Tyr Pro Asn Lys Arg Tyr Tyr Gly Gly Cys Glu						
55 60 65						
GTG GTG GAT AAA ATA GAA AGC CTA GCC ATA GAA AGG GCT AAA AAG CTT	296					
Val Val Asp Lys Ile Glu Ser Leu Ala Ile Glu Arg Ala Lys Lys Leu						
70 75 80						
TTT AAT TGC CAG TTC GCT AAC GTG CAA GCG CAT TCA GGC TCA CAA GCC	344					
Phe Asn Cys Gln Phe Ala Asn Val Gln Ala His Ser Gly Ser Gln Ala						
85 90 95						
AAT AAC GCT GTC TAT CAC GCT CTT TTA AAG CCT TAT GAC AAG ATT TTA	392					
Asn Asn Ala Val Tyr His Ala Leu Leu Lys Pro Tyr Asp Lys Ile Leu						
100 105 110						
GGC ATG GAT TTA AGC TGT GGA GGG CAT TTA ACG CAT GGC GCT AAA GTG	440					
Gly Met Asp Leu Ser Cys Gly Gly His Leu Thr His Gly Ala Lys Val						
115 120 125 130						
AGT TTA ACC GGC AAG CAT TAT CAG AGC TTT TCT TAT GGC GTG AAT TTG	488					
Ser Leu Thr Gly Lys His Tyr Gln Ser Phe Ser Tyr Gly Val Asn Leu						
135 140 145						
GAT GGC TAT ATT GAT TAT GAA GAG GCG CTA AAA ATC GCT CAA AGC GTT	536					
Asp Gly Tyr Ile Asp Tyr Glu Glu Ala Leu Lys Ile Ala Gln Ser Val						
150 155 160						
AAG CCA GAA ATC ATC GTG TGC GGG TTT TCA GCC TAT CCA AGG GAG ATT	584					
Lys Pro Glu Ile Ile Val Cys Gly Phe Ser Ala Tyr Pro Arg Glu Ile						
165 170 175						
GAT TTT AAG AAA TTT AGA GAA ATC GCT GAT GAA GTG GGG GCG TTA CTA	632					

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

CTTTTACTTT ATAATTATCG TTGGCATT TT AATATTCAAA GGAGCTTGAA ATG AGA      56
                                     Met Arg
                                     1

ATT TCT CTT TTA GCT GTA ATT TTA GCG TTA TTG TTT GTG GCT TGC CAC      104
Ile Ser Leu Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala Cys His
      5              10              15

GAA ACT AAA AAA CAA ATC TTA CAA AAC GAA GCC GAT AGC ACC CCT TCA      152
Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr Pro Ser
      20              25              30

GAA AAA ACC ATT TGG CAA CCT GAA CAA AAA TAAAAATTGT AAAAATACTC AAA      205
Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys
      35              40

GGCATT TTTT AAAATAAACG CAATAAAAAA      235

```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

Met Arg Ile Ser Leu Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala
  1              5              10              15
Cys His Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr
      20              25              30
Pro Ser Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys
      35              40

```

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...1298

```

Gln Gly Thr Pro Val Leu Ile Thr His Phe Asn Leu Asp Lys Thr Tyr
      165                      170                      175
Ala His Ile Gln Ser Ser Phe Val Tyr Gly Trp Ile Lys Val Ser Asp
      180                      185                      190
Leu Val Tyr Met His Asp Lys Asp Ile Glu Leu Leu Thr His Leu Lys
      195                      200                      205
Asp Tyr Val Met Pro Ile Lys Asp Lys Ile Pro Leu Tyr Thr Asp Tyr
      210                      215                      220
Gly Asp Phe Tyr Thr Asn Ala Arg Val Gly Glu Leu Phe Ala Leu Ile
      225                      230                      235                      240
Pro Gln Ser Gln Lys Thr Pro Gln Lys Pro Gln Lys Lys Glu Leu Lys
      245                      250                      255
Ala Tyr Gly Phe Leu Arg Asp Ala Lys Gly Tyr Ala Ala Leu Gln Ser
      260                      265                      270
Val Ile Leu Glu Glu Lys Asp Phe Phe Val Phe Pro Lys Ala Phe Asn
      275                      280                      285
Ser Glu Asn Met Ala Tyr Phe Ile Asp Thr Met Leu Gly Gln Lys Tyr
      290                      295                      300
Gly Trp Gly Gly Leu Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg
      305                      310                      315                      320
Asp Ser Phe Ala Asn Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala
      325                      330                      335
Gln Ser Arg Tyr Ala Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala
      340                      345                      350
Lys Glu Lys Glu Asp Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr
      355                      360                      365
Leu Ile Tyr Leu Lys Gly His Ile Met Leu Tyr Leu Gly Ala His Asn
      370                      375                      380
His Gln Ala Ile Val Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys
      385                      390                      395                      400
His Phe Lys Thr Leu Ser His Lys Ile Gly Gly Val Val Ile Thr Ser
      405                      410                      415
Leu Trp Leu Ala Glu Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu
      420                      425                      430
Leu Ile Asp Arg Val Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn
      435                      440                      445
Lys Thr Ser Ser Pro Leu Asn Ala Asn
      450                      455

```

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...182
- (D) OTHER INFORMATION:

```

GTC GCT CAC AGC ATT TGG TCG GTG CAA ACC CAA AAG CAT TTT AAA ACC      1257
Val Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys His Phe Lys Thr
    390                      395                      400

TTG AGC CAT AAA ATA GGA GGC GTG GTG ATC ACT TCG TTA TGG TTA GCT      1305
Leu Ser His Lys Ile Gly Gly Val Val Ile Thr Ser Leu Trp Leu Ala
    405                      410                      415                      420

GAA GAG CAT AAT GGG GCG TTT TCT AAA AAG AAA TTA TTG ATT GAT AGG      1353
Glu Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu Leu Ile Asp Arg
                425                      430                      435

GTG CTT GGA ATG AGC GAT TTG AAA GAT TTT GTC AAT AAA ACT TCA AGC      1401
Val Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn Lys Thr Ser Ser
                440                      445                      450

CCT TTA AAT GCG AAT TGATTTTCTT ATATTATGAT TACGATTTTAT CAATTTAAAA C  1457
Pro Leu Asn Ala Asn
    455

ATTTGGAGAA AGA                                                         1470

```

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```

Met Arg Tyr Phe Leu Val Val Phe Leu Phe Leu Phe Val Gly Cys Thr
 1                      5                      10                      15
Lys Lys Asp Phe Thr Leu Lys Asp Leu Ser Leu Pro Gln Glu Ala Ser
                20                      25                      30
Ser Tyr Leu Ala Ser Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile
    35                      40                      45
Asp Pro Gln Ala Leu Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala
    50                      55                      60
Trp Tyr Ser Pro Trp Leu Asp Met Lys Val Lys Ser Asn Lys Lys Glu
    65                      70                      75                      80
Val Phe Trp Ile Leu Lys Glu Met Asn Lys Ser Thr Gly Tyr Gly Glu
                85                      90                      95
Asp Leu Lys Pro Asn Ala Lys Ala Phe Asn Asp Ala Leu Ile Lys Ser
                100                      105                      110
Met Asp Ile Glu His Tyr Pro Ser Val Lys Ile Arg Ala Val Val Ala
    115                      120                      125
Arg Asp Ser Asp Val Arg Ala Val Pro Thr Asn Lys Pro Tyr Tyr Leu
    130                      135                      140
Ser Gln Lys Gly Tyr Pro Phe Asp Arg Tyr Gln Asn Ser Leu Ile Phe
    145                      150                      155                      160

```

GTT TTA ATC ACG CAT TTT AAT CTA GAT AAA ACT TAT GCC CAC ATT CAA	585
Val Leu Ile Thr His Phe Asn Leu Asp Lys Thr Tyr Ala His Ile Gln	
165 170 175 180	
AGC AGT TTT GTT TAT GGC TGG ATC AAA GTT AGC GAT TTA GTC TAC ATG	633
Ser Ser Phe Val Tyr Gly Trp Ile Lys Val Ser Asp Leu Val Tyr Met	
185 190 195	
CAC GAT AAA GAC ATA GAG CTT TTA ACC CAT CTT AAA GAT TAT GTC ATG	681
His Asp Lys Asp Ile Glu Leu Leu Thr His Leu Lys Asp Tyr Val Met	
200 205 210	
CCT ATA AAA GAT AAA ATC CCC CTT TAT ACA GAC TAT GGG GAT TTT TAC	729
Pro Ile Lys Asp Lys Ile Pro Leu Tyr Thr Asp Tyr Gly Asp Phe Tyr	
215 220 225	
ACC AAC GCC AGA GTG GGC GAA TTG TTC GCT CTC ATC CCC CAA AGT CAA	777
Thr Asn Ala Arg Val Gly Glu Leu Phe Ala Leu Ile Pro Gln Ser Gln	
230 235 240	
AAA ACA CCT CAA AAA CCC CAA AAA AAG GAA TTG AAA GCC TAT GGT TTT	825
Lys Thr Pro Gln Lys Pro Gln Lys Lys Glu Leu Lys Ala Tyr Gly Phe	
245 250 255 260	
TTG AGA GAC GCT AAG GGT TAT GCA GCT TTA CAA AGC GTG ATC TTA GAA	873
Leu Arg Asp Ala Lys Gly Tyr Ala Ala Leu Gln Ser Val Ile Leu Glu	
265 270 275	
GAA AAG GAT TTT TTT GTT TTC CCT AAG GCT TTT AAC AGC GAG AAC ATG	921
Glu Lys Asp Phe Phe Val Phe Pro Lys Ala Phe Asn Ser Glu Asn Met	
280 285 290	
GCG TAT TTT ATA GAC ACC ATG TTA GGG CAA AAA TAC GGC TGG GGC GGG	969
Ala Tyr Phe Ile Asp Thr Met Leu Gly Gln Lys Tyr Gly Trp Gly Gly	
295 300 305	
CTA TTG GGT AAT AGG GAT TGC TCG GCT TTC ACC AGA GAT AGT TTT GCT	1017
Leu Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg Asp Ser Phe Ala	
310 315 320	
AAT TTT GGT ATT TTG CTC CCC AGA AAT TCC TAT GCG CAA AGC CGT TAT	1065
Asn Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala Gln Ser Arg Tyr	
325 330 335 340	
GCG AAC AAT TAT GTG GAT TTA AGC TCT ATG AAA GCC AAA GAA AAA GAA	1113
Ala Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala Lys Glu Lys Glu	
345 350 355	
GAC TAC ATC CTT AAA AAC GCC ACG CCT TTT GGA ACG CTC ATC TAT TTA	1161
Asp Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr Leu Ile Tyr Leu	
360 365 370	
AAA GGG CAT ATC ATG CTT TAT TTA GGC GCA CAC AAC CAT CAA GCG ATA	1209
Lys Gly His Ile Met Leu Tyr Leu Gly Ala His Asn His Gln Ala Ile	
375 380 385	

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 46...1416
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

TTTAAGAAAC TATTTGCGCA TTTGATGTTA AGGTTTCTCT AAAGC ATG CGT TAT TTT      57
                                   Met Arg Tyr Phe
                                   1

CTT GTA GTT TTC TTG TTT TTG TTT GTG GGT TGC ACA AAA AAG GAT TTC      105
Leu Val Val Phe Leu Phe Leu Phe Val Gly Cys Thr Lys Lys Asp Phe
  5                      10                      15                      20

ACG CTC AAA GAT TTA TCC TTG CCC CAA GAG GCT TCA AGC TAT CTT GCA      153
Thr Leu Lys Asp Leu Ser Leu Pro Gln Glu Ala Ser Ser Tyr Leu Ala
                25                      30                      35

AGC TCT CAA AAT GGC AGT AAC AAC AAC CAA AGC ATT GAC CCC CAA GCG      201
Ser Ser Gln Asn Gly Ser Asn Asn Asn Gln Ser Ile Asp Pro Gln Ala
                40                      45                      50

TTA AGA GAA AAT CTG AAA GAG AGC TAT CTC AAA GCG TGG TAT TCC CCA      249
Leu Arg Glu Asn Leu Lys Glu Ser Tyr Leu Lys Ala Trp Tyr Ser Pro
                55                      60                      65

TGG CTA GAT ATG AAA GTC AAA AGC AAT AAA AAA GAA GTG TTT TGG ATC      297
Trp Leu Asp Met Lys Val Lys Ser Asn Lys Lys Glu Val Phe Trp Ile
  70                      75                      80

CTT AAG GAG ATG AAT AAA TCC ACC GGT TAT GGC GAA GAT CTA AAA CCC      345
Leu Lys Glu Met Asn Lys Ser Thr Gly Tyr Gly Glu Asp Leu Lys Pro
  85                      90                      95                      100

AAC GCA AAA GCT TTC AAT GAC GCA CTC ATT AAG AGC ATG GAT ATT GAG      393
Asn Ala Lys Ala Phe Asn Asp Ala Leu Ile Lys Ser Met Asp Ile Glu
                105                      110                      115

CAT TAC CCT AGC GTT AAG ATT AGG GCT GTT GTA GCG CGA GAT AGC GAT      441
His Tyr Pro Ser Val Lys Ile Arg Ala Val Val Ala Arg Asp Ser Asp
                120                      125                      130

GTG AGG GCT GTG CCT ACT AAC AAA CCT TAT TAT CTT TCT CAA AAA GGC      489
Val Arg Ala Val Pro Thr Asn Lys Pro Tyr Tyr Leu Ser Gln Lys Gly
                135                      140                      145

TAT CCT TTT GAT AGG TAT CAA AAT TCG CTG ATT TTT CAA GGC ACG CCG      537
Tyr Pro Phe Asp Arg Tyr Gln Asn Ser Leu Ile Phe Gln Gly Thr Pro
  150                      155                      160

```

```

Met Val Asn Asn Leu Lys Ser Val Ser Val Ser Ala Met Asn Thr Thr
      245      250      255
Leu Ser Gly Val Glu Thr Met Ser Gln Gln Thr Ala Thr Ile Gly Asn
      260      265      270
Leu Leu Asn Ser Ser Thr Asp Leu Ser Ser Val Ile Pro Asn Ala Gln
      275      280      285
Gly Leu Asn Ser Ala Phe Ser Thr Leu Glu Ser Ala Gln Asn Thr Leu
      290      295      300
Lys Gly Tyr Leu Asn Ser Ser Ser Ala Thr Ile Gly Gln Leu Thr Asn
      305      310      315      320
Gly Ser Asn Ala Val Val Gly Ala Leu Asp Lys Ala Ile Asn Gln Val
      325      330      335
Asp Met Ala Leu Ala Asp Leu Ser Ala Ala Asp Thr Gln Lys Thr Gln
      340      345      350
Ala Val Thr Leu Ala Thr Ala Ser Asp Ser Pro Thr Thr Thr Asp
      355      360      365
Ala Ile Asn Phe Leu Asn Ala Leu Lys Ser Asn Leu Met Ala Gln Lys
      370      375      380
Asp Ala Phe Leu Asn Val His Lys Asn Ile Gln Thr Ala Val Ala Gln
      385      390      395      400
Ala Gln Glu Thr Tyr Thr Pro Ser Val Ile Asn Thr Asn Asn Tyr Gly
      405      410      415
Gln Met Tyr Gly Val Asp Ala Met Ala Gly Tyr Lys Trp Phe Phe Gly
      420      425      430
Lys Thr Lys Arg Phe Gly Phe Arg Ser Tyr Gly Tyr Tyr Ser Tyr Asn
      435      440      445
His Ala Asn Leu Ser Phe Val Gly Ser Gln Leu Gly Ile Met Glu Gly
      450      455      460
Ala Ser Gln Val Asn Asn Phe Thr Tyr Gly Val Gly Phe Asp Val Leu
      465      470      475      480
Tyr Asn Phe Tyr Glu Ser Lys Glu Gly Tyr Asn Thr Ala Gly Leu Phe
      485      490      495
Leu Gly Phe Gly Leu Gly Gly Asp Ser Phe Ile Val Gln Gly Glu Ser
      500      505      510
Tyr Leu Lys Ser Gln Met His Ile Cys Asn Asn Thr Ala Gly Cys Ser
      515      520      525
Ala Ser Met Asn Thr Ser Tyr Phe Gln Met Pro Val Glu Phe Gly Phe
      530      535      540
Arg Ser Asn Phe Ser Lys His Ser Gly Ile Glu Val Gly Phe Lys Leu
      545      550      555      560
Pro Leu Phe Thr Asn Gln Phe Tyr Lys Glu Arg Gly Val Asp Gly Ser
      565      570      575
Val Asp Val Phe Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met
      580      585      590
Ile Asn Phe
      595

```

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

GTG TTC TAT AAA AGG AAT TTC TCT ATT TAT TTT AAC TAC ATG ATC AAC 1832
Val Phe Tyr Lys Arg Asn Phe Ser Ile Tyr Phe Asn Tyr Met Ile Asn
580 585 590

TTC TAAGCCTTTC TATTCTTTCC AATAGAGGGT TTTCTCTCTG TTGGTTTCTT TTT 1888
Phe
595

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met	Lys	Lys	Ser	Phe	Lys	Lys	Leu	Gly	Phe	Val	Ser	Leu	Ala	Ala	Ser
1				5					10					15	
Gly	Val	Leu	Leu	Gly	Ser	Met	Asn	Ala	Thr	Asp	Leu	Glu	Thr	Tyr	Ala
			20					25					30		
Ala	Leu	Gln	Lys	Ser	Ser	His	Val	Phe	Gly	Asn	Tyr	Ala	Glu	Lys	Asp
			35				40					45			
Lys	Asp	Ser	Lys	Leu	Thr	Ser	Asp	Ser	Pro	Thr	Gln	Gln	Gln	Asp	Gln
	50					55					60				
Lys	Val	Ala	Gln	Asn	Thr	Ala	Ser	Asn	Asp	Ser	Gln	Glu	Ala	Thr	Thr
65					70					75					80
Leu	Glu	Asn	Thr	Ala	Ser	Thr	Asp	Asn	Thr	Thr	Ala	Thr	Thr	Asp	Glu
				85					90					95	
Thr	Tyr	Thr	Lys	Ser	Thr	Asp	Thr	Thr	Val	Ala	Gly	Ala	Ala	Gln	Lys
			100					105					110		
Val	Glu	Thr	Asp	Asn	Thr	Ala	Val	Gln	Ser	Ala	Glu	Gln	Thr	Leu	Lys
		115					120					125			
Thr	Asp	Val	Ala	Lys	Val	Gln	Ala	Asp	Ala	Ser	Ala	Lys	Asp	Phe	Asp
	130					135					140				
Glu	Thr	Thr	Phe	Gln	Ala	Asp	Gln	Ala	Ala	Glu	Gln	Thr	Ala	Glu	Lys
145					150					155					160
Ala	Leu	Gln	Gln	Ala	Glu	Ser	Lys	Leu	Asn	Thr	Asp	Gln	Gln	Thr	Leu
				165					170					175	
Asn	Thr	Ala	Leu	Gln	Asp	Gln	Thr	Lys	Thr	Pro	Thr	Pro	Ser	Thr	Pro
			180					185					190		
Pro	Thr	Lys	Glu	Glu	Pro	Lys	His	Thr	Ala	Ser	Ser	Gly	Thr	Pro	Pro
		195					200					205			
Ala	Pro	Glu	Ser	Pro	Pro	Ala	Lys	Lys	Asp	Glu	Thr	Ser	Gly	Thr	Pro
	210					215					220				
Ser	Ala	Ser	Gly	Ser	Ser	Val	Ala	Ser	Gln	Leu	Thr	Lys	Asp	Thr	Thr
225					230					235					240

Ala	Leu	Ala	Asp	Leu	Ser	Ala	Ala	Asp	Thr	Gln	Lys	Thr	Gln	Ala	Val		
340						345					350						
ACG	CTT	GCA	ACT	GCT	AGT	GAT	AGT	CCA	ACG	ACA	ACG	ACA	GAT	GCC	ATC	1160	
Thr	Leu	Ala	Thr	Ala	Ser	Asp	Ser	Pro	Thr	Thr	Thr	Thr	Asp	Ala	Ile		
355					360					365					370		
AAT	TTC	TTA	AAC	GCG	CTA	AAA	AGC	AAT	CTA	ATG	GCT	CAA	AAA	GAC	GCT	1208	
Asn	Phe	Leu	Asn	Ala	Leu	Lys	Ser	Asn	Leu	Met	Ala	Gln	Lys	Asp	Ala		
				375					380					385			
TTT	TTG	AAT	GTG	CAT	AAA	AAC	ATT	CAA	ACC	GCT	GTC	GCT	CAA	GCC	CAG	1256	
Phe	Leu	Asn	Val	His	Lys	Asn	Ile	Gln	Thr	Ala	Val	Ala	Gln	Ala	Gln		
			390					395					400				
GAA	ACC	TAC	ACG	CCA	AGC	GTG	ATC	AAC	ACC	AAT	AAT	TAC	GGG	CAA	ATG	1304	
Glu	Thr	Tyr	Thr	Pro	Ser	Val	Ile	Asn	Thr	Asn	Asn	Tyr	Gly	Gln	Met		
		405					410						415				
TAT	GGG	GTA	GAT	GCG	ATG	GCA	GGG	TAT	AAG	TGG	TTC	TTT	GGC	AAA	ACC	1352	
Tyr	Gly	Val	Asp	Ala	Met	Ala	Gly	Tyr	Lys	Trp	Phe	Phe	Gly	Lys	Thr		
	420					425					430						
AAA	CGC	TTT	GGC	TTT	AGG	TCT	TAT	GGA	TAC	TAC	AGC	TAT	AAC	CAT	GCG	1400	
Lys	Arg	Phe	Gly	Phe	Arg	Ser	Tyr	Gly	Tyr	Tyr	Ser	Tyr	Asn	His	Ala		
435					440					445					450		
AAT	TTA	AGC	TTT	GTG	GGG	AGC	CAG	CTT	GGA	ATC	ATG	GAG	GGC	GCG	TCT	1448	
Asn	Leu	Ser	Phe	Val	Gly	Ser	Gln	Leu	Gly	Ile	Met	Glu	Gly	Ala	Ser		
				455					460					465			
CAA	GTG	AAT	AAC	TTC	ACT	TAT	GGC	GTG	GGC	TTT	GAT	GTG	CTC	TAT	AAC	1496	
Gln	Val	Asn	Asn	Phe	Thr	Tyr	Gly	Val	Gly	Phe	Asp	Val	Leu	Tyr	Asn		
				470				475					480				
TTC	TAT	GAA	AGC	AAA	GAG	GGC	TAT	AAC	ACA	GCA	GGG	TTG	TTC	TTA	GGC	1544	
Phe	Tyr	Glu	Ser	Lys	Glu	Gly	Tyr	Asn	Thr	Ala	Gly	Leu	Phe	Leu	Gly		
		485					490					495					
TTT	GGG	TTA	GGA	GGG	GAT	TCG	TTT	ATC	GTT	CAA	GGA	GAG	AGC	TAC	TTG	1592	
Phe	Gly	Leu	Gly	Gly	Asp	Ser	Phe	Ile	Val	Gln	Gly	Glu	Ser	Tyr	Leu		
	500					505					510						
AAA	TCT	CAA	ATG	CAC	ATT	TGC	AAC	AAC	ACC	GCC	GGC	TGT	TCA	GCG	AGC	1640	
Lys	Ser	Gln	Met	His	Ile	Cys	Asn	Asn	Thr	Ala	Gly	Cys	Ser	Ala	Ser		
515					520					525					530		
ATG	AAC	ACA	AGC	TAC	TTC	CAA	ATG	CCT	GTT	GAA	TTT	GGT	TTT	AGG	AGC	1688	
Met	Asn	Thr	Ser	Tyr	Phe	Gln	Met	Pro	Val	Glu	Phe	Gly	Phe	Arg	Ser		
				535					540					545			
AAT	TTC	TCT	AAA	CAC	AGC	GGG	ATT	GAA	GTG	GGC	TTT	AAA	TTG	CCT	TTA	1736	
Asn	Phe	Ser	Lys	His	Ser	Gly	Ile	Glu	Val	Gly	Phe	Lys	Leu	Pro	Leu		
				550				555					560				

115	120	125	130	
GTA GCT AAA GTT CAA GCT GAT GCT AGT GCT AAA GAT TTT GAT GAA ACC				488
Val Ala Lys Val Gln Ala Asp Ala Ser Ala Lys Asp Phe Asp Glu Thr	135	140	145	
ACT TTT CAA GCC GAT CAA GCA GCA GAG CAA ACC GCT GAA AAA GCT TTA				536
Thr Phe Gln Ala Asp Gln Ala Ala Glu Gln Thr Ala Glu Lys Ala Leu	150	155	160	
CAA CAG GCT GAG AGC AAA CTC AAC ACC GAT CAA CAG ACT TTA AAC ACA				584
Gln Gln Ala Glu Ser Lys Leu Asn Thr Asp Gln Gln Thr Leu Asn Thr	165	170	175	
GCG TTA CAA GAT CAG ACG AAA ACA CCA ACC CCA TCA ACC CCA CCA ACT				632
Ala Leu Gln Asp Gln Thr Lys Thr Pro Thr Pro Ser Thr Pro Pro Thr	180	185	190	
AAA GAG GAA CCA AAA CAC ACC GCT TCA AGC GGC ACA CCA CCA GCT CCA				680
Lys Glu Glu Pro Lys His Thr Ala Ser Ser Gly Thr Pro Pro Ala Pro	195	200	205	210
GAA AGC CCA CCA GCT AAA AAA GAT GAA ACA AGT GGC ACA CCA AGT GCT				728
Glu Ser Pro Pro Ala Lys Lys Asp Glu Thr Ser Gly Thr Pro Ser Ala	215	220	225	
AGT GGG AGT TCT GTG GCA AGC CAG CTA ACC AAA GAT ACC ACT ATG GTT				776
Ser Gly Ser Ser Val Ala Ser Gln Leu Thr Lys Asp Thr Thr Met Val	230	235	240	
AAT AAT CTT AAG AGT GTG AGC GTG AGC GCG ATG AAC ACC ACT TTA AGT				824
Asn Asn Leu Lys Ser Val Ser Val Ser Ala Met Asn Thr Thr Leu Ser	245	250	255	
GGA GTA GAA ACC ATG TCT CAA CAA ACT GCA ACG ATT GGC AAC CTT TTG				872
Gly Val Glu Thr Met Ser Gln Gln Thr Ala Thr Ile Gly Asn Leu Leu	260	265	270	
AAT AGT AGC ACC GAT TTA AGC AGT GTG ATT CCC AAC GCT CAA GGG CTA				920
Asn Ser Ser Thr Asp Leu Ser Ser Val Ile Pro Asn Ala Gln Gly Leu	275	280	285	290
AAC AGC GCG TTT AGC ACA TTA GAA AGC GCT CAA AAC ACT CTA AAA GGC				968
Asn Ser Ala Phe Ser Thr Leu Glu Ser Ala Gln Asn Thr Leu Lys Gly	295	300	305	
TAT TTA AAT TCT TCT AGC GCG ACG ATT GGG CAA TTG ACA AAC GGA TCT				1016
Tyr Leu Asn Ser Ser Ser Ala Thr Ile Gly Gln Leu Thr Asn Gly Ser	310	315	320	
AAT GCG GTT GTG GGC GCG TTA GAT AAA GCT ATC AAT CAA GTG GAT ATG				1064
Asn Ala Val Val Gly Ala Leu Asp Lys Ala Ile Asn Gln Val Asp Met	325	330	335	
GCT TTG GCC GAT CTT AGT GCA GCT GAT ACG CAA AAA ACG CAA GCC GTT				1112

145

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1835
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CACTAAAGTC AATCCAAGCG CAAGTTGGAT GAAAAAATAA GAAGGAAGTT	ATG AAA	56
	Met Lys	
	1	
AAG TCA TTC AAA AAA TTA GGC TTT GTC TCT TTA GCG GCT AGT GGC GTG		104
Lys Ser Phe Lys Lys Leu Gly Phe Val Ser Leu Ala Ala Ser Gly Val		
5 10 15		
CTT TTA GGG AGC ATG AAC GCT ACC GAT TTA GAA ACC TAC GCA GCA TTG		152
Leu Leu Gly Ser Met Asn Ala Thr Asp Leu Glu Thr Tyr Ala Ala Leu		
20 25 30		
CAA AAA TCA TCG CAT GTT TTT GGT AAT TAT GCT GAA AAG GAT AAG GAT		200
Gln Lys Ser Ser His Val Phe Gly Asn Tyr Ala Glu Lys Asp Lys Asp		
35 40 45 50		
AGT AAA TTA ACA AGC GAT TCA CCA ACG CAA CAA CAA GAT CAA AAA GTA		248
Ser Lys Leu Thr Ser Asp Ser Pro Thr Gln Gln Gln Asp Gln Lys Val		
55 60 65		
GCC CAA AAC ACC GCT TCA AAC GAC AGC CAA GAA GCG ACA ACA CTT GAA		296
Ala Gln Asn Thr Ala Ser Asn Asp Ser Gln Glu Ala Thr Thr Leu Glu		
70 75 80		
AAC ACC GCT TCT ACT GAC AAC ACA ACC GCC ACA ACT GAT GAA ACT TAT		344
Asn Thr Ala Ser Thr Asp Asn Thr Thr Ala Thr Thr Asp Glu Thr Tyr		
85 90 95		
ACA AAA AGC ACT GAC ACT ACT GTA GCT GGT GCG GCT CAA AAA GTA GAA		392
Thr Lys Ser Thr Asp Thr Thr Val Ala Gly Ala Ala Gln Lys Val Glu		
100 105 110		
ACC GAT AAC ACA GCC GTT CAA AGC GCT GAA CAA ACT TTA AAA ACA GAT		440
Thr Asp Asn Thr Ala Val Gln Ser Ala Glu Gln Thr Leu Lys Thr Asp		

His	Leu	Lys	Thr	Leu	Gly	Val	Leu	Ala	Leu	Leu	Phe	Leu	Ile	Tyr	His		
			70					75					80				
CAA	ATC	GCC	TAT	AAA	AAC	TCT	TTA	AAG	CTT	TTT	AAT	GAC	GGC	TTT	TTA	346	
Gln	Ile	Ala	Tyr	Lys	Asn	Ser	Leu	Lys	Leu	Phe	Asn	Asp	Gly	Phe	Leu		
		85					90					95					
TTC	AAA	ACT	TTG	CAT	GTT	TTT	TTG	GTT	TAT	TAC	CTT	TAT	TTA	TCG	CGC	394	
Phe	Lys	Thr	Leu	His	Val	Phe	Leu	Val	Tyr	Tyr	Leu	Tyr	Leu	Ser	Arg		
	100					105					110						
TTT	TTT	TCG	ATG	TCT	TTG	AGT	TTG	AAA	ATA	CTC	GGC	TTT	CTC	GCT	CTT	442	
Phe	Phe	Ser	Met	Ser	Leu	Ser	Leu	Lys	Ile	Leu	Gly	Phe	Leu	Ala	Leu		
115					120					125					130		
TTT	GCT	TTA	ATA	GAA	AGC	GCT	TTG	TGG	GGT	TTG	TAT	GAA	AAA	TCT	TCG	490	
Phe	Ala	Leu	Ile	Glu	Ser	Ala	Leu	Trp	Gly	Leu	Tyr	Glu	Lys	Ser	Ser		
				135				140						145			
CTA	TAAGCTTTTG	CTCTTTGTTT	TTATAGGGTT	TTGGGGGTTA	CTAGCCT											540	
Leu																	

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met	Leu	Ser	Leu	Lys	Gln	Asp	Ser	Phe	Phe	Phe	Leu	Cys	Leu	Gly	Ile		
1				5				10						15			
Leu	Gly	Phe	Tyr	Phe	Tyr	Ser	Leu	Leu	Arg	Asp	Leu	Met	Pro	Phe	Leu		
			20					25					30				
Pro	Pro	Met	Ile	Gly	Phe	Leu	Phe	Leu	Phe	Tyr	Ala	Lys	Lys	Tyr	Asp		
		35				40						45					
His	Phe	Leu	Pro	Ser	Leu	Ser	Val	Phe	Gly	Cys	Leu	Phe	Trp	Phe	Glu		
	50					55				60							
Ser	Met	His	Leu	Lys	Thr	Leu	Gly	Val	Leu	Ala	Leu	Leu	Phe	Leu	Ile		
65					70					75					80		
Tyr	His	Gln	Ile	Ala	Tyr	Lys	Asn	Ser	Leu	Lys	Leu	Phe	Asn	Asp	Gly		
			85					90					95				
Phe	Leu	Phe	Lys	Thr	Leu	His	Val	Phe	Leu	Val	Tyr	Tyr	Leu	Tyr	Leu		
		100					105						110				
Ser	Arg	Phe	Ser	Met	Ser	Leu	Ser	Leu	Lys	Ile	Leu	Gly	Phe	Leu			
	115					120					125						
Ala	Leu	Phe	Ala	Leu	Ile	Glu	Ser	Ala	Leu	Trp	Gly	Leu	Tyr	Glu	Lys		
	130					135					140						
Ser	Ser	Leu															

Gln Thr Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala
 130 135 140
 Ile Tyr Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly
 145 150 155 160
 Ser Asp Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe
 165 170 175
 Asp Ile Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp
 180 185 190
 Leu Glu Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu
 195 200 205
 His Lys Arg Asn Phe Leu Thr Thr Arg Leu Lys Ala Ser Phe Arg
 210 215 220
 Pro Thr Thr Phe
 225

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...493
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CCAAACCCTT TTGAAACACT TGCTCACTAA CCCATTATAA GCCGCAAAAA CC ATG CTC 58
 Met Leu
 1

TCT TTA AAA CAA GAT TCC TTT TTT TTC TTA TGT TTA GGA ATC CTG GGG 106
 Ser Leu Lys Gln Asp Ser Phe Phe Phe Leu Cys Leu Gly Ile Leu Gly
 5 10 15

TTT TAT TTT TAT AGC CTT TTG AGG GAT TTA ATG CCT TTT TTA CCC CCA 154
 Phe Tyr Phe Tyr Ser Leu Leu Arg Asp Leu Met Pro Phe Leu Pro Pro
 20 25 30

ATG ATT GGG TTT TTA TTC TTG TTT TAT GCG AAA AAA TAC GAT CAT TTT 202
 Met Ile Gly Phe Leu Phe Leu Phe Tyr Ala Lys Lys Tyr Asp His Phe
 35 40 45 50

TTA CCC AGT TTG AGC GTG TTT GGT TGT TTG TTT TGG TTT GAG AGC ATG 250
 Leu Pro Ser Leu Ser Val Phe Gly Cys Leu Phe Trp Phe Glu Ser Met
 55 60 65

CAT TTA AAG ACT TTA GGC GTT TTA GCT TTA TTG TTT TTA ATC TAC CAT 298

```

GTG TAT GGA GTC GCT AAT GCA AAC ATC ACT TTT TTT AAA GGC TCA GAT      536
Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly Ser Asp
      150                      155                      160

ATT TTG AGT TAT GAA ACC AGA GAG GTC TTG CTC AAG TAT TTT GAT ATT      584
Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe Asp Ile
      165                      170                      175

TTA GAT AAA GAT GAA AGA AGT TTG AAA AAC GCC TTA AAG GAT TTA GAA      632
Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp Leu Glu
      180                      185                      190

AAC CCT TTT GGG TTT GCC CCC TAC ATC AGA AAA GCT TAT GAG CAT AAA      680
Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu His Lys
      195                      200                      205                      210

AGG AAT TTT CTA ACC ACC ACC AGA TTG AAA GCT TCT TTT CGC CCA ACC      728
Arg Asn Phe Leu Thr Thr Thr Arg Leu Lys Ala Ser Phe Arg Pro Thr
      215                      220                      225

ACA TTT TAAGAGAGCG GAATGTCTTG GAATTTTGA AAACGCTCAC TCATTAGCGT AT      786
Thr Phe

```

T 787

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

Met Leu Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe
  1           5           10           15
Ala Ser Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu
      20           25           30
Leu Lys Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu
      35           40           45
Ser His Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn
      50           55           60
Gln Leu Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys
      65           70           75           80
Asn Pro Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly
      85           90           95
Ser Gln Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val
      100          105          110
Gly Ile Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu
      115          120          125

```

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...734
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

GTTTTCTACT TATGATTTTG TGGAAGAATA TTGCAAATTA AAGGAAATGC  ATG CTT      56
                                     Met Leu
                                     1

GAA AAA GTG TTT CAA GAA ATT ACC AAT AAA AGA AAG TTT TTT GCA AGT      104
Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe Ala Ser
      5                      10                      15

TCT AGC ACA GGG GAG CAG TTT GAA AAC CAA TTT AGG AAT GAA TTA AAA      152
Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu Leu Lys
      20                      25                      30

AAA CAC TTT AGC GAA ATC AAT GGC GAT TTA ACA GAA GAA TTA AGC CAT      200
Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu Ser His
      35                      40                      45                      50

ATT GAA GAA AAG CCT AAT AAA GAA ATC AAA ACC ACT TTT AAC CAA CTC      248
Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn Gln Leu
      55                      60                      65

AAA AAG CAA GTT TTA GAA AAA AAT CAC CCG CAC ACC CTT AAA AAC CCT      296
Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys Asn Pro
      70                      75                      80

TTT TCA AAC CTT ACA AGC CAT TTT TTA TAC CAG CCT TTT GGC TCA CAA      344
Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly Ser Gln
      85                      90                      95

AAT TAC CCT GAT TTT TTG GTT TTT ATT TTT GAC TAT GTG GTG GGG ATT      392
Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val Gly Ile
      100                      105                      110

GAA ATC AAG TTT TCT AAA AAC GAT AAG GGT GAA AAA AAT CTT CAA ACA      440
Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu Gln Thr
      115                      120                      125                      130

TCT CGC CCC ATG TGG AAT TCA AAC CTG CCT AAA CCC AAT GCG ATT TAT      488
Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala Ile Tyr
      135                      140                      145

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

TGTAGAATGA AATCCTAGCC AGTGAGCTAG AATTTAAATT TTTAATCAAA GGAGTCATCA      60
TGGCACACC ATG AAG AAC AAC ACG GCG GGC ACC ACC ACC ACC ATC ACC ACA      111
      Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr
        1              5              10

CAC ACC ACC ACC ACT ATC ATG GCG GTG AAC ACC ACC ATC ACC ACC ACA      159
His Thr Thr Thr Thr Ile Met Ala Val Asn Thr Thr Ile Thr Thr Thr
      15              20              25              30

GCT CTC ATC ATG AAG AAG GTT GTT GCA GCA CTA GCG ACA GTC ATC ATC      207
Ala Leu Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile
              35              40              45

AAG AAG AAG GTT GCT GCC ACG GGC ATC ACG AGT AAT ATC GGT GTG GCT      255
Lys Lys Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala
              50              55              60

AGG GGC AAC TTG ACT AGG GTT GTC TCT GGC TTT TGA CTTTAAA ATACAATCAT      308
Arg Gly Asn Leu Thr Arg Val Val Ser Gly Phe
      65              70

TCCATTCTAA CCCATTCTGA TCAAACCCGT T      339

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr His Thr
  1              5              10              15
Thr Thr Thr Ile Met Ala Val Asn Thr Thr Thr Thr Thr Thr Ala Leu
      20              25              30
Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile Lys Lys
      35              40              45
Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala Arg Gly
      50              55              60
Asn Leu Thr Arg Val Val Ser Gly Phe
      65              70

```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs

595	600	605
Leu Lys Thr His Gly Ser Asp Val Val Arg Leu Trp Val Ala Phe Asn		
610	615	620
Asp Tyr Gln Asn Asp Leu Arg Val Ser Gln Thr Phe Phe Thr Gln Thr		
625	630	635
Glu Gln His Tyr Lys Lys Phe Arg Asn Thr Leu Lys Phe Leu Leu Ala		640
	645	650
Asn Phe Ser Asp Met Asp Leu Lys Asn Leu Glu Arg Pro His Asn Phe		655
	660	665
Ser Pro Leu Asp His Phe Met Leu Glu Thr Leu Glu Thr Ile Ser Ala		670
	675	680
Gly Val Asn Ser Ala Phe Glu Glu His Asp Phe Val Lys Gly Leu Asn		685
	690	695
Ile Leu Met Ala Phe Val Thr Asn Glu Leu Ser Gly Ile Tyr Leu Asp		700
705	710	715
Ala Cys Lys Asp Ser Leu Tyr Cys Asp Ser Lys Asn Asn Glu Lys Arg		720
	725	730
Gln Ala Ile Gln Met Val Leu Leu Ala Thr Ala Ser Lys Leu Cys Tyr		735
	740	745
Phe Leu Ala Pro Ile Leu Thr His Thr Ile Glu Glu Val Leu Glu His		750
	755	760
Ser Gln Ala Leu Arg Ile Phe Leu Gln Ala Lys Asp Val Phe Asp Leu		765
	770	775
Lys Asp Ile Ser Val Ser Glu Lys Leu His Leu Lys Glu Phe Lys Lys		780
785	790	795
Pro Glu Asn Phe Glu Ala Val Leu Ala Leu Arg Ser Ala Phe Asn Glu		800
	805	810
Glu Leu Asp Arg Leu Lys Lys Glu Gly Val Ile Lys Asn Ser Leu Glu		815
	820	825
Cys Ala Ile Glu Val Lys Glu Lys Ala Leu Asp Glu Asn Leu Val Glu		830
	835	840
Glu Leu Leu Met Val Ser Phe Val Gly Ile Ala Lys Glu Lys Leu Ser		845
	850	855
Glu Thr Pro Ala Phe Thr Leu Phe Lys Ala Pro Phe Tyr Lys Cys Pro		860
865	870	875
Arg Cys Trp Arg Phe Lys Ser Glu Leu Glu Asn Thr Pro Cys Lys Arg		880
	885	890
Cys Glu Gln Val Leu Lys Glu Arg		895
	900	

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...288
- (D) OTHER INFORMATION:

Gly	Leu	Leu	Lys	Glu	Arg	His	Lys	Pro	Ile	Tyr	Trp	Ser	Tyr	Ala	Cys	
			165						170					175		
Glu	Ser	Ala	Leu	Ala	Glu	Ala	Glu	Val	Glu	Tyr	Lys	Met	Lys	Lys	Ser	
			180					185					190			
Pro	Ser	Ile	Phe	Val	Ala	Phe	Gly	Leu	Lys	Lys	Glu	Ser	Leu	Glu	Lys	
		195					200					205				
Leu	Lys	Val	Lys	Lys	Ala	Ser	Leu	Val	Ile	Trp	Thr	Thr	Thr	Pro	Trp	
	210					215					220					
Thr	Leu	Tyr	Ala	Asn	Val	Ala	Ile	Ala	Leu	Lys	Lys	Asp	Ala	Val	Tyr	
225				230						235					240	
Ala	Leu	Thr	Gln	Lys	Gly	Tyr	Leu	Val	Ala	Lys	Ala	Leu	His	Glu	Lys	
			245					250						255		
Leu	Ala	Ala	Leu	Gly	Val	Val	Asp	Asn	Glu	Ile	Thr	His	Glu	Phe	Asn	
			260					265					270			
Ser	Asn	Asp	Leu	Glu	Tyr	Leu	Val	Ala	Thr	Asn	Pro	Leu	Asn	Gln	Arg	
		275					280					285				
Asp	Ser	Leu	Val	Ala	Leu	Gly	Glu	His	Val	Gly	Leu	Glu	Asp	Gly	Thr	
	290					295					300					
Gly	Ala	Val	His	Thr	Ala	Pro	Gly	His	Gly	Glu	Glu	Asp	Tyr	Tyr	Leu	
305				310						315					320	
Gly	Leu	Arg	Tyr	Asn	Leu	Glu	Val	Leu	Met	Ser	Val	Asp	Glu	Lys	Gly	
			325					330						335		
Cys	Tyr	Asp	Glu	Gly	Ile	Ile	His	Asn	Gln	Leu	Leu	Asp	Glu	Ser	Tyr	
		340						345					350			
Leu	Gly	Glu	His	Val	Phe	Lys	Ala	Gln	Lys	Arg	Ile	Ile	Glu	Gln	Leu	
	355						360					365				
Gly	Asp	Ser	Leu	Leu	Leu	Glu	Gln	Glu	Ile	Glu	His	Ser	Tyr	Pro	His	
	370					375					380					
Cys	Trp	Arg	Thr	His	Lys	Pro	Val	Ile	Tyr	Arg	Ala	Thr	Thr	Gln	Trp	
385					390					395					400	
Phe	Ile	Leu	Met	Asp	Glu	Pro	Phe	Ile	Gln	Asn	Asp	Gly	Ser	Gln	Lys	
			405					410						415		
Thr	Leu	Arg	Glu	Val	Ala	Leu	Asp	Ala	Ile	Glu	Lys	Val	Glu	Phe	Val	
			420					425					430			
Pro	Ser	Ser	Gly	Lys	Asn	Arg	Leu	Lys	Thr	Met	Ile	Glu	Asn	Arg	Pro	
		435					440					445				
Asp	Trp	Cys	Leu	Ser	Arg	Gln	Arg	Lys	Trp	Gly	Val	Pro	Leu	Ala	Phe	
	450					455					460					
Phe	Ile	Asp	Lys	Arg	Thr	Asn	Lys	Pro	Cys	Phe	Glu	Ser	Glu	Val	Leu	
465					470					475					480	
Glu	His	Val	Ala	Asn	Leu	Phe	Glu	Lys	Lys	Gly	Cys	Asp	Val	Trp	Trp	
			485					490						495		
Glu	Tyr	Ser	Val	Lys	Asp	Leu	Leu	Pro	Pro	Ser	Tyr	Gln	Glu	Asp	Ala	
			500					505					510			
Lys	His	Tyr	Glu	Lys	Ile	Met	His	Ile	Leu	Asp	Val	Trp	Phe	Asp	Ser	
		515					520					525				
Gly	Ser	Thr	Phe	Lys	Ala	Val	Leu	Glu	Asp	Tyr	His	Gly	Glu	Lys	Gly	
	530					535					540					
Gln	Ser	Pro	Ser	Asp	Val	Ile	Leu	Glu	Gly	Ser	Asp	Gln	His	Arg	Gly	
545					550					555					560	
Trp	Phe	Gln	Ser	Ser	Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Asn	Gln	Ala	
			565					570						575		
Pro	Phe	Lys	Lys	Val	Ile	Thr	His	Gly	Phe	Ile	Val	Asp	Glu	Lys	Gly	
			580					585					590			
Glu	Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Ser	Leu	Asp	Lys	Leu	

GCT ATT GAA GTA AAA GAA AAA GCG TTG GAT GAA AAT TTA GTA GAA GAG 2604
 Ala Ile Glu Val Lys Glu Lys Ala Leu Asp Glu Asn Leu Val Glu Glu
 835 840 845

TTG CTG ATG GTA AGC TTT GTG GGG ATT GCA AAA GAA AAA TTG AGT GAA 2652
 Leu Leu Met Val Ser Phe Val Gly Ile Ala Lys Glu Lys Leu Ser Glu
 850 855 860 865

ACG CCA GCA TTC ACG CTC TTT AAA GCC CCC TTT TAT AAA TGC CCC AGG 2700
 Thr Pro Ala Phe Thr Leu Phe Lys Ala Pro Phe Tyr Lys Cys Pro Arg
 870 875 880

TGT TGG CGT TTT AAA AGC GAG CTA GAA AAC ACC CCT TGC AAG CGT TGC 2748
 Cys Trp Arg Phe Lys Ser Glu Leu Glu Asn Thr Pro Cys Lys Arg Cys
 885 890 895

GAA CAG GTT TTA AAA GAG CGA TGATAAAAGG ATAGGGCTTT TGAAAACCTTT ACAA 2803
 Glu Gln Val Leu Lys Glu Arg
 900

ACCCATAGAG TTTTACAA 2821

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met Lys Gly Asn Leu Ser Val Asn Glu Pro Lys Thr Tyr Ala Lys Trp
 1 5 10 15
 Gln Glu Gln Gln Ala Phe Lys Arg Met Gln Ala Arg Lys Asp Asn His
 20 25 30
 Gly Asp Phe Thr Leu His Asp Gly Pro Pro Tyr Ala Asn Gly His Leu
 35 40 45
 His Leu Gly His Ala Leu Asn Lys Ile Leu Lys Asp Ile Val Val Lys
 50 55 60
 Arg Glu Tyr Phe Lys Gly Lys Lys Ile Tyr Tyr Thr Pro Gly Trp Asp
 65 70 75 80
 Cys His Gly Leu Pro Ile Glu Gln Gln Ile Leu Glu Arg Leu Glu Lys
 85 90 95
 Glu Lys Thr Ser Leu Glu Asn Pro Thr Leu Phe Arg Glu Lys Cys Arg
 100 105 110
 Asp His Ala Lys Lys Phe Leu Glu Ile Gln Lys Asn Glu Phe Leu Gln
 115 120 125
 Leu Gly Val Leu Gly Asp Phe Glu Asp Pro Tyr Lys Thr Met Asp Phe
 130 135 140
 Lys Phe Glu Ala Ser Ile Tyr Arg Ala Leu Val Glu Val Ala Lys Lys
 145 150 155 160

AAA ACG CAT GGG AGC GAT GTG GTG CGT TTG TGG GTA GCG TTT AAT GAC	1932
Lys Thr His Gly Ser Asp Val Val Arg Leu Trp Val Ala Phe Asn Asp	
610 615 620 625	
TAT CAA AAC GAT TTG AGA GTC TCT CAA ACC TTT TTC ACT CAA ACA GAA	1980
Tyr Gln Asn Asp Leu Arg Val Ser Gln Thr Phe Phe Thr Gln Thr Glu	
630 635 640	
CAA CAT TAT AAA AAA TTC CGC AAC ACC CTG AAA TTC TTA CTC GCT AAT	2028
Gln His Tyr Lys Lys Phe Arg Asn Thr Leu Lys Phe Leu Leu Ala Asn	
645 650 655	
TTT AGC GAT ATG GAT CTC AAG AAT TTA GAA CGC CCC CAT AAC TTC AGC	2076
Phe Ser Asp Met Asp Leu Lys Asn Leu Glu Arg Pro His Asn Phe Ser	
660 665 670	
CCT TTA GAT CAT TTT ATG TTA GAG ACT TTA GAA ACC ATA AGC GCT GGA	2124
Pro Leu Asp His Phe Met Leu Glu Thr Leu Glu Thr Ile Ser Ala Gly	
675 680 685	
GTC AAT AGC GCG TTT GAA GAG CAT GAT TTT GTG AAA GGC TTG AAT ATT	2172
Val Asn Ser Ala Phe Glu Glu His Asp Phe Val Lys Gly Leu Asn Ile	
690 695 700 705	
TTA ATG GCG TTT GTT ACC AAT GAA TTG AGC GGG ATT TAT TTA GAC GCT	2220
Leu Met Ala Phe Val Thr Asn Glu Leu Ser Gly Ile Tyr Leu Asp Ala	
710 715 720	
TGC AAG GAT AGC TTG TAT TGC GAT AGC AAA AAC AAT GAA AAA CGC CAA	2268
Cys Lys Asp Ser Leu Tyr Cys Asp Ser Lys Asn Asn Glu Lys Arg Gln	
725 730 735	
GCC ATT CAA ATG GTT TTA CTC GCT ACA GCT AGT AAG TTG TGC TAC TTT	2316
Ala Ile Gln Met Val Leu Leu Ala Thr Ala Ser Lys Leu Cys Tyr Phe	
740 745 750	
TTA GCC CCG ATT TTA ACG CAC ACG ATT GAA GAA GTT TTA GAG CAT AGC	2364
Leu Ala Pro Ile Leu Thr His Thr Ile Glu Glu Val Leu Glu His Ser	
755 760 765	
CAA GCG CTT CGC ATT TTT TTA CAA GCC AAA GAT GTG TTT GAT TTA AAA	2412
Gln Ala Leu Arg Ile Phe Leu Gln Ala Lys Asp Val Phe Asp Leu Lys	
770 775 780 785	
GAC ATT AGC GTT TCA GAA AAA CTC CAC CTC AAA GAG TTT AAA AAA CCA	2460
Asp Ile Ser Val Ser Glu Lys Leu His Leu Lys Glu Phe Lys Lys Pro	
790 795 800	
GAA AAT TTT GAA GCC GTT TTA GCC TTG CGT TCT GCC TTT AAT GAA GAG	2508
Glu Asn Phe Glu Ala Val Leu Ala Leu Arg Ser Ala Phe Asn Glu Glu	
805 810 815	
TTA GAC CGA TTG AAA AAA GAA GGC GTC ATT AAA AAT TCG TTA GAG TGC	2556
Leu Asp Arg Leu Lys Lys Glu Gly Val Ile Lys Asn Ser Leu Glu Cys	
820 825 830	

TGG AGG ACG CAC AAG CCT GTG ATT TAC AGA GCG ACT ACG CAA TGG TTT	1260
Trp Arg Thr His Lys Pro Val Ile Tyr Arg Ala Thr Thr Gln Trp Phe	
390 395 400	
ATT TTA ATG GAT GAG CCT TTT ATC CAA AAT GAT GGC TCT CAA AAA ACC	1308
Ile Leu Met Asp Glu Pro Phe Ile Gln Asn Asp Gly Ser Gln Lys Thr	
405 410 415	
TTA AGA GAA GTG GCT TTA GAT GCG ATT GAA AAG GTG GAA TTT GTG CCA	1356
Leu Arg Glu Val Ala Leu Asp Ala Ile Glu Lys Val Glu Phe Val Pro	
420 425 430	
AGC AGC GGG AAA AAC CGC CTA AAA ACC ATG ATA GAA AAC CGC CCT GAT	1404
Ser Ser Gly Lys Asn Arg Leu Lys Thr Met Ile Glu Asn Arg Pro Asp	
435 440 445	
TGG TGC TTG AGC CGG CAA AGA AAA TGG GGC GTG CCA CTG GCC TTT TTC	1452
Trp Cys Leu Ser Arg Gln Arg Lys Trp Gly Val Pro Leu Ala Phe Phe	
450 455 460 465	
ATA GAC AAA CGC ACG AAT AAG CCT TGT TTT GAA AGC GAA GTT TTA GAG	1500
Ile Asp Lys Arg Thr Asn Lys Pro Cys Phe Glu Ser Glu Val Leu Glu	
470 475 480	
CAT GTG GCC AAT CTT TTT GAG AAA AAA GGC TGT GAT GTG TGG TGG GAG	1548
His Val Ala Asn Leu Phe Glu Lys Lys Gly Cys Asp Val Trp Trp Glu	
485 490 495	
TAT AGC GTG AAA GAT TTA TTG CCC CCT AGC TAT CAA GAG GAC GCC AAG	1596
Tyr Ser Val Lys Asp Leu Leu Pro Pro Ser Tyr Gln Glu Asp Ala Lys	
500 505 510	
CAT TAT GAG AAA ATC ATG CAC ATT TTA GAC GTG TGG TTT GAT AGT GGT	1644
His Tyr Glu Lys Ile Met His Ile Leu Asp Val Trp Phe Asp Ser Gly	
515 520 525	
AGC ACC TTT AAG GCG GTT TTA GAA GAC TAT CAT GGA GAA AAA GGG CAA	1692
Ser Thr Phe Lys Ala Val Leu Glu Asp Tyr His Gly Glu Lys Gly Gln	
530 535 540 545	
AGC CCT AGC GAT GTG ATC TTA GAA GGG AGC GAT CAG CAT AGG GGG TGG	1740
Ser Pro Ser Asp Val Ile Leu Glu Gly Ser Asp Gln His Arg Gly Trp	
550 555 560	
TTT CAA AGC TCG CTT CTA ATC GGT TGT GTT TTA AAC AAC CAA GCC CCT	1788
Phe Gln Ser Ser Leu Leu Ile Gly Cys Val Leu Asn Asn Gln Ala Pro	
565 570 575	
TTT AAA AAG GTC ATT ACG CAT GGC TTT ATC GTA GAT GAA AAG GGC GAA	1836
Phe Lys Lys Val Ile Thr His Gly Phe Ile Val Asp Glu Lys Gly Glu	
580 585 590	
AAA ATG AGT AAA TCT AAG GGC AAT GTG GTG TCT TTG GAC AAG CTG CTC	1884
Lys Met Ser Lys Ser Lys Gly Asn Val Val Ser Leu Asp Lys Leu Leu	
595 600 605	

Leu	Leu	Lys	Glu	Arg	His	Lys	Pro	Ile	Tyr	Trp	Ser	Tyr	Ala	Cys	Glu	
			165					170					175			
AGC	GCT	TTA	GCG	GAA	GCT	GAA	GTG	GAA	TAC	AAA	ATG	AAA	AAA	TCG	CCC	636
Ser	Ala	Leu	Ala	Glu	Ala	Glu	Val	Glu	Tyr	Lys	Met	Lys	Lys	Ser	Pro	
		180					185					190				
TCC	ATT	TTC	GTG	GCG	TTT	GGT	TTG	AAA	AAG	GAG	AGT	TTA	GAA	AAA	TTA	684
Ser	Ile	Phe	Val	Ala	Phe	Gly	Leu	Lys	Lys	Glu	Ser	Leu	Glu	Lys	Leu	
	195					200					205					
AAA	GTC	AAA	AAA	GCG	AGC	TTG	GTG	ATT	TGG	ACG	ACC	ACG	CCT	TGG	ACT	732
Lys	Val	Lys	Lys	Ala	Ser	Leu	Val	Ile	Trp	Thr	Thr	Thr	Pro	Trp	Thr	
210					215					220					225	
TTG	TAT	GCG	AAT	GTA	GCG	ATC	GCT	TTG	AAA	AAA	GAC	GCT	GTT	TAT	GCG	780
Leu	Tyr	Ala	Asn	Val	Ala	Ile	Ala	Leu	Lys	Lys	Asp	Ala	Val	Tyr	Ala	
				230					235					240		
CTC	ACC	CAA	AAA	GGC	TAT	TTA	GTC	GCT	AAA	GCC	TTG	CAT	GAA	AAA	TTA	828
Leu	Thr	Gln	Lys	Gly	Tyr	Leu	Val	Ala	Lys	Ala	Leu	His	Glu	Lys	Leu	
			245						250				255			
GCC	GCT	TTA	GGG	GTG	GTG	GAT	AAT	GAG	ATC	ACA	CAT	GAA	TTC	AAT	TCC	876
Ala	Ala	Leu	Gly	Val	Val	Asp	Asn	Glu	Ile	Thr	His	Glu	Phe	Asn	Ser	
		260					265					270				
AAT	GAT	TTA	GAA	TAT	TTA	GTG	GCT	ACA	AAC	CCG	CTC	AAT	CAA	AGG	GAT	924
Asn	Asp	Leu	Glu	Tyr	Leu	Val	Ala	Thr	Asn	Pro	Leu	Asn	Gln	Arg	Asp	
	275					280					285					
TCG	CTG	GTG	GCT	TTA	GGA	GAG	CAT	GTC	GGT	TTA	GAA	GAT	GGC	ACA	GGA	972
Ser	Leu	Val	Ala	Leu	Gly	Glu	His	Val	Gly	Leu	Glu	Asp	Gly	Thr	Gly	
290					295					300					305	
GCC	GTG	CAT	ACC	GCA	CCT	GGG	CAT	GGT	GAA	GAG	GAC	TAT	TAT	TTA	GGC	1020
Ala	Val	His	Thr	Ala	Pro	Gly	His	Gly	Glu	Glu	Asp	Tyr	Tyr	Leu	Gly	
				310					315					320		
TTA	AGA	TAT	AAT	TTA	GAA	GTG	TTA	ATG	TCT	GTA	GAT	GAG	AAA	GGT	TGC	1068
Leu	Arg	Tyr	Asn	Leu	Glu	Val	Leu	Met	Ser	Val	Asp	Glu	Lys	Gly	Cys	
			325					330					335			
TAT	GAT	GAG	GGC	ATT	ATC	CAT	AAC	CAA	CTA	TTA	GAT	GAA	AGC	TAT	CTG	1116
Tyr	Asp	Glu	Gly	Ile	Ile	His	Asn	Gln	Leu	Leu	Asp	Glu	Ser	Tyr	Leu	
		340					345					350				
GGC	GAG	CAT	GTT	TTT	AAG	GCT	CAA	AAA	CGC	ATT	ATA	GAG	CAA	TTG	GGC	1164
Gly	Glu	His	Val	Phe	Lys	Ala	Gln	Lys	Arg	Ile	Ile	Glu	Gln	Leu	Gly	
	355					360				365						
GAT	TCT	TTA	TTG	CTA	GAG	CAA	GAG	ATT	GAG	CAT	TCT	TAT	CCG	CAT	TGC	1212
Asp	Ser	Leu	Leu	Leu	Glu	Gln	Glu	Ile	Glu	His	Ser	Tyr	Pro	His	Cys	
370					375					380					385	

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 58...2769
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```

GATTAATCAG TGGAAGAATA CAAAGACACC CTAACTTAA ACACAACCAC CTTTTCT ATG      60
                                     Met
                                     1

AAG GGG AAT TTG AGC GTT AAT GAG CCT AAA ACT TAC GCC AAA TGG CAA      108
Lys Gly Asn Leu Ser Val Asn Glu Pro Lys Thr Tyr Ala Lys Trp Gln
                5                10                15

GAG CAA CAA GCG TTT AAA CGC ATG CAA GCT AGG AAA GAC AAC CAT GGG      156
Glu Gln Gln Ala Phe Lys Arg Met Gln Ala Arg Lys Asp Asn His Gly
                20                25                30

GAT TTC ACT TTG CAT GAC GGG CCG CCT TAT GCG AAC GGG CAT TTG CAT      204
Asp Phe Thr Leu His Asp Gly Pro Pro Tyr Ala Asn Gly His Leu His
                35                40                45

TTG GGG CAT GCC TTA AAT AAA ATT TTA AAA GAC ATT GTC GTT AAA AGA      252
Leu Gly His Ala Leu Asn Lys Ile Leu Lys Asp Ile Val Val Lys Arg
                50                55                60                65

GAA TAT TTT AAG GGG AAG AAA ATC TAT TAC ACG CCC GGT TGG GAT TGC      300
Glu Tyr Phe Lys Gly Lys Lys Ile Tyr Tyr Thr Pro Gly Trp Asp Cys
                70                75                80

CAT GGT TTG CCC ATT GAG CAG CAA ATT TTA GAG CGA TTA GAA AAA GAA      348
His Gly Leu Pro Ile Glu Gln Gln Ile Leu Glu Arg Leu Glu Lys Glu
                85                90                95

AAA ACA AGC CTA GAA AAC CCC ACG CTG TTT AGA GAA AAG TGC CGA GAT      396
Lys Thr Ser Leu Glu Asn Pro Thr Leu Phe Arg Glu Lys Cys Arg Asp
                100                105                110

CAT GCG AAG AAA TTT TTA GAA ATC CAA AAG AAT GAA TTT TTG CAA TTG      444
His Ala Lys Lys Phe Leu Glu Ile Gln Lys Asn Glu Phe Leu Gln Leu
                115                120                125

GGT GTT TTG GGG GAT TTT GAA GAT CCT TAT AAA ACC ATG GAT TTT AAA      492
Gly Val Leu Gly Asp Phe Glu Asp Pro Tyr Lys Thr Met Asp Phe Lys
                130                135                140                145

TTT GAA GCG AGC ATT TAT AGA GCC TTA GTG GAA GTG GCT AAA AAA GGG      540
Phe Glu Ala Ser Ile Tyr Arg Ala Leu Val Glu Val Ala Lys Lys Gly
                150                155                160

CTT TTG AAA GAG CGC CAC AAG CCT ATT TAT TGG AGT TAT GCA TGC GAG      588

```

TTA AAT CCC AAA CTC TTA GAG GTG GAA CAA CGC CTT ATT TAAAAGGGCG CT 687
 Leu Asn Pro Lys Leu Leu Glu Val Glu Gln Arg Leu Ile
 195 200

GAGATGGGTA GCGCTCGCTG AAGAAAGGTC GATGCGTT 725

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Met	Thr	Leu	Gly	Ile	Asp	Glu	Ala	Gly	Arg	Gly	Cys	Leu	Ala	Gly	Ser	1	5	10	15
Leu	Phe	Val	Ala	Gly	Val	Ala	Cys	Asn	Glu	Lys	Thr	Ala	Leu	Glu	Phe	20	25	30	
Leu	Lys	Met	Gly	Leu	Lys	Asp	Ser	Lys	Lys	Leu	Ser	Leu	Lys	Lys	Arg	35	40	45	
Phe	Phe	Leu	Glu	Tyr	Lys	Ile	Lys	Thr	His	Gly	Glu	Val	Gly	Phe	Phe	50	55	60	
Val	Val	Lys	Lys	Ser	Ala	Asn	Glu	Ile	Asp	Ser	Leu	Gly	Leu	Gly	Ala	65	70	75	80
Cys	Leu	Lys	Leu	Ala	Val	Gln	Glu	Ile	Leu	Glu	Asn	Gly	Cys	Ser	Leu	85	90	95	
Val	Asp	Glu	Ile	Lys	Ile	Asp	Gly	Asn	Thr	Ala	Phe	Gly	Leu	Asn	Lys	100	105	110	
Arg	Tyr	Pro	His	Ile	Gln	Thr	Ile	Lys	Gly	Asp	Glu	Thr	Ile	Ala		115	120	125	
Gln	Ile	Ala	Met	Ala	Ser	Val	Leu	Ala	Lys	Ala	Phe	Lys	Asp	Arg	Glu	130	135	140	
Met	Leu	Glu	Leu	His	Ala	Leu	Phe	Lys	Glu	Tyr	Gly	Trp	Asp	Lys	Asn	145	150	155	160
Cys	Gly	Tyr	Gly	Thr	Lys	Gln	His	Ile	Glu	Ala	Ile	Ile	Lys	Leu	Gly	165	170	175	
Ala	Thr	Pro	Phe	His	Arg	His	Ser	Phe	Thr	Leu	Lys	Asn	Arg	Ile	Leu	180	185	190	
Asn	Pro	Lys	Leu	Leu	Glu	Val	Glu	Gln	Arg	Leu	Ile					195	200		

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2821 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

GAAAACAGGA TAACGCATGA AACATGTGAG TAGGGATTTT GATACCGGTT GGGTTGCGTA      60
TCA ATG ACT CTA GGC ATT GAT GAA GCG GGT AGG GGG TGT TTG GCC GGT      108
  Met Thr Leu Gly Ile Asp Glu Ala Gly Arg Gly Cys Leu Ala Gly
    1             5             10             15

TCG CTT TTT GTG GCT GGG GTG GCG TGT AAT GAA AAA ACA GCC TTA GAA      156
Ser Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu
                20             25             30

TTT CTA AAA ATG GGT TTA AAA GAC AGC AAG AAG CTC AGC CTA AAA AAG      204
Phe Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys
                35             40             45

CGC TTT TTC TTA GAA TAT AAG ATC AAA ACG CAT GGT GAG GTG GGG TTT      252
Arg Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe
                50             55             60

TTC GTG GTT AAA AAA AGC GCA AAT GAA ATT GAT AGC TTG GGC TTA GGG      300
Phe Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly
    65             70             75

GCG TGT TTG AAA CTC GCT GTG CAA GAA ATT TTA GAA AAT GGT TGC TCT      348
Ala Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser
    80             85             90             95

TTA GTT GAT GAA ATA AAA ATA GAC GGC AAC ACG GCG TTT GGC TTG AAC      396
Leu Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn
                100             105             110

AAA CGC TAC CCC CAT ATA CAA ACC ATC ATC AAG GGC GAT GAA ACA ATC      444
Lys Arg Tyr Pro His Ile Gln Thr Ile Ile Lys Gly Asp Glu Thr Ile
                115             120             125

GCT CAA ATC GCT ATG GCG TCT GTT TTG GCG AAA GCT TTT AAG GAC AGA      492
Ala Gln Ile Ala Met Ala Ser Val Leu Ala Lys Ala Phe Lys Asp Arg
                130             135             140

GAA ATG CTA GAG TTG CAC GCT TTG TTT AAG GAA TAC GGC TGG GAT AAG      540
Glu Met Leu Glu Leu His Ala Leu Phe Lys Glu Tyr Gly Trp Asp Lys
    145             150             155

AAT TGC GGG TAT GGG ACT AAA CAA CAT ATA GAA GCG ATC ATT AAG CTA      588
Asn Cys Gly Tyr Gly Thr Lys Lys Gln His Ile Glu Ala Ile Ile Lys Leu
    160             165             170             175

GGG GCT ACG CCT TTT CAT CGG CAT AGC TTC ACG CTT AAA AAC CGC ATC      636
Gly Ala Thr Pro Phe His Arg His Ser Phe Thr Leu Lys Asn Arg Ile
                180             185             190

```


80	85	90	
GCT ATT GAC ACC ATG AAA AAG ATT GAA GCG CAA ATT TAT ATG AGC AAG			520
Ala Ile Asp Thr Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys			
95	100	105	
TAT AAA ACT TTA AGC GCG GTA GGC TTT TAATGGCAAT CTCTATTAAA AGCCCAA			574
Tyr Lys Thr Leu Ser Ala Val Gly Phe			
110	115		
AAGAAATCAA AGCTCTAAGA AAAGCCG			601

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met	Phe	Leu	Leu	Ile	Ile	Phe	Phe	Ala	Tyr	Phe	Tyr	Ser	Ser	Ile	Val
1				5					10					15	
Phe	Asn	Ser	Lys	Asp	Ile	Ala	Asp	Asn	Leu	Arg	Arg	Asn	Gly	Gly	Tyr
			20					25					30		
Ile	Pro	Gly	Leu	Arg	Pro	Gly	Glu	Gly	Thr	Ser	Ser	Phe	Leu	Asn	Ser
		35					40					45			
Val	Ala	Ser	Lys	Leu	Thr	Leu	Trp	Gly	Ser	Leu	Tyr	Leu	Ala	Leu	Ile
	50					55					60				
Ser	Thr	Val	Pro	Trp	Ile	Leu	Val	Lys	Ala	Met	Gly	Val	Pro	Phe	Tyr
65					70					75				80	
Phe	Gly	Gly	Thr	Ala	Val	Leu	Ile	Val	Val	Gln	Val	Ala	Ile	Asp	Thr
				85					90					95	
Met	Lys	Lys	Ile	Glu	Ala	Gln	Ile	Tyr	Met	Ser	Lys	Tyr	Lys	Thr	Leu
			100					105					110		
Ser	Ala	Val	Gly	Phe											
			115												

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 64...675

```

          325          330          335
Leu Cys Gln Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala
          340          345          350
Leu Ala Tyr Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile
          355          360          365
Ile Val Val Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val
          370          375          380
Tyr Asn Ala Leu Lys Gly Gly Leu Lys
385          390

```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 197...547
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

TGGTGATGCA AAACCAAAAC AAGCGCATCA TGAATTACAT TCCTATTAAG TTGAATTTAA      60
GTGGGGGTGAT CCCCCCTATT TTCGCTTCAG CTTTGCTCGT GTTCCCTTCT ACGATTTTGC      120
AGCAAGCCAC AAGCAACAAA ACCTTGCAAG CGGTTGCGNA TTTTTTAAGC CCGCAAGGTA      180
TGCCTATAAT ATTTTG ATG TTC TTG CTC ATC ATC TTT TTT GCT TAC TTT TAT      232
          Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr
              1              5              10

TCT TCT ATT GTG TTC AAT TCT AAG GAT ATT GCG GAT AAT TTG AGG CGT      280
Ser Ser Ile Val Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg
          15              20              25

AAT GGC GGG TAT ATT CCA GGG CTT AGG CCT GGA GAG GGG ACT TCA TCG      328
Asn Gly Gly Tyr Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser
          30              35              40

TTT TTA AAT TCT GTA GCG AGT AAG CTC ACT TTG TGG GGT TCA TTG TAT      376
Phe Leu Asn Ser Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr
          45              50              55              60

TTA GCG CTC ATT TCT ACC GTG CCT TGG ATT TTG GTT AAG GCT ATG GGC      424
Leu Ala Leu Ile Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly
          65              70              75

GTG CCT TTT TAC TTT GGA GGC ACA GCG GTG CTG ATT GTG GTT CAA GTC      472
Val Pro Phe Tyr Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val

```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```

Met Asn Lys Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser
 1             5             10             15
Glu Leu Leu Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala
      20             25             30
Cys Leu Lys Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys
      35             40             45
Asp Phe Val Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val
      50             55             60
Ser Asn Pro Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His
      65             70             75             80
Gly Gly Ala His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala
      85             90             95
Lys Lys Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln
      100            105            110
His Gly Val Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys
      115            120            125
Val Val Phe Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val
      130            135            140
Phe Arg Met His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly
      145            150            155            160
Ser Ala Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala
      165            170            175
Ser Ser Tyr Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro
      180            185            190
His Pro Tyr Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp
      195            200            205
Glu Val Lys Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr
      210            215            220
Val Ile Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser
      225            230            235            240
Ala Phe Leu Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala
      245            250            255
Gly Leu Gly Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly
      260            265            270
Arg Val Gly Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp
      275            280            285
Glu Gly Gln Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr
      290            295            300
Pro Gly Val Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala
      305            310            315            320
Val Tyr Glu Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu

```

AAG GAC ACG CAT TAT TTG CTA GGC ACA GCC GCC GGG CCA CAC CCT TAC	632
Lys Asp Thr His Tyr Leu Leu Gly Thr Ala Ala Gly Pro His Pro Tyr	
180 185 190 195	
CCC ACA ATG GTT AAA ACC TTT CAA AAA ATG ATA GGC GAT GAG GTT AAA	680
Pro Thr Met Val Lys Thr Phe Gln Lys Met Ile Gly Asp Glu Val Lys	
200 205 210	
AGC CAG ATT TTA GAA AAA GAA AAC CGC TTG CCT GAT TAT GTG ATC GCA	728
Ser Gln Ile Leu Glu Lys Glu Asn Arg Leu Pro Asp Tyr Val Ile Ala	
215 220 225	
TGC GTT GGA GGG GGG TCT AAC GCT ATA GGG ATA TTC AGC GCA TTT TTA	776
Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Ile Phe Ser Ala Phe Leu	
230 235 240	
AAC GAC AAA GAA GTT AAA CTC ATA GGC GTA GAG CCG GCG GGT TTA GGG	824
Asn Asp Lys Glu Val Lys Leu Ile Gly Val Glu Pro Ala Gly Leu Gly	
245 250 255	
CTA GAA ACC AAT AAG CAT GGG GCG ACT TTG AAT AAG GGG CGT GTG GGG	872
Leu Glu Thr Asn Lys His Gly Ala Thr Leu Asn Lys Gly Arg Val Gly	
260 265 270 275	
ATT TTG CAT GGG AAT AAA ACC TAT CTT TTA CAA GAT GAT GAA GGC CAG	920
Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp Glu Gly Gln	
280 285 290	
ATT GCA GAA AGC CAT AGC ATT AGC GCC GGG CTT GAT TAT CCA GGA GTG	968
Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val	
295 300 305	
GGG CCA GAA CAC AGC TAT TTA AAA GAA AGT GGG CGT GCG GTT TAT GAA	1016
Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala Val Tyr Glu	
310 315 320	
AGC GCA AGC GAT GCT GAA GCG CTA GAA GCC TTC AAG TTG TTG TGC CAA	1064
Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu Leu Cys Gln	
325 330 335	
AAA GAA GGC ATT ATC CCA GCG CTA GAA AGC TCA CAC GCC TTA GCG TAT	1112
Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Leu Ala Tyr	
340 345 350 355	
GCC TTA AAG CTC GCT CAA AAA TGC GAA GAA GAA AGC ATC ATC GTA GTG	1160
Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile Ile Val Val	
360 365 370	
AAT TTA AGC GGC AGA GGG GAT AAG GAT TTA AGC ACC GTT TAT AAC GCT	1208
Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val Tyr Asn Ala	
375 380 385	
TTA AAA GGA GGT TTA AAA TGAGGTATCA AAACATGTTT GAAACCTTAA AAA	1259
Leu Lys Gly Gly Leu Lys	
390	

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TAAGGATAAA ATCAAGCGAT TAGCCCGAAT TTTAAGAGAG TATTAAG	ATG AAT AAA	56
	Met Asn Lys	
	1	
AAA GCG TAT TTT GGG GAG TTT GGA GGG AGT TTT GTT TCG GAG TTG TTA		104
Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu		
5 10 15		
GTG CCT GCA TTA AGA GAA TTA GAA CAG GCG TTT GAT GCG TGT TTG AAA		152
Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys		
20 25 30 35		
GAT GAA AAA TTC CAA AAA GAA TAT TTT CGT CTT TTA AAG GAT TTT GTG		200
Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys Asp Phe Val		
40 45 50		
GGC CGT CCT AGC CCT TTA ACC TTG TGT CAA AAT ATC GTT TCT AAC CCT		248
Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val Ser Asn Pro		
55 60 65		
AAA GTC AAG CTT TAT TTA AAA CGA GAG GAT TTA ATC CAT GGC GGG GCG		296
Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His Gly Gly Ala		
70 75 80		
CAT AAG ACT AAT CAA GCC TTA GGG CAA GCC CTT TTA GCG AAA AAA ATG		344
His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala Lys Lys Met		
85 90 95		
GGT AAA ACA AGG ATC ATC GCT GAA ACA GGC GCC GGT CAG CAT GGC GTG		392
Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Val		
100 105 110 115		
GCG ACG GCT ATC GCT TGC GCA TTA TTG AAC TTA AAA TGC GTG GTT TTT		440
Ala Thr Ala Ile Ala Cys Ala Leu Leu Asn Leu Lys Cys Val Val Phe		
120 125 130		
ATG GGA TCT AAA GAC ATC AAG CGC CAG GAA ATG AAT GTT TTT AGA ATG		488
Met Gly Ser Lys Asp Ile Lys Arg Gln Glu Met Asn Val Phe Arg Met		
135 140 145		
CAC TTA TTA GGC GCT GAA GTG AGA GAG GTT AAT TCA GGG AGC GCG ACG		536
His Leu Leu Gly Ala Glu Val Arg Glu Val Asn Ser Gly Ser Ala Thr		
150 155 160		
CTT AAA GAC GCT GTG AAT GAA GCC TTA AGA GAT TGG GCG AGC AGT TAC		584
Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Ala Ser Ser Tyr		
165 170 175		

Ile	Pro	Thr	Asn	Gly	Val	Ser	Asp	Thr	Asn	Asn	Leu	Ile	Asn	Leu	Leu
			915					920					925		
Thr	Glu	Phe	Ile	Lys	Thr	Ala	Gly	Phe	Ile	Gln	Asn	Asn	Asp	Ser	Ser
			930				935				940				
Val	Ser	Thr	Ser	Leu	Thr	Ser	Ala	Phe	Gln	Ala	Ile	Thr	Ser	Ala	Ile
945					950					955					960
Ser	Gln	Gly	Phe	Gln	Ala	Leu	Gln	Asn	Asp	Ile	Ser	Pro	Asn	Ala	Ile
				965					970					975	
Leu	Thr	Leu	Leu	Gln	Glu	Ile	Thr	Ser	Asn	Thr	Thr	Thr	Ile	Gln	Ser
			980						985				990		
Phe	Ser	Gln	Thr	Leu	Arg	Gln	Leu	Gly	Asp	Lys	Thr	Phe	Phe	Met	
			995				1000					1005			
Ala	Gln	Gln	Lys	Leu	Ile	Asp	Ala	Met	Ile	Asn	Ala	Arg	Asn	Gln	Val
1010					1015						1020				
Gln	Asn	Ala	Gln	Asn	Gln	Ala	Asn	Asn	Tyr	Gly	Ser	Gln	Pro	Val	Leu
025					1030					1035					1040
Ser	Gln	Tyr	Ala	Ala	Ala	Lys	Ser	Thr	Gln	His	Gly	Met	Ser	Asn	Gly
				1045					1050				1055		
Leu	Gly	Val	Gly	Leu	Gly	Tyr	Lys	Tyr	Phe	Phe	Gly	Lys	Ala	Arg	Lys
			1060				1065					1070			
Leu	Gly	Leu	Arg	His	Tyr	Phe	Phe	Phe	Asp	Tyr	Gly	Phe	Ser	Glu	Ile
			1075				1080				1085				
Gly	Leu	Ala	Asn	Gln	Ser	Val	Lys	Ala	Asn	Ile	Phe	Ala	Tyr	Gly	Val
1090					1095						1100				
Gly	Thr	Asp	Phe	Leu	Trp	Asn	Leu	Phe	Arg	Arg	Thr	Tyr	Asn	Thr	Lys
105				1110						1115				1120	
Ala	Leu	Asn	Phe	Gly	Leu	Phe	Ala	Gly	Val	Gln	Leu	Gly	Gly	Ala	Thr
				1125					1130				1135		
Trp	Leu	Ser	Ser	Leu	Arg	Gln	Gln	Ile	Ile	Asp	Asn	Trp	Gly	Ser	Ala
			1140					1145				1150			
Asn	Asp	Ile	His	Ser	Thr	Asn	Phe	Gln	Val	Ala	Leu	Asn	Phe	Gly	Val
			1155				1160				1165				
Arg	Thr	Asn	Phe	Ala	Glu	Phe	Lys	Arg	Phe	Ala	Lys	Lys	Phe	His	Asn
			1170				1175				1180				
Gln	Gly	Val	Ile	Ser	Gln	Lys	Ser	Val	Glu	Phe	Gly	Ile	Lys	Val	Pro
185				1190						1195				1200	
Leu	Ile	Asn	Gln	Ala	Tyr	Leu	Asn	Ser	Ala	Gly	Ala	Asp	Val	Ser	Tyr
				1205					1210				1215		
Arg	Arg	Leu	Tyr	Thr	Phe	Tyr	Ile	Asn	Tyr	Ile	Met	Gly	Phe		
			1220					1225				1230			

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...1226

Val	Gln	Thr	Ile	Asn	Gly	Lys	Glu	Gln	Ile	Gly	Val	Asn	Ser	Phe	Asn	465	470	475	480
Leu	Val	Ser	Gln	Val	Trp	Ser	Val	Tyr	Asn	Ser	Leu	Lys	Thr	Ser	Glu	485	490	495	
Glu	Asn	Leu	Gln	Lys	Asn	Ala	Asn	Ile	Leu	Cys	Ala	Asn	Gly	Thr	Gln	500	505	510	
Ser	Gly	Thr	Ser	Ser	Cys	Asn	Ser	Ser	Ser	Gly	Gly	Leu	Ser	Ile	Ser	515	520	525	
Gly	Asn	Ala	Gln	Leu	Gln	Asn	Ile	Leu	Ser	Pro	Thr	Ser	Gly	Thr	Thr	530	535	540	
Thr	Asn	Thr	Gln	Ala	Lys	Ser	Asn	Ala	Pro	Lys	Leu	Lys	Ala	Met	Val	545	550	555	560
Val	Val	Asn	Asn	Glu	Glu	Glu	Ala	Lys	Thr	Ala	Asn	Leu	Ala	Gln	Ser	565	570	575	
Ser	Gly	Thr	Thr	Thr	Gln	Ser	Pro	Asn	Ser	Thr	Val	Met	Gly	Ala	Leu	580	585	590	
Asn	Thr	Val	Leu	Gln	Asn	Val	Ser	Asn	Phe	Gln	Gln	Ser	Ile	Gln	Asn	595	600	605	
Ala	Phe	Gln	Asn	Gln	Glu	Ser	Asn	Ile	Gln	Ala	Trp	Ala	Asn	Ala	Ile	610	615	620	
Tyr	Asn	Thr	Asn	Gly	Ser	Gln	Ser	Gln	Glu	Met	Thr	Pro	Asn	Asn	Asn	625	630	635	640
Gln	Asp	Leu	Arg	Ile	Gln	Leu	Arg	Ala	Asn	Phe	Tyr	Gln	Leu	Ile	Asn	645	650	655	
Thr	Ile	Asn	Gln	Gln	Val	Pro	Thr	Asp	Met	Asn	Ala	Leu	Ile	Asn	Gln	660	665	670	
Ser	Gln	Gln	Thr	Gln	Gln	Thr	Ser	Gly	Ser	Ala	Ser	Asn	Asn	Asn	Ala	675	680	685	
Cys	Ala	Ser	Gly	Met	Ser	Gly	Ser	Asn	Gly	Asn	Trp	Cys	Tyr	Gln	Gln	690	695	700	
Trp	Ser	Asp	Ser	Lys	Ala	Tyr	Tyr	Ser	Gly	Leu	Gln	Ser	Ala	Leu	Gly	705	710	715	720
Tyr	Gln	Thr	Gln	Ala	Thr	Thr	Gln	Ser	Gly	Ser	Asn	Gly	Gly	Asn	Ser	725	730	735	
Ile	Thr	Tyr	Asn	Val	Gln	Gln	Ile	Thr	Leu	Thr	Ser	Asn	Gly	Leu	Leu	740	745	750	
Asn	Gln	Ile	Ile	Thr	Asn	Leu	Lys	Ser	Val	Asn	Gly	Gly	Asn	Gly	Ala	755	760	765	
Ser	Gly	Thr	Gly	Ser	Gly	Asn	Gly	Thr	Ser	Gln	Ile	Asn	Thr	Ala	Tyr	770	775	780	
Gln	Met	Leu	Thr	Asp	Ala	Ser	Asp	Gly	Lys	Leu	Gly	Thr	Tyr	Ser	Ser	785	790	795	800
Ser	Ser	Gly	Ser	Asn	Asn	Gly	Tyr	Thr	Pro	Cys	Asn	Ser	Thr	Asn	Gly	805	810	815	
Ser	Asn	Lys	Thr	Ser	Gly	Asn	Asn	Cys	Tyr	Glu	Pro	Asn	Lys	Gln	Gln	820	825	830	
Asn	Ala	Thr	Thr	Ala	Thr	Ala	Thr	Thr	Asp	Ser	Asn	Leu	Gln	Lys	Val	835	840	845	
Tyr	Asn	Asp	Ala	Gln	Lys	Ile	Ala	Asn	Ile	Ile	Ala	Ser	Ser	Gly	Asn	850	855	860	
Asn	Lys	Gly	Val	Glu	Asn	Gly	Leu	Lys	Gln	Phe	Phe	Glu	Ala	Leu	Lys	865	870	875	880
Asn	Asn	Ser	Ser	Ser	Ser	Ser	Asn	Leu	Cys	Gly	Asn	Gly	Ser	Ser	Gly	885	890	895	
Ser	Ser	Gly	Thr	Thr	Cys	Ser	Gly	Trp	Leu	Ile	Asn	Leu	Leu	Gly	Ala				

			20					25				30					
Gly	Gly	Thr	Gln	Gln	Phe	Ile	Asn	Asn	Lys	Gln	Leu	Leu	Glu	Asn	Gln		
		35					40					45					
Asn	Ile	Ile	Asn	Ser	Val	Thr	Gln	Ser	Ala	Ile	Asn	Ile	Ala	Gly	Pro		
	50					55					60						
Thr	Thr	Gly	Leu	Ile	Thr	Leu	Ser	Ser	Gln	Thr	Val	Ile	Asp	Ala	Leu		
65					70					75					80		
Gly	Tyr	Gly	Val	Ser	Asn	Thr	Val	Gly	Asn	Gln	Leu	Glu	Gly	Ile	Ser		
			85					90						95			
Asn	Ile	Leu	Asn	Gln	Ile	Gly	Lys	Arg	Lys	Asp	Phe	Tyr	Ser	Ser	Arg		
		100					105						110				
Gln	Ile	Ser	Ser	Ile	Ser	Gln	Gln	Ile	Ile	Gly	Leu	Lys	Gly	Ser	Ser		
	115					120					125						
Asp	Pro	Leu	Lys	Ala	His	Ser	Ser	Gln	Ile	Thr	Ala	Lys	Leu	Leu	Ser		
	130					135					140						
Asn	Thr	Gln	Ser	Ala	Phe	Asp	Gln	Gly	Ile	Ala	Leu	Ser	Thr	Asn	Ile		
145				150						155					160		
Ile	Ser	Ser	Ile	Asn	Ser	Leu	Asn	Pro	Ser	Asn	Asn	Thr	Gln	Glu	Val		
			165					170						175			
Lys	Lys	Gln	Leu	Gln	Asn	Thr	Ala	Gln	Ser	Met	Thr	Glu	Leu	Leu	Gln		
		180						185					190				
Gln	Ile	Glu	His	Ser	Ile	Thr	Lys	Thr	Thr	Ser	Thr	Thr	Tyr	Ala	Gln		
	195					200					205						
Ser	Leu	Leu	Ser	Asn	Leu	Thr	Asp	Ala	Val	Asn	Ala	Ser	Ser	Asn	Asn		
	210					215					220						
Thr	Ala	Tyr	Val	Ser	Ala	Leu	Val	Asn	Ala	Leu	Asn	Thr	Leu	Gly	Val		
225				230						235					240		
Gly	Val	Phe	Pro	Thr	Thr	Thr	Thr	Thr	His	Val	Val	Leu	Asn	Pro	Pro		
		245						250						255			
Gly	Gln	Val	Val	Phe	Tyr	Pro	Thr	Asn	Ser	Ile	Leu	Gly	Ser	Thr	Ser		
		260						265					270				
Ser	Asn	Ser	Asn	Asn	Gln	Gln	Gln	Tyr	Asn	Asn	Thr	Leu	Leu	Met	Asn		
	275					280						285					
Thr	Leu	Gln	Gly	Thr	Leu	Ser	Ala	Asn	Thr	Gln	Asn	Asn	Pro	Asn	Gly		
	290					295					300						
Cys	Ala	Asn	Gln	Val	Gln	Cys	Leu	Glu	Gln	Phe	Ile	Gln	Asn	Leu	Ala		
305				310						315					320		
Pro	Leu	Ala	Ala	Thr	Pro	Thr	Ser	Asn	Asn	Gln	Ala	Asn	Gln	Gln	Val		
			325					330						335			
Gln	Ala	Ile	Ala	Gln	Lys	Leu	Gln	Ser	Val	Ala	Ile	Asn	Thr	Leu	Asp		
		340						345					350				
Asn	Asn	Ala	Ile	Asn	Asn	Thr	Thr	Tyr	Asn	Leu	Asn	Asn	Leu	His	Asn		
	355					360						365					
Ala	Leu	Asn	Phe	Gln	Ala	Tyr	Glu	Ser	Thr	Ile	Glu	Gln	Tyr	Asn	Asn		
	370					375					380						
Ala	Leu	Lys	Gln	Ile	Ser	Trp	Ile	Ser	Phe	Thr	Glu	Pro	Lys	Asn	Leu		
385				390						395					400		
Leu	Lys	Asn	Thr	Ser	Asn	Asn	Tyr	Gln	Ile	Gly	Thr	Val	Thr	Asn	Ala		
		405						410						415			
Gln	Gly	Gln	Asn	Ile	Ser	Ala	Tyr	Asp	Cys	Met	Thr	Ala	Thr	Gly	Ser		
	420							425					430				
Leu	Ser	Ser	Asn	Ala	Ser	Ser	Gly	Ile	Ser	Cys	Ser	Ala	Thr	Ser	Ser		
	435					440						445					
Thr	Ser	Ser	Thr	Asn	Ser	Phe	Asp	Asn	Ser	Leu	Val	Ala	Thr	Ser	Lys		
	450					455					460						

GCC AAT CAA AGC GTG AAA GCG AAT ATC TTT GCT TAT GGG GTA GGC ACG 3368
 Ala Asn Gln Ser Val Lys Ala Asn Ile Phe Ala Tyr Gly Val Gly Thr
 1095 1100 1105

GAT TTT TTA TGG AAC TTA TTC AGG AGG ACT TAC AAC ACT AAA GCG TTG 3416
 Asp Phe Leu Trp Asn Leu Phe Arg Arg Thr Tyr Asn Thr Lys Ala Leu
 1110 1115 1120

AAT TTT GGG CTA TTT GCT GGG GTC CAA CTG GGC GGC GCA ACC TGG CTT 3464
 Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr Trp Leu
 1125 1130 1135

AGC TCC TTA AGG CAA CAA ATC ATT GAC AAC TGG GGG AGT GCT AAT GAC 3512
 Ser Ser Leu Arg Gln Gln Ile Ile Asp Asn Trp Gly Ser Ala Asn Asp
 1140 1145 1150

ATC CAT TCA ACG AAT TTT CAA GTG GCG CTG AAT TTT GGG GTG CGC ACC 3560
 Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val Arg Thr
 1155 1160 1165 1170

AAC TTC GCG GAG TTT AAG CGT TTT GCT AAG AAA TTC CAC AAT CAA GGG 3608
 Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn Gln Gly
 1175 1180 1185

GTC ATC AGC CAA AAG AGC GTG GAA TTT GGG ATC AAA GTG CCT CTC ATC 3656
 Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro Leu Ile
 1190 1195 1200

AAT CAA GCG TAT TTG AAT AGC GCT GGA GCT GAT GTG AGT TAC AGG AGG 3704
 Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr Arg Arg
 1205 1210 1215

CTT TAT ACT TTT TAT ATC AAT TAC ATC ATG GGG TTT TAAAAAAGGG TGTGTC 3756
 Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe
 1220 1225 1230

ATGGAAATCT TACAATTCAT CGGCTATGGG AATATGG 3793

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Ile Lys Lys Ala Arg Lys Phe Ile Pro Phe Phe Leu Ile Gly Ser
 1 5 10 15
 Leu Leu Ala Glu Asp Asn Gly Trp Tyr Met Ser Val Gly Tyr Gln Ile

GGC GTT GAA AAC GGC TTA AAA CAA TTC TTT GAA GCG TTA AAA AAT AAT	2696
Gly Val Glu Asn Gly Leu Lys Gln Phe Phe Glu Ala Leu Lys Asn Asn	
870 875 880	
AGC AGC AGT CTC AGT AAT TTA TGT GGT AAT GGT AGT AGC GGT AGT AGT	2744
Ser Ser Ser Leu Ser Asn Leu Cys Gly Asn Gly Ser Ser Gly Ser Ser	
885 890 895	
GGC ACT ACT TGC TCC GGT TGG CTT ATC AAC CTT TTA GGG GCA ATC CCC	2792
Gly Thr Thr Cys Ser Gly Trp Leu Ile Asn Leu Leu Gly Ala Ile Pro	
900 905 910	
ACC AAT GGA GTG AGC GAT ACG AAT AAT TTA ATT AAT CTG CTC ACT GAA	2840
Thr Asn Gly Val Ser Asp Thr Asn Asn Leu Ile Asn Leu Leu Thr Glu	
915 920 925 930	
TTC ATT AAA ACC GCC GGG TTT ATC CAA AAT AAT GAT AGT AGT GTA TCT	2888
Phe Ile Lys Thr Ala Gly Phe Ile Gln Asn Asn Asp Ser Ser Val Ser	
935 940 945	
ACT AGT CTT ACA AGC GCT TTT CAA GCC ATT ACG AGC GCT ATT TCT CAA	2936
Thr Ser Leu Thr Ser Ala Phe Gln Ala Ile Thr Ser Ala Ile Ser Gln	
950 955 960	
GGG TTT CAA GCC TTA CAA AAC GAT ATT AGC CCT AAT GCG ATT TTA ACC	2984
Gly Phe Gln Ala Leu Gln Asn Asp Ile Ser Pro Asn Ala Ile Leu Thr	
965 970 975	
TTG CTC CAA GAG ATT ACT TCT AAC ACC ACC ACC ATT CAG TCA TTC TCG	3032
Leu Leu Gln Glu Ile Thr Ser Asn Thr Thr Thr Ile Gln Ser Phe Ser	
980 985 990	
CAA ACC TTA CGG CAG CTT TTA GGG GAT AAA ACA TTC TTT ATG GCG CAA	3080
Gln Thr Leu Arg Gln Leu Leu Gly Asp Lys Thr Phe Phe Met Ala Gln	
995 1000 1005 1010	
CAA AAG CTC ATT GAT GCG ATG ATT AAC GCC AGA AAT CAG GTT CAA AAC	3128
Gln Lys Leu Ile Asp Ala Met Ile Asn Ala Arg Asn Gln Val Gln Asn	
1015 1020 1025	
GCG CAA AAT CAA GCC AAT AAC TAC GGC TCT CAA CCC GTT TTA AGC CAG	3176
Ala Gln Asn Gln Ala Asn Asn Tyr Gly Ser Gln Pro Val Leu Ser Gln	
1030 1035 1040	
TAT GCG GCC GCT AAA AGC ACC CAA CAT GGC ATG AGC AAT GGT TTA GGG	3224
Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met Ser Asn Gly Leu Gly	
1045 1050 1055	
GTT GGT TTG GGC TAT AAA TAC TTC TTT GGT AAA GCG AGA AAA TTA GGC	3272
Val Gly Leu Gly Tyr Lys Tyr Phe Phe Gly Lys Ala Arg Lys Leu Gly	
1060 1065 1070	
CTT AGG CAT TAT TTT TTC TTT GAT TAC GGC TTT AGT GAA ATA GGC CTA	3320
Leu Arg His Tyr Phe Phe Phe Asp Tyr Gly Phe Ser Glu Ile Gly Leu	
1075 1080 1085 1090	

TTA CGC ATC CAA TTG AGG GCG AAT TTT TAC CAG CTC ATC AAT ACC ATT	2024
Leu Arg Ile Gln Leu Arg Ala Asn Phe Tyr Gln Leu Ile Asn Thr Ile	
645 650 655	
AAC CAG CAA GTG CCT ACA GAC ATG AAT GCT TTA ATT AAT CAA AGC CAA	2072
Asn Gln Gln Val Pro Thr Asp Met Asn Ala Leu Ile Asn Gln Ser Gln	
660 665 670	
CAA ACC CAA CAA ACA AGC GGA TCA GCA AGC AAT AAT AAC GCA TGC GCG	2120
Gln Thr Gln Gln Thr Ser Gly Ser Ala Ser Asn Asn Asn Ala Cys Ala	
675 680 685 690	
AGT GGA ATG AGT GGG AGT AAT GGT AAC TGG TGC TAT CAG CAA TGG TCC	2168
Ser Gly Met Ser Gly Ser Asn Gly Asn Trp Cys Tyr Gln Gln Trp Ser	
695 700 705	
GAT TCT AAG GCT TAT TAC AGC GGG TTG CAA AGC GCT TTA GGG TAT CAA	2216
Asp Ser Lys Ala Tyr Tyr Ser Gly Leu Gln Ser Ala Leu Gly Tyr Gln	
710 715 720	
ACG CAA GCG ACA ACT CAA AGC GGG AGC AAT GGT GGG AAC AGC ATC ACC	2264
Thr Gln Ala Thr Thr Gln Ser Gly Ser Asn Gly Gly Asn Ser Ile Thr	
725 730 735	
TAC AAT GTC CAA CAA ATC ACG CTC ACT AGT AAT GGT TTG CTC AAC CAA	2312
Tyr Asn Val Gln Gln Ile Thr Leu Thr Ser Asn Gly Leu Leu Asn Gln	
740 745 750	
ATC ATC ACA AAT CTT AAG AGC GTT AAT GGA GGC AAT GGC GCG AGT GGT	2360
Ile Ile Thr Asn Leu Lys Ser Val Asn Gly Gly Asn Gly Ala Ser Gly	
755 760 765 770	
ACA GGC AGT GGG AAT GGC ACC AGT CAA ATC AAC ACA GCC TAC CAG ATG	2408
Thr Gly Ser Gly Asn Gly Thr Ser Gln Ile Asn Thr Ala Tyr Gln Met	
775 780 785	
CTC ACA GAC GCC AGC GAT GGG AAA TTA GGG ACT TAT AGT AGT AGT AGT	2456
Leu Thr Asp Ala Ser Asp Gly Lys Leu Gly Thr Tyr Ser Ser Ser Ser	
790 795 800	
GGC AGT AAT AAC GGC TAT ACG CCA TGC AAT AGC ACC AAT GGG AGC AAT	2504
Gly Ser Asn Asn Gly Tyr Thr Pro Cys Asn Ser Thr Asn Gly Ser Asn	
805 810 815	
AAA ACG AGT GGG AAC AAT TGT TAT GAA CCC AAC AAA CAA CAA AAC GCC	2552
Lys Thr Ser Gly Asn Asn Cys Tyr Glu Pro Asn Lys Gln Gln Asn Ala	
820 825 830	
ACC ACC GCA ACC GCC ACA ACC GAC AGC AAT TTA CAA AAA GTC TAT AAT	2600
Thr Thr Ala Thr Ala Thr Thr Asp Ser Asn Leu Gln Lys Val Tyr Asn	
835 840 845 850	
GAC GCC CAA AAA ATA GCC AAC ATT ATC GCC AGC TCT GGG AAC AAT AAA	2648
Asp Ala Gln Lys Ile Ala Asn Ile Ile Ala Ser Ser Gly Asn Asn Lys	
855 860 865	

CAA AAT ATC AGC GCC TAT GAT TGC ATG ACT GCT ACC GGA AGC CTT TCT	1352
Gln Asn Ile Ser Ala Tyr Asp Cys Met Thr Ala Thr Gly Ser Leu Ser	
420 425 430	
AGC AAT GCT TCT AGC GGG ATT TCA TGC TCA GCC ACA AGC TCC ACA AGT	1400
Ser Asn Ala Ser Ser Gly Ile Ser Cys Ser Ala Thr Ser Ser Thr Ser	
435 440 445 450	
TCC ACA AAT AGC TTT GAC AAT TCT TTA GTC GCT ACC TCC AAA GTC CAA	1448
Ser Thr Asn Ser Phe Asp Asn Ser Leu Val Ala Thr Ser Lys Val Gln	
455 460 465	
ACC ATC AAC GGC AAA GAG CAG ATC GGC GTG AAT TCT TTT AAC CTT GTC	1496
Thr Ile Asn Gly Lys Glu Gln Ile Gly Val Asn Ser Phe Asn Leu Val	
470 475 480	
TCT CAA GTG TGG AGC GTT TAT AAT TCT TTA AAA ACT TCA GAA GAA AAT	1544
Ser Gln Val Trp Ser Val Tyr Asn Ser Leu Lys Thr Ser Glu Glu Asn	
485 490 495	
TTG CAA AAA AAC GCC AAT ATT TTA TGC GCT AAT GGG ACG CAA TCT GGG	1592
Leu Gln Lys Asn Ala Asn Ile Leu Cys Ala Asn Gly Thr Gln Ser Gly	
500 505 510	
ACA AGC TCA TGC AAT AGC TCT TCA GGG GGT TTG AGC ATC AGC GGG AAC	1640
Thr Ser Ser Cys Asn Ser Ser Ser Gly Gly Leu Ser Ile Ser Gly Asn	
515 520 525 530	
GCC CAA TTG CAA AAT ATT TTA AGC CCT ACT AGT GGG ACT ACC ACT AAT	1688
Ala Gln Leu Gln Asn Ile Leu Ser Pro Thr Ser Gly Thr Thr Thr Asn	
535 540 545	
ACT CAA GCT AAA AGC AAC GCT CCC AAA CTA AAA GCG ATG GTG GTG GTG	1736
Thr Gln Ala Lys Ser Asn Ala Pro Lys Leu Lys Ala Met Val Val Val	
550 555 560	
AAT AAT GAA GAA GAA GCT AAA ACG GCC AAT TTA GCC CAA AGC AGC GGG	1784
Asn Asn Glu Glu Glu Ala Lys Thr Ala Asn Leu Ala Gln Ser Ser Gly	
565 570 575	
ACA ACC ACA CAA TCT CCT AAC AGC ACG GTG ATG GGA GCT TTA AAC ACC	1832
Thr Thr Thr Gln Ser Pro Asn Ser Thr Val Met Gly Ala Leu Asn Thr	
580 585 590	
GTG TTG CAA AAT GTC AGC AAT TTC CAA CAA AGC ATT CAA AAC GCT TTT	1880
Val Leu Gln Asn Val Ser Asn Phe Gln Gln Ser Ile Gln Asn Ala Phe	
595 600 605 610	
CAA AAC CAA GAA AGT AAT ATC CAA GCT TGG GCG AAT GCG ATT TAT AAC	1928
Gln Asn Gln Glu Ser Asn Ile Gln Ala Trp Ala Asn Ala Ile Tyr Asn	
615 620 625	
ACT AAT GGG AGT CAG TCG CAA GAG ATG ACA CCT AAC AAT AAC CAA GAT	1976
Thr Asn Gly Ser Gln Ser Gln Glu Met Thr Pro Asn Asn Asn Gln Asp	
630 635 640	

Glu	His	Ser	Ile	Thr	Lys	Thr	Thr	Ser	Thr	Thr	Tyr	Ala	Gln	Ser	Leu	
195					200					205					210	
CTC	TCC	AAT	CTA	ACC	GAT	GCG	GTG	AAT	GCC	TCT	AGC	AAT	AAT	ACC	GCT	728
Leu	Ser	Asn	Leu	Thr	Asp	Ala	Val	Asn	Ala	Ser	Ser	Asn	Asn	Thr	Ala	
			215					220						225		
TAT	GTG	AGC	GCT	CTT	GTT	AAC	GCT	TTA	AAC	ACT	TTA	GGG	GTA	GGG	GTT	776
Tyr	Val	Ser	Ala	Leu	Val	Asn	Ala	Leu	Asn	Thr	Leu	Gly	Val	Gly	Val	
			230					235					240			
TTC	CCC	ACC	ACA	ACC	ACA	ACG	CAT	GTG	GTG	TTA	AAC	CCA	CCG	GGA	CAA	824
Phe	Pro	Thr	Thr	Thr	Thr	Thr	His	Val	Val	Leu	Asn	Pro	Pro	Gly	Gln	
		245					250					255				
GTC	GTA	TTC	TAT	CCA	ACC	AAT	TCC	ATT	TTA	GGC	TCT	ACT	TCT	TCA	AAC	872
Val	Val	Phe	Tyr	Pro	Thr	Asn	Ser	Ile	Leu	Gly	Ser	Thr	Ser	Ser	Asn	
	260					265					270					
AGC	AAT	AAC	CAA	CAA	CAA	TAC	AAC	AAC	ACC	CTT	TTA	ATG	AAC	ACC	TTA	920
Ser	Asn	Asn	Gln	Gln	Gln	Tyr	Asn	Asn	Thr	Leu	Leu	Met	Asn	Thr	Leu	
275					280				285						290	
CAA	GGG	ACA	TTA	AGC	GCT	AAT	ACT	CAA	AAT	AAC	CCC	AAT	GGT	TGC	GCC	968
Gln	Gly	Thr	Leu	Ser	Ala	Asn	Thr	Gln	Asn	Asn	Pro	Asn	Gly	Cys	Ala	
			295					300						305		
AAT	CAA	GTC	CAG	TGT	TTG	GAG	CAA	TTC	ATC	CAA	AAT	TTA	GCC	CCT	TTA	1016
Asn	Gln	Val	Gln	Cys	Leu	Glu	Gln	Phe	Ile	Gln	Asn	Leu	Ala	Pro	Leu	
		310						315					320			
GCC	GCA	ACC	CCC	ACT	TCA	AAC	AAC	CAG	GCC	AAC	CAG	CAA	GTC	CAA	GCC	1064
Ala	Ala	Thr	Pro	Thr	Ser	Asn	Asn	Gln	Ala	Asn	Gln	Gln	Val	Gln	Ala	
		325					330					335				
ATC	GCT	CAA	AAG	CTT	CAA	AGC	GTT	GCT	ATC	AAC	ACT	TTA	GAC	AAC	AAT	1112
Ile	Ala	Gln	Lys	Leu	Gln	Ser	Val	Ala	Ile	Asn	Thr	Leu	Asp	Asn	Asn	
	340					345					350					
GCG	ATC	AAC	AAC	ACC	ACC	TAT	AAT	TTA	AAC	AAT	TTG	CAC	AAC	GCT	TTG	1160
Ala	Ile	Asn	Asn	Thr	Thr	Tyr	Asn	Leu	Asn	Asn	Leu	His	Asn	Ala	Leu	
355				360					365					370		
AAT	TTC	CAA	GCC	TAT	GAA	AGC	ACG	ATA	GAA	CAA	TAC	AAT	AAC	GCT	TTA	1208
Asn	Phe	Gln	Ala	Tyr	Glu	Ser	Thr	Ile	Glu	Gln	Tyr	Asn	Asn	Ala	Leu	
			375					380						385		
AAA	CAA	ATT	TCT	TGG	ATC	AGT	TTT	ACT	GAG	CCT	AAA	AAC	TTA	CTC	AAA	1256
Lys	Gln	Ile	Ser	Trp	Ile	Ser	Phe	Thr	Glu	Pro	Lys	Asn	Leu	Leu	Lys	
		390						395					400			
AAC	ACT	TCC	AAT	AAC	TAC	CAA	ATC	GGC	ACC	GTT	ACC	AAC	GCT	CAA	GGG	1304
Asn	Thr	Ser	Asn	Asn	Tyr	Gln	Ile	Gly	Thr	Val	Thr	Asn	Ala	Gln	Gly	
		405					410						415			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TTATGTGGGC TACAACATAG GCTTTTGGATT AAACAAAATA AGGGAAAAAT ATG ATA	56
Met Ile	
1	
AAA AAA GCT AGA AAA TTC ATA CCA TTC TTT TTA ATT GGC TCC CTC TTA	104
Lys Lys Ala Arg Lys Phe Ile Pro Phe Phe Leu Ile Gly Ser Leu Leu	
5 10 15	
GCT GAA GAC AAT GGC TGG TAT ATG TCT GTA GGC TAT CAA ATC GGT GGC	152
Ala Glu Asp Asn Gly Trp Tyr Met Ser Val Gly Tyr Gln Ile Gly Gly	
20 25 30	
ACG CAA CAA TTC ATC AAT AAC AAA CAA CTT TTA GAA AAT CAA AAT ATC	200
Thr Gln Gln Phe Ile Asn Asn Lys Gln Leu Leu Glu Asn Gln Asn Ile	
35 40 45 50	
ATC AAC AGC GTA ACC CAA AGC GCG ATC AAC ATT GCA GGG CCT ACT ACC	248
Ile Asn Ser Val Thr Gln Ser Ala Ile Asn Ile Ala Gly Pro Thr Thr	
55 60 65	
GGC CTT ATC ACT TTA AGC TCT CAA ACC GTC ATT GAC GCT TTA GGC TAT	296
Gly Leu Ile Thr Leu Ser Ser Gln Thr Val Ile Asp Ala Leu Gly Tyr	
70 75 80	
GGC GTG AGT AAC ACT GTT GGC AAC CAA TTA GAG GGC ATT TCT AAT ATC	344
Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser Asn Ile	
85 90 95	
TTG AAT CAA ATT GGC AAA AGA AAA GAC TTT TAT TCT AGC CGT CAA ATC	392
Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg Gln Ile	
100 105 110	
TCT AGC ATT TCC CAA CAA ATC ATA GGG CTT AAA GGA AGC TCT GAT CCC	440
Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser Asp Pro	
115 120 125 130	
TTA AAA GCC CAT TCT TCA CAG ATC ACA GCC AAA CTC CTT TCC AAC ACC	488
Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser Asn Thr	
135 140 145	
CAA AGC GCG TTT GAT CAG GGC ATC GCG CTA AGC ACT AAC ATC ATT AGC	536
Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile Ile Ser	
150 155 160	
TCT ATC AAT AGC CTA AAC CCT AGC AAC AAC ACC CAA GAG GTT AAA AAA	584
Ser Ile Asn Ser Leu Asn Pro Ser Asn Asn Thr Gln Glu Val Lys Lys	
165 170 175	
CAG CTC CAA AAC ACC GCG CAA TCC ATG ACA GAA TTG TTG CAA CAA ATT	632
Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln Gln Ile	
180 185 190	
GAA CAC AGC ATC ACT AAA ACC ACT AGC ACC ACT TAC GCG CAA TCC TTA	680

```

Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu Leu
      165      170      175
Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp Glu
      180      185      190
Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu Thr
      195      200      205
Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr His
      210      215      220
Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys Val
      225      230      235      240
Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu Phe
      245      250      255
Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu Glu
      260      265      270
Lys Thr Asn Ile Lys Gln Val Ile Ile Leu Thr His Asn Thr Tyr Phe
      275      280      285
Tyr Lys Glu Ile Thr Leu Glu Cys Asp Leu Lys Arg Tyr Gln Gly Lys
      290      295      300
Tyr Ser Phe Trp Ile Ile Lys Lys Asp Asn Asn Val Ser Lys Ile Lys
      305      310      315      320
Asp Tyr Lys Glu Asn Pro Ile Lys Asn Ser Tyr Glu Leu Leu Trp Gln
      325      330      335
Glu Val Lys Gln Ala Lys Glu Asn Asn Ala Ser Trp Val Ser Leu Gln
      340      345      350
Asn Val Met Arg Arg Ile Ile Glu Tyr Tyr Phe Arg Ile Leu Gly Gly
      355      360      365
Phe Lys His Asn Asp Ser Leu Ser Glu Cys Phe Glu Asn Ile Glu Glu
      370      375      380
Lys Arg Val Cys Asn Ser Phe Ile Ser Trp Phe Asn Asp Gly Ser His
      385      390      395      400
Gly Ile Ser Asp Asp Leu Phe Met Gln Ser Gln Asp Thr Ser Ile Glu
      405      410      415
Thr Tyr Leu Lys Val Phe Glu Lys Ile Phe Lys Glu Thr Gly His Glu
      420      425      430
Ala His Tyr Lys Met Met Met Arg Met Lys
      435      440

```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...3740
- (D) OTHER INFORMATION:

```

GGT TTT AAA CAT AAT GAT AGC TTG AGT GAA TGT TTT GAA AAT ATT GAA      2114
Gly Phe Lys His Asn Asp Ser Leu Ser Glu Cys Phe Glu Asn Ile Glu
      370                      375                      380

GAA AAA CGA GTG TGT AAT TCT TTC ATT TCA TGG TTT AAT GAT GGC TCT      2162
Glu Lys Arg Val Cys Asn Ser Phe Ile Ser Trp Phe Asn Asp Gly Ser
      385                      390                      395

CAT GGG ATT TCA GAT GAT TTG TTT ATG CAA AGT CAA GAT ACA AGT ATT      2210
His Gly Ile Ser Asp Asp Leu Phe Met Gln Ser Gln Asp Thr Ser Ile
      400                      405                      410                      415

GAG ACA TAT TTA AAA GTT TTT GAA AAA ATA TTT AAA GAA ACC GGT CAT      2258
Glu Thr Tyr Leu Lys Val Phe Glu Lys Ile Phe Lys Glu Thr Gly His
      420                      425                      430

GAA GCT CAT TAT AAA ATG ATG ATG AGA ATG AAG TAATTGAATT AAAAACAAGG      2311
Glu Ala His Tyr Lys Met Met Met Arg Met Lys
      435                      440

AATAACATGC GAATCGTATT TATGGGAACG      2341

```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu Asp
 1           5           10           15
Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp Thr
      20           25           30
Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn Gly
      35           40           45
Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn Phe
      50           55           60
Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu Ile
      65           70           75           80
Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys Asp
      85           90           95
Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe Leu
      100          105          110
Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr Cys
      115          120          125
Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu Asn
      130          135          140
Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu Lys
      145          150          155          160

```


AAT CAA GAA GAG GTA AAG AAA TTA GAA AAT GAA ATT AAG GAA TTA GAA	1442
Asn Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu	
145 150 155	
AAA ACT ATG GTA AGC ATA AAG CCC ATT GTC AAT GAA ATC AAT ACG CTT	1490
Lys Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu	
160 165 170 175	
TTA AAA GGG TAT GGA TTC GCG AAT TTT AGT TTG GCA TGC ACT GAA GAT	1538
Leu Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp	
180 185 190	
GAA AAA TTT TAT CGT ATT CAA AGA GAA GAT GGT CAA TTA GTA GGA GAA	1586
Glu Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu	
195 200 205	
ACA CTG AGC GAG GGT GAA GTT ACT TTC ATC ACT TTC TTA TAT TAT TAT	1634
Thr Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr	
210 215 220	
CAT TTA GCA AAA GGC TCT TTA GAA GAG AAC GAT ATA TCA AAA AAT AAG	1682
His Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys	
225 230 235	
GTT TTA GTG ATT GAT GAC CCC ATT TCA AGT TTG GAT AGC AAT ATA TTG	1730
Val Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu	
240 245 250 255	
TTT ATA GTG AGT GTT TTA GTT AAA GAT CTT ATG AAA GAA GCC ATG GAA	1778
Phe Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu	
260 265 270	
GAA AAA ACA AAC ATC AAG CAA GTT ATT ATA CTA ACC CAC AAC ACA TAT	1826
Glu Lys Thr Asn Ile Lys Gln Val Ile Ile Leu Thr His Asn Thr Tyr	
275 280 285	
TTT TAC AAG GAA ATT ACA TTA GAA TGT GAT TTA AAA CGC TAT CAA GGG	1874
Phe Tyr Lys Glu Ile Thr Leu Glu Cys Asp Leu Lys Arg Tyr Gln Gly	
290 295 300	
AAA TAT TCT TTT TGG ATA ATT AAA AAG GAT AAT AAT GTT TCA AAA ATT	1922
Lys Tyr Ser Phe Trp Ile Ile Lys Lys Asp Asn Asn Val Ser Lys Ile	
305 310 315	
AAA GAT TAT AAA GAA AAT CCC ATT AAA AAT TCC TAT GAA TTG CTA TGG	1970
Lys Asp Tyr Lys Glu Asn Pro Ile Lys Asn Ser Tyr Glu Leu Leu Trp	
320 325 330 335	
CAA GAA GTA AAA CAA GCA AAA GAA AAT AAT GCT TCT TGG GTA TCT TTA	2018
Gln Glu Val Lys Gln Ala Lys Glu Asn Asn Ala Ser Trp Val Ser Leu	
340 345 350	
CAA AAT GTT ATG CGA AGA ATT ATT GAG TAT TAC TTT AGG ATT TTA GGC	2066
Gln Asn Val Met Arg Arg Ile Ile Glu Tyr Tyr Phe Arg Ile Leu Gly	
355 360 365	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ATTGTGAATT	AGGAGTGAGC	GTGAATAGTA	ATGGCAATAA	AGACAAACAA	CAGCAGAATG	60
TAAGCAGTGG	GATTTCTCAA	ATCTCATTA	AAAAGGTGGC	AAC TTTTGAT	GAAAATGGGG	120
CGAGTTTTGA	GAATTTAAAT	TCTATCAACT	TTATTTATGG	GGCTAATGGG	AGCGGTAAGA	180
CAACCACTTC	TAGTTTTTTA	AAAAATCTAG	CTGAAAATGG	GATTGAAGAC	AAGTTTGCTA	240
ATAGTAAAAT	AGCATGGTAT	AACAATGAGA	GTTTAAAGAT	TGAAGTTTAT	AACAAGCAAT	300
TTAAAGAAGA	GCAATTGAGA	AACTCTCAAG	TTAAAGGCAT	TTTTACGCTC	GGTAAAAAAA	360
CGAACGAGAA	TTTAGAAAAA	ATTGAAAGCA	AGAAAGAATC	AATAAACAAA	GAGAATGAAA	420
AGAAAATAAA	AAATGAAGCA	AGCTTGCAAG	TTTTAACACA	AAAAAAGGAA	AAGGAAGAAA	480
AGGATTTTGC	TGATAGGTGT	TGGGAAAAAC	TTTATAAGAA	AAATGAAGAG	GATTTTAAAG	540
AAACGCTAGA	AGGCTTTAAG	CGTAAAGAGA	AGTTTAAAGA	AAAAATCCTT	AAGGAATTTG	600
AAAACGATAA	ATACAATCAA	AGCGAAATAG	TAGGGTTAGA	AAAAATTAAAG	AAAAAAATTG	660
AGATTGTTTT	TGGTGAAAAC	CAAACAGAAT	TGGCACTATT	GGAATGCAAT	TTAACAGATT	720
TTGATTTTAT	TGAAAATCAT	TCTATTTGGG	AACAAAAAAT	TGTAGGGAGT	GGTGATGCAG	780
CCATTGCAGA	TTTAATAAAA	AGATTAAGCA	ATGAAGATTG	GGTAGCTCAA	GGTAGAGAAT	840
ATATAAAAGA	TAATAGTATA	TGCCCTTTCT	GTCAAAAAGA	AACCATTACC	GAAGAATTTA	900
AAAAACAAC	AGAATCTTAT	TTTGATACAA	GTTATCAAGA	ATCTATTGAA	ACGATCAAGG	960
AAAAG ATG GAA GAC TAC GCA AGC AGA ACC GCT GGA GCA CTG GAG CGA CTT						1010
Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu						
1	5		10		15	
GAT AAG ATT GTT GAA ACA GAA CAG AAG AAT CAA CAA ACT AAA TTG GAC						1058
Asp Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp						
	20		25		30	
ACA GAA AAT TTG AAA ATA ATT ATT GAA ACT TTG AGA AGT AAA ATC AAT						1106
Thr Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn						
	35		40		45	
GGG AAT CAG CAA AAG ATG CTT GAT AAA AGT AAA GAA ATG AGC AGA AAT						1154
Gly Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn						
	50		55		60	
TTT AAG CTT GAT AGC ACT AAA AAC GAG ATA GAC GCA ATT AAA GAT TTG						1202
Phe Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu						
	65		70		75	
ATT AAA AAG GCT AAT GAG CAA ATA GCC AAT TAT AAT GAG ATG ATA AAG						1250
Ile Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys						
	80		85		90	95
GAT ATT GAA AAA CAG AAA AAG AGT TGT AAG GAA CAA ACT TGG AAA TTT						1298
Asp Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe						
	100		105		110	
CTA GTC AAT GAA TTT AAA AGT GAT ATA CAA GAA TAT AAT AAA AAG TAT						1346
Leu Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr						
	115		120		125	
TGC GGT TTG GAG AAA GGA ATA AAC AAT TTA GAG AAA GCA ATT AGT GAA						1394
Cys Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu						
	130		135		140	

165

170

GTCAGCATTT AGTAAATAGC AGAGAA

616

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met	Gly	Leu	Lys	Asn	Leu	Ser	Thr	Leu	Leu	Val	Phe	Leu	Phe	Phe	Cys
1				5				10					15		
Leu	Gly	Cys	Val	Ser	Asn	Phe	Asn	Glu	Asp	Thr	Tyr	Thr	Leu	Asp	Leu
			20					25					30		
Val	Leu	Glu	Lys	Lys	Ile	Gln	Ala	Ser	Arg	Lys	Gly	Glu	Ile	Thr	Gln
			35				40					45			
Asp	Asn	Val	Pro	Ile	Ile	Thr	Ala	Ile	Ala	Thr	His	Leu	Asn	Asp	Val
		50				55					60				
Asp	Ser	Gly	Thr	Tyr	Tyr	Asp	His	Glu	Tyr	Phe	Leu	Val	Glu	Ile	Phe
65					70					75				80	
Thr	Gln	Asn	Asn	Asp	Trp	Ile	Asp	Asp	Gly	Tyr	Ile	Ser	Tyr	Glu	Leu
			85						90					95	
Phe	Gly	Thr	Lys	Pro	Ile	Gly	Ser	Glu	Pro	Leu	Trp	Val	Arg	Glu	Ile
			100					105					110		
Thr	Lys	Asp	Glu	Phe	Asp	Gly	Ile	Leu	Glu	Thr	Thr	Asn	Arg	Trp	Ser
		115				120						125			
Arg	Ala	Phe	Leu	Leu	Ala	Phe	Asn	Lys	Leu	Asp	Tyr	Leu	Ala	Val	Gln
		130				135					140				
Glu	Ala	Lys	Leu	Glu	Leu	Asp	Ala	Tyr	Ser	Leu	Gly	Lys	Ile	Val	Phe
145					150					155				160	
Asn	Phe	Ala	Tyr	Gln	Val	Pro	Leu	Pro	Gln	Phe					
			165						170						

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 966...2291
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...563
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TATAATATAG ATTTTATTTT AGCTAAAAAT GGCATGGGTT TTAGCAAGGA ATG GGC	56
Met Gly	
1	
TTG AAA AAT CTC TCA ACA CTT CTG GTG TTT TTA TTC TTT TGT TTA GGG	104
Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys Leu Gly	
5 10 15	
TGT GTG AGC AAT TTT AAT GAA GAC ACT TAC ACG CTA GAC TTA GTT TTA	152
Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu Val Leu	
20 25 30	
GAA AAA AAG ATC CAA GCC AGC AGG AAA GGT GAA ATC ACC CAA GAT AAT	200
Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln Asp Asn	
35 40 45 50	
GTG CCT ATC ATC ACG GCT ATC GCT ACG CAT TTA AAC GAT GTG GAT AGC	248
Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val Asp Ser	
55 60 65	
GGC ACT TAC TAT GAC CAT GAG TAT TTT TTA GTG GAG ATT TTC ACG CAA	296
Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe Thr Gln	
70 75 80	
AAT AAC GAC TGG ATA GAT GAT GGC TAT ATT TCT TAT GAA CTT TTT GGC	344
Asn Asn Asp Trp Ile Asp Asp Gly Tyr Ile Ser Tyr Glu Leu Phe Gly	
85 90 95	
ACA AAA CCT ATA GGC TCA GAG CCT TTA TGG GTG CGA GAA ATC ACA AAA	392
Thr Lys Pro Ile Gly Ser Glu Pro Leu Trp Val Arg Glu Ile Thr Lys	
100 105 110	
GAT GAA TTT GAT GGC ATT TTA GAA ACC ACG AAC AGG TGG AGC AGA GCT	440
Asp Glu Phe Asp Gly Ile Leu Glu Thr Thr Asn Arg Trp Ser Arg Ala	
115 120 125 130	
TTT TTG CTC GCT TTT AAC AAA TTG GAT TAT TTA GCG GTT CAA GAA GCC	488
Phe Leu Leu Ala Phe Asn Lys Leu Asp Tyr Leu Ala Val Gln Glu Ala	
135 140 145	
AAA CTA GAG CTT GAT GCC TAT AGT TTG GGC AAG ATT GTT TTT AAT TTC	536
Lys Leu Glu Leu Asp Ala Tyr Ser Leu Gly Lys Ile Val Phe Asn Phe	
150 155 160	
GCT TAT CAA GTC CCC CTA CCT CAA TTT TAATGCGCTT AGATTACGCC TTATTCA	590
Ala Tyr Gln Val Pro Leu Pro Gln Phe	

```

Gln Asp Leu Leu Leu Phe His Pro Tyr Glu Ser Phe Glu Pro Val Ile
 290                295                300
Asp Leu Ile Glu Gln Ala Ala Ser Asp Pro Ala Thr Leu Ser Ile Lys
305                310                315                320
Met Thr Leu Tyr Arg Val Gly Lys His Ser Pro Ile Val Lys Ala Leu
                325                330                335
Ile Glu Ala Ala Ser Lys Ile Gln Val Ser Val Leu Val Glu Leu Lys
                340                345                350
Ala Arg Phe Asp Glu Glu Ser Asn Leu His Trp Ala Lys Ala Leu Glu
                355                360                365
Arg Ala Gly Ala Leu Val Val Tyr Gly Val Phe Lys Leu Lys Val His
                370                375                380
Ala Lys Met Leu Leu Ile Thr Lys Lys Thr Asp Asn Gln Leu Arg His
385                390                395                400
Phe Thr His Leu Ser Thr Gly Asn Tyr Asn Pro Leu Ser Ala Lys Val
                405                410                415
Tyr Thr Asp Val Ser Phe Phe Ser Ala Lys Asn Glu Ile Ala Asn Asp
                420                425                430
Ile Ile Lys Leu Phe His Ser Leu Leu Thr Ser Ser Ala Thr Asn Ser
                435                440                445
Ala Leu Glu Thr Leu Phe Met Ala Pro Lys Gln Ile Lys Pro Lys Ile
                450                455                460
Ile Glu Leu Ile Gln Asn Glu Met Asn His Gln Gln Glu Gly Tyr Ile
465                470                475                480
Ile Leu Lys Ala Asn Ala Leu Val Asp Ser Glu Ile Ile Glu Trp Leu
                485                490                495
Tyr Gln Ala Ser Gln Lys Gly Val Lys Ile Asp Leu Ile Ile Arg Gly
                500                505                510
Ile Cys Cys Leu Lys Pro Gln Val Lys Gly Leu Ser Glu Asn Ile Arg
                515                520                525
Val Tyr Ser Ile Val Gly Lys Tyr Leu Glu His Ala Arg Ile Tyr Tyr
                530                535                540
Phe Lys His Glu Asn Ile Tyr Phe Ser Ser Ala Asp Leu Met Pro Arg
545                550                555                560
Asn Leu Glu Arg Arg Val Glu Leu Leu Ile Pro Ala Thr Asn Pro Lys
                565                570                575
Ile Ala His Lys Leu Leu His Ile Leu Glu Ile Gln Leu Lys Asp Thr
                580                585                590
Leu Lys Arg Tyr Glu Leu Asn Ser Lys Gly Arg Tyr Ile Lys Val Ser
                595                600                605
Asn Pro Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala
        610                615                620
Leu Lys Thr Phe
625

```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

ACC TTT TAAGGGTTAT CGTTCAAATC ATAAAAGATA AGGATTTAAA TGCTTTATTC AT 1986
Thr Phe

T

1987

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```

Met Ile Arg Val Ala Gly Leu Lys Gln Leu Tyr Glu His Lys Ile Ala
 1             5             10             15
Ser Lys Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile
          20             25             30
Lys His Tyr Leu Ala His Glu Ile Glu Glu Arg Glu Leu Glu Phe Gln
          35             40             45
Lys Ile Gln Ala Leu Leu Phe Lys Lys Gly Leu Cys Ile Thr Pro Tyr
          50             55             60
Asn Glu Leu Asn Leu Glu Gln Lys Ala Lys Ala Lys Thr Tyr Phe Lys
65             70             75             80
Glu Gln Leu Tyr Ala Leu Val Leu Pro Phe Lys Leu Asp Ser Ser His
          85             90             95
Thr Phe Pro Pro Leu Ala Asn Leu Thr Phe Ala Leu Phe Ala Arg Ile
          100            105            110
Lys Asp Lys Glu Thr Gln Ile Ile Ser Tyr Ala Leu Ile Lys Leu Pro
          115            120            125
Ser Phe Ile Phe Arg Phe Val Glu Leu Glu Lys Gly Leu Phe Val Leu
          130            135            140
Ala Glu Glu Ile Val Glu Ala His Leu Glu Glu Leu Phe Leu Glu His
          145            150            155            160
Glu Ile Leu Asp Cys Met Ala Phe Arg Val Thr Cys Asp Ala Asp Ile
          165            170            175
Ala Ile Thr Glu Asp Glu Ala His Asp Tyr Ala Asp Leu Met Ser Lys
          180            185            190
Ser Leu Arg Lys Arg Asn Gln Gly Glu Ile Val Arg Leu Gln Thr Gln
          195            200            205
Lys Gly Ser Gln Glu Leu Leu Lys Thr Leu Leu Ala Ser Leu Arg Ser
          210            215            220
Phe Gln Thr His Ser Tyr Lys Lys His Lys Leu Thr Gly Met His Ile
          225            230            235            240
Tyr Lys Ser Ala Ile Met Leu Asn Leu Gly Asp Leu Trp Glu Leu Val
          245            250            255
Asn His Ser Asp Phe Lys Ala Leu Lys Ser Pro Asn Phe Thr Pro Lys
          260            265            270
Ile His Pro His Phe Asn Glu Asn Asp Leu Phe Lys Ser Ile Glu Lys
          275            280            285

```

CAT	TTA	AGC	ACG	GGC	AAT	TAC	AAC	CCT	TTG	AGC	GCT	AAA	GTC	TAT	ACC	1304
His	Leu	Ser	Thr	Gly	Asn	Tyr	Asn	Pro	Leu	Ser	Ala	Lys	Val	Tyr	Thr	
		405					410					415				
GAT	GTG	AGT	TTT	TTT	AGC	GCT	AAA	AAT	GAA	ATC	GCT	AAC	GAC	ATT	ATC	1352
Asp	Val	Ser	Phe	Phe	Ser	Ala	Lys	Asn	Glu	Ile	Ala	Asn	Asp	Ile	Ile	
	420					425					430					
AAG	CTT	TTC	CAT	TCC	TTG	CTC	ACT	AGC	AGC	GCG	ACT	AAT	AGC	GCA	TTA	1400
Lys	Leu	Phe	His	Ser	Leu	Leu	Thr	Ser	Ser	Ala	Thr	Asn	Ser	Ala	Leu	
435					440					445					450	
GAA	ACG	CTT	TTT	ATG	GCA	CCC	AAA	CAA	ATC	AAG	CCT	AAA	ATC	ATT	GAA	1448
Glu	Thr	Leu	Phe	Met	Ala	Pro	Lys	Gln	Ile	Lys	Pro	Lys	Ile	Ile	Glu	
				455				460							465	
CTC	ATT	CAA	AAT	GAA	ATG	AAT	CAC	CAA	CAA	GAA	GGC	TAT	ATC	ATT	TTA	1496
Leu	Ile	Gln	Asn	Glu	Met	Asn	His	Gln	Gln	Glu	Gly	Tyr	Ile	Ile	Leu	
		470						475					480			
AAA	GCC	AAC	GCC	CTA	GTG	GAT	AGC	GAA	ATC	ATT	GAA	TGG	CTC	TAT	CAA	1544
Lys	Ala	Asn	Ala	Leu	Val	Asp	Ser	Glu	Ile	Ile	Glu	Trp	Leu	Tyr	Gln	
	485					490					495					
GCC	TCT	CAA	AAA	GGG	GTT	AAA	ATT	GAT	CTC	ATT	ATT	AGA	GGG	ATT	TGC	1592
Ala	Ser	Gln	Lys	Gly	Val	Lys	Ile	Asp	Leu	Ile	Ile	Arg	Gly	Ile	Cys	
	500					505					510					
TGT	TTA	AAG	CCC	CAA	GTC	AAG	GGC	TTG	AGC	GAA	AAT	ATC	AGG	GTG	TAT	1640
Cys	Leu	Lys	Pro	Gln	Val	Lys	Gly	Leu	Ser	Glu	Asn	Ile	Arg	Val	Tyr	
515					520					525					530	
TCT	ATC	GTG	GGG	AAA	TAT	TTA	GAA	CAT	GCA	CGC	ATT	TAT	TAT	TTT	AAA	1688
Ser	Ile	Val	Gly	Lys	Tyr	Leu	Glu	His	Ala	Arg	Ile	Tyr	Tyr	Phe	Lys	
				535				540						545		
CAT	GAA	AAT	ATT	TAT	TTT	TCT	AGC	GCG	GAT	TTA	ATG	CCC	AGG	AAT	TTA	1736
His	Glu	Asn	Ile	Tyr	Phe	Ser	Ser	Ala	Asp	Leu	Met	Pro	Arg	Asn	Leu	
		550						555					560			
GAA	AGG	CGC	GTG	GAA	TTG	CTC	ATT	CCA	GCC	ACA	AAC	CCA	AAG	ATC	GCT	1784
Glu	Arg	Arg	Val	Glu	Leu	Leu	Ile	Pro	Ala	Thr	Asn	Pro	Lys	Ile	Ala	
	565					570						575				
CAT	AAA	TTG	TTG	CAT	ATT	TTA	GAA	ATC	CAA	CTC	AAA	GAC	ACC	TTA	AAA	1832
His	Lys	Leu	Leu	His	Ile	Leu	Glu	Ile	Gln	Leu	Lys	Asp	Thr	Leu	Lys	
	580					585					590					
CGC	TAC	GAG	TTA	AAT	TCT	AAA	GGC	CGT	TAC	ATT	AAA	GTT	TCA	AAC	CCT	1880
Arg	Tyr	Glu	Leu	Asn	Ser	Lys	Gly	Arg	Tyr	Ile	Lys	Val	Ser	Asn	Pro	
595					600					605					610	
AAC	GAT	CCT	TTA	AAT	TCG	CAG	GAT	TAT	TTT	GAA	AAA	CAA	GCC	CTT	AAA	1928
Asn	Asp	Pro	Leu	Asn	Ser	Gln	Asp	Tyr	Phe	Glu	Lys	Gln	Ala	Leu	Lys	
				615					620					625		

ACT GAA GAT GAA GCG CAT GAT TAT GCA GAT TTG ATG AGT AAG AGT TTG	632
Thr Glu Asp Glu Ala His Asp Tyr Ala Asp Leu Met Ser Lys Ser Leu	
180 185 190	
AGG AAA CGC AAT CAA GGC GAA ATC GTG CGC TTG CAA ACC CAA AAA GGG	680
Arg Lys Arg Asn Gln Gly Glu Ile Val Arg Leu Gln Thr Gln Lys Gly	
195 200 205 210	
AGT CAA GAG CTT TTA AAA ACC CTC TTA GCG TCT TTA AGG AGT TTT CAA	728
Ser Gln Glu Leu Leu Lys Thr Leu Leu Ala Ser Leu Arg Ser Phe Gln	
215 220 225	
ACC CAC TCT TAC AAA AAG CAC AAA CTC ACC GGC ATG CAT ATC TAT AAA	776
Thr His Ser Tyr Lys Lys His Lys Leu Thr Gly Met His Ile Tyr Lys	
230 235 240	
AGC GCG ATC ATG CTC AAT TTA GGG GAT TTG TGG GAA TTA GTC AAT CAT	824
Ser Ala Ile Met Leu Asn Leu Gly Asp Leu Trp Glu Leu Val Asn His	
245 250 255	
AGC GAT TTT AAA GCG CTC AAA TCG CCC AAT TTC ACA CCC AAA ATC CAC	872
Ser Asp Phe Lys Ala Leu Lys Ser Pro Asn Phe Thr Pro Lys Ile His	
260 265 270	
CCT CAT TTC AAT GAA AAC GAT CTT TTC AAA TCT ATA GAA AAA CAG GAT	920
Pro His Phe Asn Glu Asn Asp Leu Phe Lys Ser Ile Glu Lys Gln Asp	
275 280 285 290	
CTG TTG CTG TTT CAT CCT TAT GAA AGT TTT GAG CCT GTG ATT GAT TTA	968
Leu Leu Leu Phe His Pro Tyr Glu Ser Phe Glu Pro Val Ile Asp Leu	
295 300 305	
ATA GAG CAA GCC GCT AGC GAT CCA GCC ACC CTT TCT ATC AAA ATG ACG	1016
Ile Glu Gln Ala Ala Ser Asp Pro Ala Thr Leu Ser Ile Lys Met Thr	
310 315 320	
CTT TAT CGT GTG GGC AAG CAT TCC CCC ATT GTC AAA GCT TTG ATT GAA	1064
Leu Tyr Arg Val Gly Lys His Ser Pro Ile Val Lys Ala Leu Ile Glu	
325 330 335	
GCG GCG AGC AAG ATT CAA GTG AGC GTT TTA GTG GAA TTA AAA GCG CGC	1112
Ala Ala Ser Lys Ile Gln Val Ser Val Leu Val Glu Leu Lys Ala Arg	
340 345 350	
TTT GAT GAA GAG AGC AAT CTG CAC TGG GCA AAA GCT TTA GAA AGG GCG	1160
Phe Asp Glu Glu Ser Asn Leu His Trp Ala Lys Ala Leu Glu Arg Ala	
355 360 365 370	
GGC GCG TTA GTC GTT TAT GGC GTT TTC AAA CTC AAA GTG CAT GCT AAA	1208
Gly Ala Leu Val Val Tyr Gly Val Phe Lys Leu Lys Val His Ala Lys	
375 380 385	
ATG CTA TTG ATC ACT AAA AAA ACA GAC AAC CAA TTA CGC CAT TTC ACC	1256
Met Leu Leu Ile Thr Lys Lys Thr Asp Asn Gln Leu Arg His Phe Thr	
390 395 400	

(B) LOCATION: 51...1934

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCGCTTGAA ATTTTATGCC ATTTATGACA CGAATTTAGA CGAATTTTAC ATG ATA	56
Met Ile	
1	
AGA GTG GCA GGG CTT AAA CAA CTC TAT GAG CAT AAA ATC GCC TCT AAA	104
Arg Val Ala Gly Leu Lys Gln Leu Tyr Glu His Lys Ile Ala Ser Lys	
5 10 15	
GGC ATT GAT GGC GCA AGC CCT GAA GAA CAA TTA GAA AAA ATC AAG CAT	152
Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile Lys His	
20 25 30	
TAT TTA GCG CAT GAA ATT GAA GAA AGG GAG TTA GAA TTC CAA AAA ATC	200
Tyr Leu Ala His Glu Ile Glu Glu Arg Glu Leu Glu Phe Gln Lys Ile	
35 40 45 50	
CAA GCC CTA CTC TTT AAA AAA GGG CTT TGT ATC ACC CCC TAT AAT GAA	248
Gln Ala Leu Leu Phe Lys Lys Gly Leu Cys Ile Thr Pro Tyr Asn Glu	
55 60 65	
TTG AAT TTA GAG CAA AAA GCG AAG GCT AAA ACC TAT TTT AAA GAG CAG	296
Leu Asn Leu Glu Gln Lys Ala Lys Ala Lys Thr Tyr Phe Lys Glu Gln	
70 75 80	
CTT TAC GCG TTA GTT TTG CCT TTT AAA TTG GAT TCT TCA CAC ACT TTC	344
Leu Tyr Ala Leu Val Leu Pro Phe Lys Leu Asp Ser Ser His Thr Phe	
85 90 95	
CCG CCT TTA GCG AAT TTG ACT TTC GCG CTT TTT GCC CGC ATC AAA GAC	392
Pro Pro Leu Ala Asn Leu Thr Phe Ala Leu Phe Ala Arg Ile Lys Asp	
100 105 110	
AAA GAA ACC CAA ATT ATC TCC TAT GCG CTC ATC AAA CTC CCC TCT TTT	440
Lys Glu Thr Gln Ile Ile Ser Tyr Ala Leu Ile Lys Leu Pro Ser Phe	
115 120 125 130	
ATC TTC CGT TTT GTA GAG CTA GAA AAA GGC TTG TTT GTG TTA GCT GAA	488
Ile Phe Arg Phe Val Glu Leu Glu Lys Gly Leu Phe Val Leu Ala Glu	
135 140 145	
GAA ATC GTG GAA GCG CAT TTA GAA GAA TTG TTT TTA GAG CAT GAG ATT	536
Glu Ile Val Glu Ala His Leu Glu Glu Leu Phe Leu Glu His Glu Ile	
150 155 160	
TTA GAT TGC ATG GCG TTT AGG GTA ACT TGC GAT GCG GAT ATT GCT ATC	584
Leu Asp Cys Met Ala Phe Arg Val Thr Cys Asp Ala Asp Ile Ala Ile	
165 170 175	

Glu	Val	Asn	Asp	Pro	Leu	Gly	Met	Ser	Gly	Thr	Arg	Leu	Glu	Val	Phe
				165					170					175	
Ile	His	Ile	Val	Tyr	Thr	Glu	Lys	Asn	Asn	Ile	Glu	Asn	Leu	Glu	Lys
			180					185					190		
Ile	Met	Ile	Gln	Ser	Gly	Val	Glu	Ile	Glu	Asn	Ile	Val	Ile	Asn	Ser
		195					200					205			
Tyr	Ala	Ala	Ser	Ile	Ala	Thr	Leu	Ser	Asn	Asp	Glu	Arg	Glu	Leu	Gly
	210					215					220				
Val	Ala	Cys	Val	Asp	Met	Gly	Gly	Glu	Thr	Cys	Asn	Leu	Thr	Ile	Tyr
225					230					235					240
Ser	Gly	Asn	Ser	Ile	Arg	Tyr	Asn	Lys	Tyr	Leu	Pro	Val	Gly	Ser	His
			245					250						255	
His	Leu	Thr	Thr	Asp	Leu	Ser	His	Met	Leu	Asn	Thr	Pro	Phe	Pro	Tyr
			260					265						270	
Ala	Glu	Glu	Val	Lys	Ile	Lys	Tyr	Gly	Asp	Leu	Ser	Phe	Glu	Gly	Gly
		275					280					285			
Glu	Glu	Thr	Pro	Ser	Gln	Asn	Val	Gln	Ile	Pro	Thr	Thr	Gly	Ser	Asp
		290				295					300				
Gly	His	Glu	Ser	His	Ile	Val	Pro	Leu	Ser	Glu	Ile	Gln	Thr	Ile	Met
305					310					315					320
Arg	Glu	Arg	Ala	Leu	Glu	Thr	Phe	Lys	Ile	Ile	His	Arg	Ser	Ile	Gln
			325					330						335	
Asp	Ser	Gly	Leu	Glu	Glu	His	Leu	Gly	Gly	Gly	Val	Val	Leu	Thr	Gly
			340					345					350		
Gly	Met	Ala	Leu	Met	Lys	Gly	Ile	Lys	Glu	Leu	Ala	Arg	Thr	His	Phe
		355					360					365			
Thr	Asn	Tyr	Pro	Val	Arg	Leu	Ala	Ala	Pro	Val	Glu	Lys	Tyr	Asn	Ile
		370				375					380				
Met	Gly	Met	Phe	Glu	Asp	Leu	Lys	Asp	Pro	Arg	Phe	Ser	Val	Val	Val
385					390					395					400
Gly	Leu	Ile	Leu	Tyr	Lys	Ala	Gly	Gly	His	Thr	Asn	Tyr	Glu	Arg	Asp
			405						410					415	
Ser	Lys	Gly	Val	Ile	Arg	Tyr	His	Glu	Ser	Asp	Asp	Tyr	Thr	Arg	Thr
			420					425					430		
Ala	His	Gln	Ser	Ser	Pro	Thr	Pro	His	Ile	His	Ser	Ser	Pro	Thr	Glu
		435					440					445			
Arg	Asn	Leu	Ser	Asp	Leu	Lys	Ala	Pro	Ser	Ala	Pro	Leu	Asn	Thr	Ala
		450				455					460				
Lys	Asn	Asp	Asp	Phe	Leu	Pro	Ile	Lys	Pro	Thr	Glu	Gln	Lys	Gly	Phe
465					470					475					480
Phe	Lys	Ser	Phe	Leu	Asp	Lys	Ile	Ser	Lys	Phe	Phe				
				485					490						

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

GGG GTT ATC CGC TAC CAT GAA AGC GAT GAT TAC ACA AGA ACA GCC CAT 1352
 Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr Ala His
 420 425 430

CAA TCA AGC CCT ACC CCC CAT ATC CAT TCA TCG CCC ACA GAA AGG AAT 1400
 Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu Arg Asn
 435 440 445 450

TTG AGC GAT TTA AAA GCC CCT AGT GCT CCT TTA AAC ACC GCT AAA AAC 1448
 Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala Lys Asn
 455 460 465

GAT GAC TTT TTA CCT ATA AAA CCC ACC GAA CAA AAA GGT TTT TTT AAA 1496
 Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys
 470 475 480

AGT TTC CTT GAT AAG ATT TCT AAA TTC TTT TAAGATACAG CCATTTCTTT ATG 1549
 Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe
 485 490

CGATAAAAAC GCCTTGATGG TTATCAAAAG 1579

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Glu His Lys Glu Ile Val Ile Gly Val Asp Leu Gly Ser Arg Lys
 1 5 10 15
 Ile Cys Ala Ile Val Ala Glu Phe Lys Glu Gly Ile Leu Arg Ile Ile
 20 25 30
 Gly Thr Ala His Gln Asp Ser Lys Glu Ile Asn Ser Lys Ala Ile Lys
 35 40 45
 Arg Gly Arg Ile Asn Ser Leu Ala His Ala Ser Asn Ala Ile Lys Glu
 50 55 60
 Val Ile Asn Ser Ala Lys Lys Met Ala Gly Leu Asn Ala Asp Glu Asp
 65 70 75 80
 Arg Asn Asn Pro Met Pro His Phe Gly Glu Tyr His Pro Lys Thr Lys
 85 90 95
 Ala Ile Val Ser Phe Ser Gly Ala Tyr Thr Glu Ser Ile Arg Asp Val
 100 105 110
 Thr Gly Val Ala Ser Thr Lys Asp Asn Val Val Thr Ile Asp Glu Ile
 115 120 125
 Asn Arg Ala Ile Asn Ser Ala Cys Ala Lys Ala Gly Leu Asp Asn Asp
 130 135 140
 Lys His Ile Leu His Ala Leu Pro Tyr Arg Phe Thr Leu Asp Lys Gln
 145 150 155 160

ATC CAA TCT GGG GTA GAG ATT GAA AAC ATC GTG ATC AAT TCT TAT GCA	680
Ile Gln Ser Gly Val Glu Ile Glu Asn Ile Val Ile Asn Ser Tyr Ala	
195 200 205 210	
GCC TCG ATT GCC ACC TTA TCT AAT GAT GAA AGG GAA TTG GGC GTG GCT	728
Ala Ser Ile Ala Thr Leu Ser Asn Asp Glu Arg Glu Leu Gly Val Ala	
215 220 225	
TGC GTG GAT ATG GGC GGA GAG ACA TGC AAC CTT ACG ATT TAT AGC GGC	776
Cys Val Asp Met Gly Gly Glu Thr Cys Asn Leu Thr Ile Tyr Ser Gly	
230 235 240	
AAT TCC ATA CGC TAT AAC AAA TAT TTG CCC GTA GGC TCT CAC CAT TTA	824
Asn Ser Ile Arg Tyr Asn Lys Tyr Leu Pro Val Gly Ser His His Leu	
245 250 255	
ACC ACG GAT TTA TCG CAC ATG CTC AAC ACC CCA TTC CCT TAC GCT GAA	872
Thr Thr Asp Leu Ser His Met Leu Asn Thr Pro Phe Pro Tyr Ala Glu	
260 265 270	
GAA GTT AAG ATC AAA TAC GGG GAT CTT TCT TTT GAA GGC GGC GAA GAA	920
Glu Val Lys Ile Lys Tyr Gly Asp Leu Ser Phe Glu Gly Gly Glu Glu	
275 280 285 290	
ACG CCC TCT CAA AAT GTC CAA ATC CCT ACC ACC GGC TCG GAT GGC CAT	968
Thr Pro Ser Gln Asn Val Gln Ile Pro Thr Thr Gly Ser Asp Gly His	
295 300 305	
GAA AGC CAT ATT GTG CCG CTT AGT GAA ATC CAA ACT ATC ATG AGA GAA	1016
Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met Arg Glu	
310 315 320	
AGG GCT TTA GAA ACT TTT AAA ATC ATC CAC AGG AGC ATT CAA GAT AGC	1064
Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln Asp Ser	
325 330 335	
GGC TTA GAA GAG CAT TTG GGC GGA GGC GTT GTG TTA ACC GGT GGG ATG	1112
Gly Leu Glu Glu His Leu Gly Gly Gly Val Val Leu Thr Gly Gly Met	
340 345 350	
GCT TTA ATG AAA GGG ATC AAA GAA TTA GCC AGA ACC CAT TTC ACT AAT	1160
Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe Thr Asn	
355 360 365 370	
TAC CCG GTG CGT TTG GCA GCC CCT GTG GAA AAA TAC AAT ATC ATG GGC	1208
Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile Met Gly	
375 380 385	
ATG TTT GAA GAT TTG AAA GAC CCT CGC TTT TCA GTC GTA GTT GGC TTG	1256
Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Gly Leu	
390 395 400	
ATT TTA TAC AAA GCA GGG GGG CAT ACC AAT TAT GAA AGA GAC TCT AAA	1304
Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp Ser Lys	
405 410 415	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAAAACGCTA TAAGATAGTC AAATACATTC AATAAATGCA AGGGGAAATC ATG GAA	56
Met Glu	
1	
CAT AAA GAA ATC GTT ATA GGG GTT GAT CTA GGC TCT AGA AAG ATT TGC	104
His Lys Glu Ile Val Ile Gly Val Asp Leu Gly Ser Arg Lys Ile Cys	
5 10 15	
GCG ATA GTG GCT GAA TTT AAA GAA GGG ATT TTG CGC ATC ATT GGC ACG	152
Ala Ile Val Ala Glu Phe Lys Glu Gly Ile Leu Arg Ile Ile Gly Thr	
20 25 30	
GCC CAT CAA GAC TCC AAA GAA ATC AAT TCA AAA GCC ATT AAA AGA GGG	200
Ala His Gln Asp Ser Lys Glu Ile Asn Ser Lys Ala Ile Lys Arg Gly	
35 40 45 50	
CGT ATC AAT AGC CTT GCT CAC GCT TCC AAC GCC ATT AAA GAA GTG ATT	248
Arg Ile Asn Ser Leu Ala His Ala Ser Asn Ala Ile Lys Glu Val Ile	
55 60 65	
AAT AGC GCT AAA AAA ATG GCA GGT TTG AAC GCT GAT GAA GAC AGA AAT	296
Asn Ser Ala Lys Lys Met Ala Gly Leu Asn Ala Asp Glu Asp Arg Asn	
70 75 80	
AAC CCC ATG CCC CAT TTT GGG GAA TAC CAC CCT AAA ACT AAG GCG ATT	344
Asn Pro Met Pro His Phe Gly Glu Tyr His Pro Lys Thr Lys Ala Ile	
85 90 95	
GTT TCT TTT TCT GGG GCT TAT ACT GAA AGC ATT AGA GAT GTT ACC GGT	392
Val Ser Phe Ser Gly Ala Tyr Thr Glu Ser Ile Arg Asp Val Thr Gly	
100 105 110	
GTA GCG AGC ACC AAA GAT AAT GTG GTA ACC ATT GAT GAA ATC AAT CGC	440
Val Ala Ser Thr Lys Asp Asn Val Val Thr Ile Asp Glu Ile Asn Arg	
115 120 125 130	
GCT ATC AAT AGT GCA TGC GCT AAA GCA GGC TTA GAT AAC GAC AAA CAT	488
Ala Ile Asn Ser Ala Cys Ala Lys Ala Gly Leu Asp Asn Asp Lys His	
135 140 145	
ATT TTG CAT GCT CTC CCC TAT CGC TTC ACT TTA GAC AAA CAA GAA GTG	536
Ile Leu His Ala Leu Pro Tyr Arg Phe Thr Leu Asp Lys Gln Glu Val	
150 155 160	
AAT GAC CCT TTA GGG ATG AGC GGG ACT CGC TTG GAA GTC TTT ATC CAC	584
Asn Asp Pro Leu Gly Met Ser Gly Thr Arg Leu Glu Val Phe Ile His	
165 170 175	
ATT GTC TAT ACA GAA AAA AAC AAC ATT GAA AAT TTA GAA AAA ATC ATG	632
Ile Val Tyr Thr Glu Lys Asn Asn Ile Glu Asn Leu Glu Lys Ile Met	
180 185 190	

Gly	Trp	Leu	Ser	Ile	Asp	Met	Tyr	His	Gln	Met	Leu	Lys	Asp	Gly	Met	
		115					120					125				
Asp	Phe	Trp	Tyr	Lys	Glu	Asp	Gly	Leu	Leu	Met	Ile	Tyr	Thr	Leu	Glu	
	130					135					140					
Glu	Ser	Phe	Glu	Lys	Lys	Leu	Lys	Thr	Cys	Asp	Asn	Ser	Gly	Ala	Tyr	
145					150					155					160	
Lys	Ile	Leu	Ser	Ala	Lys	Glu	Thr	Lys	Glu	Tyr	Met	Pro	Val	Val	Asn	
				165					170						175	
Asp	Asn	Ile	Cys	Gly	Ser	Val	Leu	Leu	Thr	Glu	Asn	Ala	His	Val	Asp	
			180					185					190			
Pro	Gly	Glu	Val	Met	His	Ser	Leu	Gln	Glu	Tyr	Leu	Gln	Asn	Val	Gly	
		195					200					205				
Val	Glu	Phe	Leu	Tyr	Asn	Glu	Glu	Val	Ile	Asp	Phe	Glu	Phe	Lys	Asn	
		210				215					220					
Asn	Leu	Ile	Glu	Gly	Val	Ile	Thr	His	Lys	Glu	Lys	Ile	Gln	Ala	Glu	
225					230					235					240	
Thr	Ile	Ile	Leu	Ala	Thr	Gly	Ala	Asn	Pro	Thr	Leu	Ile	Lys	Lys	Thr	
				245					250						255	
Lys	Asn	Asp	Phe	Leu	Met	Met	Gly	Ala	Lys	Gly	Tyr	Ser	Ile	Thr	Phe	
			260					265					270			
Lys	Met	Pro	Glu	Glu	Leu	Lys	Pro	Lys	Thr	Ser	Ser	Leu	Phe	Ala	Asp	
		275					280					285				
Ile	Phe	Met	Ala	Met	Thr	Pro	Arg	Arg	Asp	Thr	Val	Arg	Ile	Thr	Ser	
	290					295					300					
Lys	Leu	Glu	Leu	Asn	Thr	Asn	Asn	Ala	Leu	Ile	Asp	Lys	Glu	Gln	Ile	
305					310					315					320	
Ala	Asn	Met	Lys	Lys	Asn	Leu	Ala	Ala	Phe	Thr	Gln	Pro	Phe	Glu	Met	
				325					330						335	
Lys	Asp	Ala	Ile	Glu	Trp	Cys	Gly	Phe	Arg	Pro	Leu	Thr	Pro	Asn	Asp	
			340					345					350			
Ile	Pro	Tyr	Leu	Gly	Tyr	Asp	Lys	Arg	Tyr	Lys	Asn	Leu	Ile	His	Ala	
	355						360					365				
Thr	Gly	Leu	Gly	Trp	Leu	Gly	Ile	Thr	Phe	Gly	Pro	Ala	Ile	Gly	Lys	
	370					375					380					
Ile	Ile	Ala	Asn	Leu	Ser	Gln	Asp	Gly	Ala	Asn	Glu	Lys	Asn	Ala	Asp	
385					390					395					400	
Ile	Met	Leu	Phe	Ser	Ala	Phe	Phe	Arg	Asp							
				405				410								

(2) INFORMATION FOR SEO ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1526
(D) OTHER INFORMATION:

```

Leu Glu Leu Asn Thr Asn Asn Ala Leu Ile Asp Lys Glu Gln Ile Ala
      310                      315                      320

AAC ATG AAA AAG AAT TTA GCC GCT TTC ACG CAG CCT TTT GAA ATG AAA      1065
Asn Met Lys Lys Asn Leu Ala Ala Phe Thr Gln Pro Phe Glu Met Lys
      325                      330                      335

GAC GCC ATA GAG TGG TGC GGT TTC AGA CCC TTA ACC CCT AAT GAT ATT      1113
Asp Ala Ile Glu Trp Cys Gly Phe Arg Pro Leu Thr Pro Asn Asp Ile
      340                      345                      350

CCT TAT TTG GGC TAT GAC AAA CGC TAT AAA AAC TTA ATC CAT GCG ACA      1161
Pro Tyr Leu Gly Tyr Asp Lys Arg Tyr Lys Asn Leu Ile His Ala Thr
      355                      360                      365

GGG CTA GGG TGG CTT GGC ATC ACT TTT GGC CCA GCC ATT GGT AAA ATC      1209
Gly Leu Gly Trp Leu Gly Ile Thr Phe Gly Pro Ala Ile Gly Lys Ile
      370                      375                      380                      385

ATC GCC AAT TTG AGC CAA GAC GGA GCG AAT GAA AAA AAT GCC GAT ATT      1257
Ile Ala Asn Leu Ser Gln Asp Gly Ala Asn Glu Lys Asn Ala Asp Ile
      390                      395                      400

ATG CTT TTT TCT GCA TTT TTT AGG GAT TAAGGAATTT CTTTTTTAAA CCCTAGT      1311
Met Leu Phe Ser Ala Phe Phe Arg Asp
      405                      410

TTATTAAGGA GTTTTTATGG AAAC      1335

```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

Met Lys Lys Glu Val Val Val Ile Gly Gly Gly Ile Val Gly Leu Ser
 1                      5                      10                      15
Cys Ala Tyr Ser Met His Lys Leu Gly His Lys Val Cys Val Ile Glu
      20                      25                      30
Lys Asn Asp Gly Ala Asn Gly Thr Ser Phe Gly Asn Ala Gly Leu Ile
      35                      40                      45
Ser Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp
      50                      55                      60
Thr Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe
      65                      70                      75                      80
Gly Leu Asn Leu Lys Leu Tyr Gln Trp Ile Leu Lys Phe Val Lys Ser
      85                      90                      95
Ala Asn Ala Lys Ser Thr His Arg Thr Met Ala Leu Phe Glu Arg Tyr

```

-283-

Thr Phe Lys Val Asn Ala Ala His Asn Pro Leu Ser Thr His Ala Arg
 1235 1240 1245
 Val Met Met Gly Gly Glu Leu Lys Leu Ala Lys Glu Val Phe Leu Asn
 1250 1255 1260
 Leu Gly Phe Val Tyr Leu His Asn Leu Ile Ser Asn Ile Gly His Phe
 265 1270 1275 1280
 Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
 1285 1290

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...1284
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

TTAGTAGAAA TTGAAGCGAT AGCCATTAAG TAATTTATTA AAGGGACTAT CAGC	57
Met	
1	
AAA AAA GAG GTC GTG GTC ATA GGC GGT GGG ATT GTA GGG CTT TCT TGT	105
Lys Lys Glu Val Val Val Ile Gly Gly Gly Ile Val Gly Leu Ser Cys	
5 10 15	
GCG TAT TCT ATG CAC AAG TTA GGC CAT AAG GTC TGC GTG ATA GAA AAA	153
Ala Tyr Ser Met His Lys Leu Gly His Lys Val Cys Val Ile Glu Lys	
20 25 30	
AAC GAT GGC GCA AAC GGC ACT TCT TTT GGG AAT GCT GGG CTT ATT TCT	201
Asn Asp Gly Ala Asn Gly Thr Ser Phe Gly Asn Ala Gly Leu Ile Ser	
35 40 45	
GCG TTT AAA AAA GCC CCA CTC TCA TGC CCT GGT GTG GTG TTA GAC ACC	249
Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp Thr	
50 55 60 65	
CTG AAG CTC ATG CTC AAA AAC CAA GCC CCT TTA AAA TTC CAT TTC GGG	297
Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe Gly	
70 75 80	
CTT AAT TTA AAG CTC TAT CAA TGG ATT TTA AAA TTT GTA AAA AGC GCG	345
Leu Asn Leu Lys Leu Tyr Gln Trp Ile Leu Lys Phe Val Lys Ser Ala	

785					790					795				800	
Tyr	Lys	Tyr	Leu	Ile	Gly	Lys	Ala	Trp	Lys	Asn	Ile	Gly	Ile	Ser	Lys
				805					810					815	
Thr	Ala	Asn	Gly	Ser	Lys	Ile	Ser	Val	Tyr	Tyr	Leu	Gly	Asn	Ser	Thr
			820					825					830		
Pro	Thr	Glu	Lys	Gly	Gly	Asn	Thr	Thr	Asn	Leu	Pro	Thr	Asn	Thr	Thr
		835					840					845			
Ser	Asn	Val	Arg	Ser	Ala	Asn	Asn	Ala	Leu	Ala	Gln	Asn	Ala	Pro	Phe
	850					855					860				
Ala	Gln	Pro	Ser	Ala	Thr	Pro	Asn	Leu	Val	Ala	Ile	Asn	Gln	His	Asp
865					870				875						880
Phe	Gly	Thr	Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala	Asn	Arg	Ser	Lys	Asp
			885					890						895	
Ile	Asp	Thr	Leu	Tyr	Ala	Asn	Ser	Gly	Ala	Gln	Gly	Arg	Asp	Leu	Leu
			900					905					910		
Gln	Thr	Leu	Leu	Ile	Asp	Ser	His	Asp	Ala	Gly	Tyr	Ala	Arg	Gln	Met
		915					920					925			
Ile	Asp	Asn	Thr	Ser	Thr	Gly	Glu	Ile	Thr	Lys	Gln	Leu	Asn	Ala	Ala
	930					935					940				
Thr	Thr	Thr	Leu	Asn	Asn	Ile	Ala	Ser	Leu	Glu	His	Lys	Thr	Ser	Ser
945					950					955					960
Leu	Gln	Thr	Leu	Ser	Leu	Ser	Asn	Ala	Met	Ile	Leu	Asn	Ser	Arg	Leu
			965					970						975	
Val	Asn	Leu	Ser	Arg	Arg	His	Thr	Asn	Asn	Ile	Asp	Ser	Phe	Ala	Gln
		980						985					990		
Arg	Leu	Gln	Ala	Leu	Lys	Asp	Gln	Lys	Phe	Ala	Ser	Leu	Glu	Ser	Ala
		995				1000					1005				
Ala	Glu	Val	Leu	Tyr	Gln	Phe	Ala	Pro	Lys	Tyr	Glu	Lys	Pro	Thr	Asn
	1010					1015					1020				
Val	Trp	Ala	Asn	Ala	Ile	Gly	Gly	Thr	Ser	Leu	Asn	Asn	Gly	Gly	Asn
025					1030					1035					1040
Ala	Ser	Leu	Tyr	Gly	Thr	Ser	Ala	Gly	Val	Asp	Ala	Tyr	Leu	Asn	Gly
			1045					1050					1055		
Glu	Val	Glu	Ala	Ile	Val	Gly	Gly	Phe	Gly	Ser	Tyr	Gly	Tyr	Ser	Ser
		1060				1065						1070			
Phe	Asn	Asn	Gln	Ala	Asn	Ser	Leu	Asn	Ser	Gly	Ala	Asn	Asn	Thr	Asn
	1075					1080					1085				
Phe	Gly	Val	Tyr	Ser	Arg	Ile	Phe	Ala	Asn	Gln	His	Glu	Phe	Asp	Phe
	1090				1095						1100				
Glu	Ala	Gln	Gly	Ala	Leu	Gly	Ser	Asp	Gln	Ser	Ser	Leu	Asn	Phe	Lys
105					1110					1115				1120	
Ser	Ala	Leu	Leu	Arg	Asp	Leu	Asn	Gln	Ser	Tyr	Asn	Tyr	Leu	Ala	Tyr
			1125					1130					1135		
Ser	Ala	Ala	Thr	Arg	Ala	Ser	Tyr	Gly	Tyr	Asp	Phe	Ala	Phe	Phe	Arg
		1140					1145					1150			
Asn	Ala	Leu	Val	Leu	Lys	Pro	Ser	Val	Gly	Val	Ser	Tyr	Asn	His	Leu
	1155					1160					1165				
Gly	Ser	Thr	Asn	Phe	Lys	Ser	Asn	Ser	Asn	Gln	Val	Ala	Leu	Lys	Asn
	1170					1175					1180				
Gly	Ser	Ser	Ser	Gln	His	Leu	Phe	Asn	Ala	Ser	Ala	Asn	Val	Glu	Ala
185					1190					1195					1200
Arg	Tyr	Tyr	Tyr	Gly	Asp	Thr	Ser	Tyr	Phe	Tyr	Met	Asn	Ala	Gly	Val
			1205					1210					1215		
Leu	Gln	Glu	Phe	Ala	Asn	Phe	Gly	Ser	Ser	Asn	Ala	Val	Ser	Leu	Asn
		1220					1225					1230			

Asn Ser Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn
 355 360 365
 Ser Ala Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro
 370 375 380
 Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr
 385 390 395 400
 Asn Ala Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr
 405 410 415
 Thr Asn Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser
 420 425 430
 Asn Gln Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn
 435 440 445
 Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr
 450 455 460
 Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp
 465 470 475 480
 Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu Gly Arg
 485 490 495
 Phe Val Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile
 500 505 510
 Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr
 515 520 525
 Gly Lys Val Asn Ile Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala
 530 535 540
 Val Lys Asn Phe Asn Ile Asn Glu Leu Val Val Lys Thr Asn Gly Val
 545 550 555 560
 Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser
 565 570 575
 Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser
 580 585 590
 Gly Gly Val Lys Phe Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe
 595 600 605
 Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg Asn Ile Lys Asn Val
 610 615 620
 Glu Ile Thr Arg Lys Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly
 625 630 635 640
 Thr Ser Lys Leu Met Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val
 645 650 655
 Met Asp Tyr Ser Gln Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile
 660 665 670
 Asn Asn Gln Gly Thr Ile Asn Tyr Leu Val Arg Gly Gly Gln Val Ala
 675 680 685
 Thr Leu Asn Val Gly Asn Ala Ala Ala Met Phe Phe Ser Asn Asn Val
 690 695 700
 Asp Ser Ala Thr Gly Phe Tyr Gln Pro Leu Met Lys Ile Asn Ser Ala
 705 710 715 720
 Gln Asp Leu Ile Lys Asn Lys Glu His Val Leu Leu Lys Ala Lys Ile
 725 730 735
 Ile Gly Tyr Gly Asn Val Ser Leu Gly Thr Asn Ser Ile Ser Asn Val
 740 745 750
 Asn Leu Ile Glu Gln Phe Lys Glu Arg Leu Ala Leu Tyr Asn Asn Asn
 755 760 765
 Asn Arg Met Asp Ile Cys Val Val Arg Asn Thr Asp Asp Ile Lys Ala
 770 775 780
 Cys Gly Thr Ala Ile Gly Asn Gln Ser Met Val Asn Asn Pro Asp Asn

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
 1           5           10           15
Leu Ala Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His
          20           25           30
Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
          35           40           45
Ala Thr Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly
          50           55           60
Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65           70           75           80
Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
          85           90           95
Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
          100          105          110
Trp Asp Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln
          115          120          125
Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn
          130          135          140
Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
145          150          155          160
Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
          165          170          175
Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala
          180          185          190
Lys Asn Ile Leu Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly
          195          200          205
Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
          210          215          220
Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp
225          230          235          240
Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn
          245          250          255
Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
          260          265          270
Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn
          275          280          285
His Leu Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala
          290          295          300
Ser Asn Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
305          310          315          320
Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys
          325          330          335
Asp Lys Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln
          340          345          350

```

Val Tyr Ser Arg Ile Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala	
1095 1100 1105	
CAA GGG GCG CTA GGG AGT GAT CAA TCA AGC TTG AAT TTC AAA AGC GCT	3416
Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Ala	
1110 1115 1120	
CTA TTG CGA GAT TTG AAT CAA AGC TAT AAT TAC TTA GCC TAT AGC GCT	3464
Leu Leu Arg Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala	
1125 1130 1135	
GCA ACA AGA GCG AGC TAT GGT TAT GAC TTT GCA TTT TTT AGG AAC GCT	3512
Ala Thr Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala	
1140 1145 1150	
TTG GTG TTA AAA CCA AGC GTG GGC GTG AGC TAT AAC CAT TTA GGT TCA	3560
Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser	
1155 1160 1165 1170	
ACC AAC TTT AAA AGC AAT AGC AAT CAA GTG GCT TTG AAA AAT GGC TCT	3608
Thr Asn Phe Lys Ser Asn Ser Asn Gln Val Ala Leu Lys Asn Gly Ser	
1175 1180 1185	
AGC AGT CAG CAT TTA TTC AAC GCT AGC GCT AAT GTG GAA GCG CGC TAT	3656
Ser Ser Gln His Leu Phe Asn Ala Ser Ala Asn Val Glu Ala Arg Tyr	
1190 1195 1200	
TAT TAT GGG GAC ACT TCA TAC TTC TAT ATG AAC GCT GGA GTT TTA CAA	3704
Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Met Asn Ala Gly Val Leu Gln	
1205 1210 1215	
GAA TTT GCT AAC TTT GGT TCT AGC AAT GCG GTA TCT TTA AAC ACC TTT	3752
Glu Phe Ala Asn Phe Gly Ser Ser Asn Ala Val Ser Leu Asn Thr Phe	
1220 1225 1230	
AAA GTG AAT GCC GCA CAC AAT CCT TTA AGT ACC CAT GCC AGA GTG ATG	3800
Lys Val Asn Ala Ala His Asn Pro Leu Ser Thr His Ala Arg Val Met	
1235 1240 1245 1250	
ATG GGT GGG GAA TTA AAA TTA GCT AAA GAA GTG TTT TTG AAT TTG GGC	3848
Met Gly Gly Glu Leu Lys Leu Ala Lys Glu Val Phe Leu Asn Leu Gly	
1255 1260 1265	
TTT GTT TAT TTG CAC AAT TTG ATT TCC AAT ATA GGC CAT TTC GCT TCC	3896
Phe Val Tyr Leu His Asn Leu Ile Ser Asn Ile Gly His Phe Ala Ser	
1270 1275 1280	
AAT TTA GGA ATG AGG TAT AGT TTC TAAATACCGC TCTTAAACCC ATGCTCAAAG	3950
Asn Leu Gly Met Arg Tyr Ser Phe	
1285 1290	
CATGGGTTTG AAATCTTACA AAA	3973

(2) INFORMATION FOR SEQ ID NO:138:

870						875						880						
ACC	ATT	GAA	AGC	GTG	TTT	GAA	TTG	GCT	AAC	CGC	TCT	AAA	GAT	ATT	GAC	2744		
Thr	Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala	Asn	Arg	Ser	Lys	Asp	Ile	Asp			
885						890						895						
ACG	CTT	TAT	GCT	AAC	TCA	GGC	GCG	CAA	GGC	AGG	GAT	CTC	TTA	CAA	ACC	2792		
Thr	Leu	Tyr	Ala	Asn	Ser	Gly	Ala	Gln	Gly	Arg	Asp	Leu	Leu	Gln	Thr			
900						905						910						
TTA	TTG	ATT	GAT	AGC	CAT	GAT	GCG	GGT	TAT	GCC	AGA	CAA	ATG	ATT	GAT	2840		
Leu	Leu	Ile	Asp	Ser	His	Asp	Ala	Gly	Tyr	Ala	Arg	Gln	Met	Ile	Asp			
915						920						930						
AAC	ACA	AGC	ACC	GGT	GAA	ATC	ACC	AAG	CAA	TTG	AAT	GCG	GCC	ACT	ACC	2888		
Asn	Thr	Ser	Thr	Gly	Glu	Ile	Thr	Lys	Gln	Leu	Asn	Ala	Ala	Thr	Thr			
935						940						945						
ACT	TTA	AAC	AAC	ATA	GCC	AGT	TTA	GAG	CAT	AAG	ACA	AGC	AGC	TTA	CAA	2936		
Thr	Leu	Asn	Asn	Ile	Ala	Ser	Leu	Glu	His	Lys	Thr	Ser	Ser	Leu	Gln			
950						955						960						
ACT	TTG	AGC	TTG	AGT	AAT	GCG	ATG	ATC	TTA	AAT	TCT	CGT	TTA	GTC	AAT	2984		
Thr	Leu	Ser	Leu	Ser	Asn	Ala	Met	Ile	Leu	Asn	Ser	Arg	Leu	Val	Asn			
965						970						975						
CTC	TCC	AGA	AGG	CAC	ACC	AAT	AAT	ATT	GAC	TCA	TTC	GCC	CAA	CGC	TTA	3032		
Leu	Ser	Arg	Arg	His	Thr	Asn	Asn	Ile	Asp	Ser	Phe	Ala	Gln	Arg	Leu			
980						985						990						
CAA	GCT	TTA	AAA	GAC	CAA	AAA	TTC	GCT	TCT	TTA	GAA	AGC	GCG	GCG	GAA	3080		
Gln	Ala	Leu	Lys	Asp	Gln	Lys	Phe	Ala	Ser	Leu	Glu	Ser	Ala	Ala	Glu			
995						1000						1005						1010
GTG	TTG	TAT	CAA	TTT	GCC	CCT	AAA	TAT	GAA	AAA	CCT	ACC	AAT	GTT	TGG	3128		
Val	Leu	Tyr	Gln	Phe	Ala	Pro	Lys	Tyr	Glu	Lys	Pro	Thr	Asn	Val	Trp			
1015						1020						1025						
GCT	AAC	GCT	ATT	GGG	GGA	ACG	AGC	TTG	AAT	AAT	GGC	GGC	AAC	GCT	TCA	3176		
Ala	Asn	Ala	Ile	Gly	Gly	Thr	Ser	Leu	Asn	Asn	Gly	Gly	Asn	Ala	Ser			
1030						1035						1040						
TTG	TAT	GGC	ACA	AGT	GCG	GGC	GTA	GAT	GCC	TAC	CTT	AAT	GGG	GAA	GTG	3224		
Leu	Tyr	Gly	Thr	Ser	Ala	Gly	Val	Asp	Ala	Tyr	Leu	Asn	Gly	Glu	Val			
1045						1050						1055						
GAA	GCC	ATT	GTG	GGC	GGT	TTT	GGA	AGC	TAT	GGT	TAT	AGC	TCT	TTT	AAT	3272		
Glu	Ala	Ile	Val	Gly	Gly	Phe	Gly	Ser	Tyr	Gly	Tyr	Ser	Ser	Phe	Asn			
1060						1065						1070						
AAT	CAA	GCG	AAC	TCT	CTT	AAC	TCT	GGA	GCC	AAT	AAC	ACT	AAT	TTT	GGC	3320		
Asn	Gln	Ala	Asn	Ser	Leu	Asn	Ser	Gly	Ala	Asn	Asn	Thr	Asn	Phe	Gly			
1075						1080						1085						1090
GTG	TAT	AGC	CGT	ATC	TTT	GCT	AAC	CAG	CAT	GAA	TTT	GAT	TTT	GAA	GCT	3368		

TAT AGT CAA TTT TCA AAT TTA ACC ATT CAG GGG GAT TTC ATC AAC AAT	2072
Tyr Ser Gln Phe Ser Asn Leu Thr Ile Gln Gly Asp Phe Ile Asn Asn	
660 665 670	
CAA GGC ACT ATC AAT TAT TTG GTC CGA GGC GGG CAA GTA GCC ACC TTG	2120
Gln Gly Thr Ile Asn Tyr Leu Val Arg Gly Gly Gln Val Ala Thr Leu	
675 680 685 690	
AAT GTA GGC AAT GCG GCA GCT ATG TTC TTT AGT AAT AAT GTG GAT AGC	2168
Asn Val Gly Asn Ala Ala Ala Met Phe Phe Ser Asn Asn Val Asp Ser	
695 700 705	
GCG ACT GGG TTT TAC CAA CCG CTC ATG AAG ATT AAC AGC GCT CAA GAT	2216
Ala Thr Gly Phe Tyr Gln Pro Leu Met Lys Ile Asn Ser Ala Gln Asp	
710 715 720	
CTC ATT AAA AAT AAA GAA CAT GTC TTA TTG AAA GCG AAA ATC ATC GGT	2264
Leu Ile Lys Asn Lys Glu His Val Leu Leu Lys Ala Lys Ile Ile Gly	
725 730 735	
TAT GGC AAT GTT TCT TTA GGC ACT AAC AGC ATT AGT AAT GTT AAT CTA	2312
Tyr Gly Asn Val Ser Leu Gly Thr Asn Ser Ile Ser Asn Val Asn Leu	
740 745 750	
ATA GAG CAA TTC AAA GAG CGC CTA GCC CTT TAC AAC AAC AAT AAC CGC	2360
Ile Glu Gln Phe Lys Glu Arg Leu Ala Leu Tyr Asn Asn Asn Asn Arg	
755 760 765 770	
ATG GAT ATT TGT GTG GTG CGA AAT ACT GAT GAC ATT AAA GCA TGC GGG	2408
Met Asp Ile Cys Val Val Arg Asn Thr Asp Asp Ile Lys Ala Cys Gly	
775 780 785	
ACG GCT ATC GGC AAT CAA AGC ATG GTG AAT AAC CCC GAC AAT TAC AAG	2456
Thr Ala Ile Gly Asn Gln Ser Met Val Asn Asn Pro Asp Asn Tyr Lys	
790 795 800	
TAT CTT ATC GGT AAA GCA TGG AAG AAC ATA GGG ATC AGC AAA ACA GCT	2504
Tyr Leu Ile Gly Lys Ala Trp Lys Asn Ile Gly Ile Ser Lys Thr Ala	
805 810 815	
AAT GGC TCT AAA ATT TCG GTG TAT TAT TTA GGC AAT TCT ACG CCT ACT	2552
Asn Gly Ser Lys Ile Ser Val Tyr Tyr Leu Gly Asn Ser Thr Pro Thr	
820 825 830	
GAG AAA GGT GGC AAT ACC ACA AAT TTA CCT ACA AAC ACC ACT AGC AAT	2600
Glu Lys Gly Gly Asn Thr Thr Asn Leu Pro Thr Asn Thr Thr Ser Asn	
835 840 845 850	
GTG CGT TCT GCC AAC AAC GCC CTT GCG CAA AAC GCT CCT TTC GCT CAA	2648
Val Arg Ser Ala Asn Asn Ala Leu Ala Gln Asn Ala Pro Phe Ala Gln	
855 860 865	
CCT AGC GCC ACT CCT AAT TTA GTC GCT ATC AAT CAG CAT GAT TTT GGC	2696
Pro Ser Ala Thr Pro Asn Leu Val Ala Ile Asn Gln His Asp Phe Gly	

GCG AGC GGG CGC ACC CTT TTA GTG GAA AAT CTA ACC GGG AAT ATC ACC	1400
Ala Ser Gly Arg Thr Leu Leu Val Glu Asn Leu Thr Gly Asn Ile Thr	
435 440 445 450	
GTT GAT GGG CCT TTA AGA GTG AAT AAT CAA GTG GGT GGT TAT GCT TTG	1448
Val Asp Gly Pro Leu Arg Val Asn Asn Gln Val Gly Gly Tyr Ala Leu	
455 460 465	
GCA GGA TCA AGC GCG AAT TTT GAG TTT AAG GCT GGT ACG GAT ACC AAA	1496
Ala Gly Ser Ser Ala Asn Phe Glu Phe Lys Ala Gly Thr Asp Thr Lys	
470 475 480	
AAC GGC ACA GCC ACT TTT AAT AAC GAT ATT AGT TTG GGA AGA TTT GTG	1544
Asn Gly Thr Ala Thr Phe Asn Asn Asp Ile Ser Leu Gly Arg Phe Val	
485 490 495	
AAT TTA AAA GTG GAT GCT CAT ACA GCT AAT TTT AAA GGT ATT GAT ACT	1592
Asn Leu Lys Val Asp Ala His Thr Ala Asn Phe Lys Gly Ile Asp Thr	
500 505 510	
GGT AAT GGT GGT TTC AAC ACC TTA GAT TTT AGT GGC GTT ACA GGT AAG	1640
Gly Asn Gly Gly Phe Asn Thr Leu Asp Phe Ser Gly Val Thr Gly Lys	
515 520 525 530	
GTC AAT ATC AAC AAG CTC ATT ACG GCT TCC ACT AAT GTG GCC GTT AAA	1688
Val Asn Ile Asn Lys Leu Ile Thr Ala Ser Thr Asn Val Ala Val Lys	
535 540 545	
AAC TTC AAC ATT AAT GAA TTG GTT GTT AAG ACC AAT GGG GTG AGT GTG	1736
Asn Phe Asn Ile Asn Glu Leu Val Val Lys Thr Asn Gly Val Ser Val	
550 555 560	
GGG GAA TAC ACT CAT TTT AGC GAA GAT ATA GGC AGT CAA TCG CGC ATC	1784
Gly Glu Tyr Thr His Phe Ser Glu Asp Ile Gly Ser Gln Ser Arg Ile	
565 570 575	
AAT ACC GTG CGT TTG GAA ACT GGC ACT AGG TCA ATC TTT TCT GGG GGT	1832
Asn Thr Val Arg Leu Glu Thr Gly Thr Arg Ser Ile Phe Ser Gly Gly	
580 585 590	
GTC AAA TTT AAA AGC GGT GAA AAA CTG GTT ATA GAT GAG TTT TAC TAT	1880
Val Lys Phe Lys Ser Gly Glu Lys Leu Val Ile Asp Glu Phe Tyr Tyr	
595 600 605 610	
AGC CCT TGG AAT TAT TTT GAC GCT AGG AAT ATT AAA AAT GTT GAA ATC	1928
Ser Pro Trp Asn Tyr Phe Asp Ala Arg Asn Ile Lys Asn Val Glu Ile	
615 620 625	
ACC AGA AAA TTC GCT TCT TCA ACC CCA GAA AAC CCT TGG GGC ACA TCA	1976
Thr Arg Lys Phe Ala Ser Ser Thr Pro Glu Asn Pro Trp Gly Thr Ser	
630 635 640	
AAG CTT ATG TTT AAT AAT CTA ACC CTG GGT CAA AAT GCG GTC ATG GAC	2024
Lys Leu Met Phe Asn Asn Leu Thr Leu Gly Gln Asn Ala Val Met Asp	
645 650 655	

GCC GGG AGG AAA GCC AGC TCT ACG GTT TTA ACT TTG CAA GCT TCA GAA	728
Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala Ser Glu	
215 220 225	
GGG ATT ACT AGC AGT AAA AAT GCG GAA ATT TCT CTT TAT GAT GGC GCC	776
Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp Gly Ala	
230 235 240	
ACG CTC AAT TTG GCT TCA AAC AGC GTT AAA TTA ATG GGT AAT GTG TGG	824
Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn Val Trp	
245 250 255	
ATG GGC CGT TTG CAA TAT GTG GGA GCG TAT TTG GCC CCT TCA TAC AGC	872
Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser Tyr Ser	
260 265 270	
ACG ATA AAC ACT TCA AAA GTG ACA GGG GAA GTG AAT TTT AAC CAT CTC	920
Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn His Leu	
275 280 285 290	
ACT GTG GGC GAT CAC AAC GCC GCT CAA GCA GGC ATT ATC GCT AGT AAC	968
Thr Val Gly Asp His Asn Ala Ala Gln Ala Gly Ile Ile Ala Ser Asn	
295 300 305	
AAG ACT CAT ATT GGC ACA CTG GAT TTG TGG CAA AGC GCG GGA CTA AAC	1016
Lys Thr His Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly Leu Asn	
310 315 320	
ATT ATC GCC CCT CCA GAA GGC GGT TAT AAG GAT AAA CCT AAG GAT AAA	1064
Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Lys Asp Lys	
325 330 335	
CCT AGT AAC ACC ACG CAA AAT AAT GCT AAC AAC AAC CAA CAA AAC AGC	1112
Pro Ser Asn Thr Thr Gln Asn Asn Ala Asn Asn Asn Gln Gln Asn Ser	
340 345 350	
GCT CAA AAC AAT AGT AAC ACT CAG GTT ATT AAC CCA CCC AAT AGC GCG	1160
Ala Gln Asn Asn Ser Asn Thr Gln Val Ile Asn Pro Pro Asn Ser Ala	
355 360 365 370	
CAA AAA ACA GAA ATT CAA CCC ACG CAA GTC ATT GAT GGG CCT TTT GCT	1208
Gln Lys Thr Glu Ile Gln Pro Thr Gln Val Ile Asp Gly Pro Phe Ala	
375 380 385	
GGT GGC AAA GAC ACG GTT GTC AAT ATT GAT CGC ATC AAC ACT AAC GCT	1256
Gly Gly Lys Asp Thr Val Val Asn Ile Asp Arg Ile Asn Thr Asn Ala	
390 395 400	
GAT GGC ACG ATT AAA GTG GGA GGG TAT AAA GCT TCT CTT ACC ACC AAT	1304
Asp Gly Thr Ile Lys Val Gly Gly Tyr Lys Ala Ser Leu Thr Thr Asn	
405 410 415	
GCG GCT CAT TTG CAT ATC GGC AAA GGC GGT ATC AAT CTG TCC AAT CAA	1352
Ala Ala His Leu His Ile Gly Lys Gly Gly Ile Asn Leu Ser Asn Gln	
420 425 430	

AAAGTCGCAC CCTTTGTGCA AAAATCGTTT TACAAGAAGA AAGGAAAAAA ATG GAA	56
Met Glu	
1	
ATA CAA CAA ACA CAC CGC AAA ATC AAT CGC CCT TTG GTT TCT CTC GCT	104
Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser Leu Ala	
5 10 15	
TTA GTA GGA GCG TTA GTC AGC ATC ACA CCG CAA CAA AGT CAT GCC GCC	152
Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Ser His Ala Ala	
20 25 30	
TTT TTC ACA ACC GTG ATC ATT CCA GCC ATT GTT GGG GGG ATT GCT ACA	200
Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile Ala Thr	
35 40 45 50	
GGC GCT GCT GTA GGA ACG GTC TCA GGG CTT CTT GGC TGG GGG CTA AAA	248
Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly Leu Lys	
55 60 65	
CAA GCC GAA GAA GCC AAT AAA ACC CCA GAT AAA CCC GAT AAA GTT TGG	296
Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys Val Trp	
70 75 80	
CGC ATT CAA GCA GGA AAA GGC TTT AAT GAA TTC CCT AAC AAG GAA TAC	344
Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys Glu Tyr	
85 90 95	
GAC TTA TAC AGA TCC CTA CTA TCT AGT AAG ATT GAT GGA GGC TGG GAT	392
Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly Trp Asp	
100 105 110	
TGG GGG AAT GCC GCT ACG CAT TAT TGG GTC AAA GGC GGG CAA TGG AAC	440
Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln Trp Asn	
115 120 125 130	
AAG CTT GAA GTG GAT ATG AAA GAC GCT GTA GGG ACT TAT AAT CTC TCA	488
Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn Leu Ser	
135 140 145	
GGG CTA AGA AAC TTT ACT GGT GGG GAT TTA GAT GTC AAT ATG CAA AAA	536
Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met Gln Lys	
150 155 160	
GCC ACT TTG CGC TTG GGC CAA TTC AAT GGC AAT TCT TTC ACA AGC TAT	584
Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr Ser Tyr	
165 170 175	
AAG GAT AGC GCT GAT CGC ACC ACG AGA GTG GAT TTC AAC GCT AAA AAT	632
Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala Lys Asn	
180 185 190	
ATC TTA ATT GAT AAT TTT TTA GAA ATC AAT AAT CGT GTG GGT TCT GGA	680
Ile Leu Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly Ser Gly	
195 200 205 210	

```

Gly Phe Asp Lys Ala Thr Ser Leu Ser Phe Ile Gln Ala Trp Met Thr
      260                      265                      270
Ser Leu Ser Tyr Ser Phe Gln Leu Tyr Phe Asp Phe Ser Gly Tyr Cys
      275                      280                      285
Asp Met Ala Ile Gly Ile Gly Leu Phe Phe Asn Ile Lys Leu Pro Ile
      290                      295                      300
Asn Phe Asn Ser Pro Tyr Lys Ala Leu Asn Ile Gln Asp Phe Trp Arg
      305                      310                      315                      320
Arg Trp His Ile Thr Leu Ser Arg Phe Leu Lys Glu Tyr Leu Tyr Ile
      325                      330                      335
Pro Leu Gly Gly Asn Arg Val Lys Glu Leu Ile Val Tyr Arg Asn Leu
      340                      345                      350
Ile Leu Val Phe Leu Ile Gly Gly Phe Trp His Gly Ala Gly Trp Thr
      355                      360                      365
Phe Ile Ile Trp Gly Leu Leu His Gly Ile Ala Leu Ser Val His Arg
      370                      375                      380
Ala Tyr Ser His Ala Thr Arg Lys Phe His Phe Thr Met Pro Lys Ile
      385                      390                      395                      400
Leu Ala Trp Leu Ile Thr Phe Asn Phe Ile Asn Leu Ala Trp Val Phe
      405                      410                      415
Phe Arg Ala Lys Asn Leu Glu Ser Ala Leu Lys Val Leu Lys Gly Met
      420                      425                      430
Val Gly Leu Asn Gly Val Ser Leu Cys His Leu Ser Lys Glu Ala Ser
      435                      440                      445
Glu Phe Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met
      450                      455                      460
Tyr Ala Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser
      465                      470                      475                      480
Phe Cys Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp
      485                      490                      495
Trp Ile Lys Thr Thr Ser Ala Cys Leu Leu Leu Ser Ile Gly Phe Leu
      500                      505                      510
Phe Ile Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe
      515                      520                      525

```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...3920
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

AAA ACA ACA AGC GCT TGT TTG TTG CTC TCT ATA GGT TTT TTA TTT ATT      1592
Lys Thr Thr Ser Ala Cys Leu Leu Leu Ser Ile Gly Phe Leu Phe Ile
    500                      505                      510

TTT GCC AGT TCT CAA TCG GTA TTT TTG TAT TTT AAT TTT TAGGACACTG CT    1643
Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe
    515                      520                      525

ATGGAATTTT ATAAAAACA AACTTTAATC ATTGTTTCTT T                        1684

```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Met Leu Ala Ser Ile Ile Ser Ile Leu Arg Val Phe Val Leu Leu Phe
 1          5          10          15
Asn Thr Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly
    20          25          30
Tyr Phe Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu
    35          40          45
Trp Leu Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys
    50          55          60
Tyr Leu Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala
    65          70          75          80
Leu Lys Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu
    85          90          95
Ile Leu Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr
    100         105         110
Thr Asp Phe Phe Leu Thr Asn Phe Asn Leu Ile Trp Lys Ser His Phe
    115         120         125
Glu Thr Leu His Leu Ile Leu Pro Leu Ala Ile Ser Phe Phe Thr Leu
    130         135         140
Gln Gln Ile Ala Tyr Leu Met Asp Thr Tyr Lys Gln Asn Gln Ile Met
    145         150         155         160
Gln Pro Lys Met Arg Glu Arg Val Ser Glu Asn Ala Pro Ile Leu Leu
    165         170         175
Asn Pro Pro Thr Ser Phe Phe Ser Leu Ser His Phe Leu Asp Tyr Ala
    180         185         190
Leu Phe Val Ser Phe Phe Pro Gln Leu Ile Ala Gly Pro Ile Val His
    195         200         205
His Ser Glu Met Met Pro Gln Phe Lys Asp Lys Asn Asn Gln Tyr Leu
    210         215         220
Asn Tyr Arg Asn Ile Ala Leu Gly Leu Phe Ile Phe Ser Ile Gly Leu
    225         230         235         240
Phe Lys Lys Val Val Ile Ala Asp Asn Thr Ala His Phe Ala Asp Phe
    245         250         255

```

TCT TAT TCG TTC CAG CTG TAT TTT GAT TTT AGC GGT TAT TGC GAT ATG	920
Ser Tyr Ser Phe Gln Leu Tyr Phe Asp Phe Ser Gly Tyr Cys Asp Met	
275 280 285 290	
GCT ATA GGC ATT GGC CTC TTT TTT AAC ATC AAA CTC CCT ATC AAT TTT	968
Ala Ile Gly Ile Gly Leu Phe Phe Asn Ile Lys Leu Pro Ile Asn Phe	
295 300 305	
AAT AGC CCC TAT AAG GCT TTG AAT ATC CAA GAT TTT TGG AGG AGG TGG	1016
Asn Ser Pro Tyr Lys Ala Leu Asn Ile Gln Asp Phe Trp Arg Arg Trp	
310 315 320	
CAT ATC ACT TTG AGC CGC TTC TTA AAA GAG TAT TTG TAT ATC CCT TTA	1064
His Ile Thr Leu Ser Arg Phe Leu Lys Glu Tyr Leu Tyr Ile Pro Leu	
325 330 335	
GGG GGT AAT AGG GTG AAA GAA TTA ATC GTG TAT AGG AAT TTA ATT TTA	1112
Gly Gly Asn Arg Val Lys Glu Leu Ile Val Tyr Arg Asn Leu Ile Leu	
340 345 350	
GTG TTT TTG ATT GGG GGG TTT TGG CAT GGG GCT GGT TGG ACT TTT ATC	1160
Val Phe Leu Ile Gly Gly Phe Trp His Gly Ala Gly Trp Thr Phe Ile	
355 360 365 370	
ATT TGG GGG CTA TTG CAT GGG ATT GCT TTG AGC GTT CAT AGA GCG TAT	1208
Ile Trp Gly Leu Leu His Gly Ile Ala Leu Ser Val His Arg Ala Tyr	
375 380 385	
TCT CAT GCC ACT AGA AAA TTC CAT TTC ACT ATG CCA AAG ATT TTA GCA	1256
Ser His Ala Thr Arg Lys Phe His Phe Thr Met Pro Lys Ile Leu Ala	
390 395 400	
TGG CTC ATC ACT TTT AAT TTT ATC AAT CTC GCA TGG GTG TTT TTT AGA	1304
Trp Leu Ile Thr Phe Asn Phe Ile Asn Leu Ala Trp Val Phe Phe Arg	
405 410 415	
GCC AAA AAT TTA GAA AGC GCT TTG AAG GTT TTA AAG GGG ATG GTT GGT	1352
Ala Lys Asn Leu Glu Ser Ala Leu Lys Val Leu Lys Gly Met Val Gly	
420 425 430	
TTG AAT GGT GTT TCG CTT TGT CAT CTT TCA AAA GAG GCA TCA GAG TTT	1400
Leu Asn Gly Val Ser Leu Cys His Leu Ser Lys Glu Ala Ser Glu Phe	
435 440 445 450	
TTA AAT CGT GTC AAT GAT AAC ATG ATC ATG CAC ACC ATA ATG TAT GCA	1448
Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met Tyr Ala	
455 460 465	
TCC CCC ACA TTT AAA ATG TGT GTT TTG ATG ATA ATC ATC TCT TTT TGT	1496
Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser Phe Cys	
470 475 480	
TTA AAA AAT AGT TCC CAT TTA TAC CAA TCC AAT CAA ATG GAT TGG ATT	1544
Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp Trp Ile	
485 490 495	

GTA TTG GCT AGT TTG TTT TTT TAT GCT TTT TGG AAT GTG AAG TAT TTG	248
Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys Tyr Leu	
55 60 65	
CCC TTA TTG GTT GGC TCT ATT GTT TTT AAT TAT TTT GTG GCT TTG AAA	296
Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala Leu Lys	
70 75 80	
ATC CAT CAA ACC CAG CCA AAT GCA TAT AAA AGA TTA TGG CTT ATT TTG	344
Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu Ile Leu	
85 90 95	
GGC TTG ATC GCT AAT GTT TCA CTT TTA GGA TTT TTC AAA TAC ACT GAT	392
Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr Thr Asp	
100 105 110	
TTT TTC TTA ACC AAT TTC AAT CTA ATA TGG AAG AGC CAT TTT GAA ACC	440
Phe Phe Leu Thr Asn Phe Asn Leu Ile Trp Lys Ser His Phe Glu Thr	
115 120 125 130	
TTG CAT TTA ATC TTG CCT TTA GCG ATC AGC TTT TTC ACT TTG CAA CAA	488
Leu His Leu Ile Leu Pro Leu Ala Ile Ser Phe Phe Thr Leu Gln Gln	
135 140 145	
ATC GCT TAC TTG ATG GAC ACT TAT AAG CAA AAT CAA ATC ATG CAG CCC	536
Ile Ala Tyr Leu Met Asp Thr Tyr Lys Gln Asn Gln Ile Met Gln Pro	
150 155 160	
AAA ATG AGA GAG AGA GTG AGT GAA AAC GCT CCT ATT TTA TTA AAT CCT	584
Lys Met Arg Glu Arg Val Ser Glu Asn Ala Pro Ile Leu Leu Asn Pro	
165 170 175	
CCC ACT TCA TTT TTT TCA CTT TCG CAT TTT TTA GAT TAC GCT TTA TTT	632
Pro Thr Ser Phe Phe Ser Leu Ser His Phe Leu Asp Tyr Ala Leu Phe	
180 185 190	
GTG AGT TTC TTC CCT CAA CTC ATT GCA GGG CCT ATT GTG CAT CAT AGC	680
Val Ser Phe Phe Pro Gln Leu Ile Ala Gly Pro Ile Val His His Ser	
195 200 205 210	
GAG ATG ATG CCT CAA TTT AAA GAT AAA AAC AAT CAA TAT TTG AAT TAC	728
Glu Met Met Pro Gln Phe Lys Asp Lys Asn Asn Gln Tyr Leu Asn Tyr	
215 220 225	
AGA AAT ATC GCT TTA GGC TTG TTT ATC TTT TCT ATC GGT TTG TTT AAA	776
Arg Asn Ile Ala Leu Gly Leu Phe Ile Phe Ser Ile Gly Leu Phe Lys	
230 235 240	
AAG GTC GTG ATT GCA GAT AAT ACC GCT CAT TTT GCT GAT TTT GGA TTT	824
Lys Val Val Ile Ala Asp Asn Thr Ala His Phe Ala Asp Phe Gly Phe	
245 250 255	
GAT AAG GCG ACT AGC TTA AGT TTT ATT CAA GCA TGG ATG ACT TCT TTA	872
Asp Lys Ala Thr Ser Leu Ser Phe Ile Gln Ala Trp Met Thr Ser Leu	
260 265 270	

```

1           5           10           15
Ser Leu Val Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu
20           25           30
Ile Asp Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Gln
35           40           45
Lys Thr Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile
50           55           60
Val Pro Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser
65           70           75           80
Tyr Tyr Leu Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys
85           90           95
Ile Asp Ile Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys
100          105          110
Ser Val Ser Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys
115          120          125
Glu Asn Gln Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg
130          135          140
Thr Phe Gln Phe
145

```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1631
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```

CCTTTCTTTA TTCTCATTGC ATCTTG TGGG ATCATT TTTT TATTA ATG CTA      56
                                   Met Leu
                                   1

GCT TCC ATC ATC TCA ATT TTA AGG GTT TTT GTT TTG TTA TTC AAC ACG      104
Ala Ser Ile Ile Ser Ile Leu Arg Val Phe Val Leu Leu Phe Asn Thr
5           10           15

CCG TTA TTC ATC TTT GCT TTT TTG CCT GTT GGT TTT TTA GGG TAT TTT      152
Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly Tyr Phe
20           25           30

ATC TTG CAA GCT TAT GCT AAA AAT CCC CTG TTC CCT AAA CTA TGG CTA      200
Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu Trp Leu
35           40           45           50

```

CGC ATG AAT AAA AAT TAT CTT TTA ATC TTT TTG TTG TTA GCG AGT CTT	104
Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala Ser Leu	
5 10 15	
GTT GCT AGA GAG AAG GAC GCT TCT TCA AAC CTT TTT GAT TTG ATT GAT	152
Val Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu Ile Asp	
20 25 30	
AAG GGG ATC AAC AGA GAA CAA GAA TTA AAA GAG CAG GAG CAA AAA ACG	200
Lys Gly Ile Asn Arg Glu Gln Glu Leu Lys Glu Gln Glu Lys Thr	
35 40 45 50	
CGC TTA AAA CTG GCT CAA AGC CCT TTA GTA GCG TTA GAG ATT GTC CCC	248
Arg Leu Lys Leu Ala Gln Ser Pro Leu Val Ala Leu Glu Ile Val Pro	
55 60 65	
CAA GAA ACG CCC TAT TTA GAA TGG CAA GGG GCT AGG GAG TCG TAT TAT	296
Gln Glu Thr Pro Tyr Leu Glu Trp Gln Gly Ala Arg Glu Ser Tyr Tyr	
70 75 80	
TTA AAG GTG AGC GCT GTA GTG GAG AGC GTG GTT ATC TTA AAA ATT GAC	344
Leu Lys Val Ser Ala Val Val Glu Ser Val Val Ile Leu Lys Ile Asp	
85 90 95	
ATC AAT CAA GGG CGT TCT TGC TCG CTC TAC CCC ACG CCT AAA AGC GTT	392
Ile Asn Gln Gly Arg Ser Cys Ser Leu Tyr Pro Thr Pro Lys Ser Val	
100 105 110	
TCT TTA GTG AGG AAT CAA AGC GTA GCC TAT GAA ATT TTA TGC GAA AAC	440
Ser Leu Val Arg Asn Gln Ser Val Ala Tyr Glu Ile Leu Cys Glu Asn	
115 120 125 130	
CAA CCC CTA TGG ATA GAA GTA AGC ACC AAT TTA GGC AAA CGC ACC TTT	488
Gln Pro Leu Trp Ile Glu Val Ser Thr Asn Leu Gly Lys Arg Thr Phe	
135 140 145	
CAG TTT TAACCTGCAA CCAACATTAA AGAATGCCTT TAGCATTTTA AAACCCCTTT AT	546
Gln Phe	
C	547

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Asn Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala


```

Ser Val Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met
      20              25              30
Tyr Leu Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp
      35              40              45
Val Val Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp
      50              55              60
Phe Leu Asn Gln Ser Lys Ala Ser Ser Ala Lys Ala Arg Leu Lys Gln
      65              70              75              80
Leu Asn Ala Gly Ile Glu Ile Glu Ala Phe Glu Glu Arg Phe Lys Ala
      85              90              95
His Asn Ala Leu Ser Leu Ile Glu Pro Tyr Asp Phe Ile Ile Asp Ala
      100             105             110
Thr Asp Asn Phe Asn Ala Lys Phe Leu Ile Asn Asp Ala Cys Val Leu
      115             120             125
Ala Gln Lys Pro Tyr Ser His Ala Gly Val Leu Glu Tyr Arg Gly Gln
      130             135             140
Ser Met Ser Val Leu Pro His Ser Ala Cys Leu Ala Cys Val Phe Asp
      145             150             155             160
Lys Pro Pro Lys Lys Gly Leu Asn Pro Ile Ser Gly Leu Phe Gly Val
      165             170             175
Leu Pro Gly Val Leu Gly Cys Ile Gln Ala Ser Glu Cys Leu Lys Tyr
      180             185             190
Phe Leu Gly Phe Glu Thr Leu Leu Ile Asn Thr Leu Leu Ile Ala Asp
      195             200             205
Ile Lys Thr Met Asp Phe Lys Lys Ile Gln Ala Pro Lys Asn Pro Glu
      210             215             220
Cys Arg Val Cys Gly Thr His Lys Ile Thr His Leu Gln Asp Tyr Glu
      225             230             235             240
Ile

```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...494
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

AAAATTCATT CTATTTTAGA TAATGAGTTC AATCCCCACA AACAGCAAGA ATG AAT
                                     Met Asn

```

56

1

85					90					95						
GCT	CTT	TCT	CTC	ATA	GAG	CCT	TAT	GAT	TTT	ATC	ATA	GAC	GCC	ACG	GAC	392
Ala	Leu	Ser	Leu	Ile	Glu	Pro	Tyr	Asp	Phe	Ile	Ile	Asp	Ala	Thr	Asp	
100					105					110						
AAT	TTT	AAC	GCT	AAA	TTT	TTG	ATC	AAT	GAC	GCT	TGC	GTG	TTA	GCC	CAA	440
Asn	Phe	Asn	Ala	Lys	Phe	Leu	Ile	Asn	Asp	Ala	Cys	Val	Leu	Ala	Gln	
115					120					125					130	
AAA	CCC	TAT	TCG	CAT	GCC	GGG	GTT	TTA	GAA	TAC	AGG	GGG	CAA	AGC	ATG	488
Lys	Pro	Tyr	Ser	His	Ala	Gly	Val	Leu	Glu	Tyr	Arg	Gly	Gln	Ser	Met	
135					140					145						
AGC	GTT	TTA	CCC	CAT	AGC	GCA	TGC	TTA	GCG	TGC	GTT	TTT	GAT	AAG	CCC	536
Ser	Val	Leu	Pro	His	Ser	Ala	Cys	Leu	Ala	Cys	Val	Phe	Asp	Lys	Pro	
150					155					160						
CCT	AAA	AAG	GGA	TTA	AAT	CCC	ATT	TCA	GGG	CTT	TTT	GGG	GTC	TTA	CCC	584
Pro	Lys	Lys	Gly	Leu	Asn	Pro	Ile	Ser	Gly	Leu	Phe	Gly	Val	Leu	Pro	
165					170					175						
GGA	GTT	TTA	GGG	TGT	ATC	CAA	GCG	AGC	GAA	TGC	CTT	AAA	TAT	TTT	TTA	632
Gly	Val	Leu	Gly	Cys	Ile	Gln	Ala	Ser	Glu	Cys	Leu	Lys	Tyr	Phe	Leu	
180					185					190						
GGG	TTT	GAA	ACT	TTA	CTT	ATA	AAT	ACT	TTA	CTT	ATA	GCC	GAT	ATT	AAA	680
Gly	Phe	Glu	Thr	Leu	Leu	Ile	Asn	Thr	Leu	Leu	Ile	Ala	Asp	Ile	Lys	
195					200					205					210	
ACG	ATG	GAT	TTT	AAA	AAA	ATT	CAA	GCA	CCC	AAA	AAC	CCT	GAA	TGT	AGG	728
Thr	Met	Asp	Phe	Lys	Lys	Ile	Gln	Ala	Pro	Lys	Asn	Pro	Glu	Cys	Arg	
215					220					225						
GTT	TGT	GGC	ACG	CAT	AAA	ATC	ACG	CAT	TTA	CAG	GAT	TAT	GAA	ATT	TAGAT	778
Val	Cys	Gly	Thr	His	Lys	Ile	Thr	His	Leu	Gln	Asp	Tyr	Glu	Ile		
230					235					240						
TAAGGGGTAA GTTTTGGATT TATCAACCAT ATTAGGCTTG GTATTGGC															826	

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met	Leu	Glu	Asp	Val	Gly	Glu	Glu	Gly	Gln	Leu	Lys	Leu	Leu	Lys	Ser
1				5				10						15	

```

      1             5             10             15
Phe Leu Asp Arg Phe Gly Glu Lys Met Glu Glu Ser Lys Glu Arg Lys
      20             25             30
Gln Leu Leu Ile Ala Ser Leu Ala Pro Leu Ala Gly Phe Ala Ala Arg
      35             40             45
Ile Ser Pro Gly Leu Leu Ser Leu Leu Gly Leu Met Leu Ala Met Gly
      50             55             60
Cys Ala Asn Phe Trp Ile
      65             70

```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...773
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

TGGCTTAATT GTTAAGCCGG CTAGAAAAAG AGCGTTATTT GCGCCATATC  ATG CTA      56
                                     Met Leu
                                     1

GAA GAT GTG GGC GAA GAG GGT CAA TTG AAG CTT TTA AAA TCT AGC GTT      104
Glu Asp Val Gly Glu Glu Gly Gln Leu Lys Leu Leu Lys Ser Ser Val
      5             10             15

TTA GTC ATT GGG GCT GGG GGT CTT GGA TCG GCG GTT TTG ATG TAT TTG      152
Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met Tyr Leu
      20             25             30

TGT GCC GCT GGG ATA GGA AAA ATC GGT ATT GTA GAT TTT GAT GTA GTA      200
Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp Val Val
      35             40             45             50

GAT ATG AGT AAT TTG CAA CGC CAA ATC ATC CAT TCA CAG GAT TTT TTA      248
Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp Phe Leu
      55             60             65

AAC CAA TCT AAA GCC TCT AGC GCG AAA GCG CGC TTA AAA CAA CTC AAT      296
Asn Gln Ser Lys Ala Ser Ser Ala Lys Ala Arg Leu Lys Gln Leu Asn
      70             75             80

GCG GGT ATT GAA ATA GAG GCT TTT GAA GAA CGC TTT AAG GCT CAT AAC      344
Ala Gly Ile Glu Ile Glu Ala Phe Glu Glu Arg Phe Lys Ala His Asn

```

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...261
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```

GTAAGCTAGA GTTTATGCAA AGGGAGATGA GTAGCCTAGA AGCTAAGCAT T ATG ATT      57
                                   Met Ile
                                   1

CAG TTA AAA TCA AAT TTG GAT TGG TAC GCA GAT TAT TTG AAT TTT TTA      105
Gln Leu Lys Ser Asn Leu Asp Trp Tyr Ala Asp Tyr Leu Asn Phe Leu
      5              10              15

GAT CGC TTT GGG GAA AAA ATG GAA GAA TCC AAA GAG CGA AAA CAA CTC      153
Asp Arg Phe Gly Glu Lys Met Glu Glu Ser Lys Glu Arg Lys Gln Leu
      20              25              30

CTG ATC GCT TCC CTT GCA CCT CTT GCG GGC TTT GCT GCA AGA ATA TCG      201
Leu Ile Ala Ser Leu Ala Pro Leu Ala Gly Phe Ala Ala Arg Ile Ser
      35              40              45              50

CCG GGA TTA TTG AGC TTA TTG GGT TTG ATG CTG GCA ATG GGG TGT GCA      249
Pro Gly Leu Leu Ser Leu Leu Gly Leu Met Leu Ala Met Gly Cys Ala
      55              60              65

AAT TTT TGG ATT TAGAAACCAA TCTGTGCAAG ATTTATGAAT CGCGCCCGTT AA      303
Asn Phe Trp Ile
      70
  
```

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ile Gln Leu Lys Ser Asn Leu Asp Trp Tyr Ala Asp Tyr Leu Asn

```

Asn Phe Asn Ile Ala Ser Asp Pro Asp Met Ala Arg Leu Val Leu Ser
      100                      105                      110
Leu Pro Leu Val Ala Met Asp Ser Val Gly Ala Gly Ala Gly Ser Phe
      115                      120                      125
Val Arg Ile Asp Pro His Ser Arg Ser Val Lys Leu Gly Pro Asp Ser
      130                      135                      140
Ala Gly Tyr Arg Val Gly Thr Cys Trp Lys Asp Ser Gly Leu Asp Thr
      145                      150                      155                      160
Val Ser Val Thr Asp Cys His Ile Val Leu Gly Tyr Leu Asn Pro Asp
      165                      170                      175
Asn Phe Leu Gly Gly Leu Ile Lys Leu Asp Val Asp Arg Ala Lys Lys
      180                      185                      190
His Ile Lys Glu Gln Ile Ala Asp Pro Leu Gly Ile Ser Val Glu Asp
      195                      200                      205
Ala Ala Ala Gly Val Ile Glu Leu Leu Asp Leu Glu Leu Lys Glu Tyr
      210                      215                      220
Leu Arg Ser Asn Ile Ser Ala Lys Gly Tyr Ser Pro Ser Asp Phe Val
      225                      230                      235                      240
Cys Phe Ser Tyr Gly Gly Ala Gly Pro Val His Thr Tyr Gly Tyr Thr
      245                      250                      255
Glu Gly Leu Gly Phe Lys Asp Val Val Val Pro Ala Trp Ala Ala Gly
      260                      265                      270
Phe Ser Ala Phe Gly Cys Ala Cys Ala Asp Phe Glu Tyr Arg Tyr Asp
      275                      280                      285
Lys Ser Val Asp Ile Ala Ile Pro Gln Tyr Ser Ser Asp Lys Ser Lys
      290                      295                      300
Ile Asp Ala Cys Lys Ile Ile Gln Asp Ala Trp Asp Glu Leu Thr Leu
      305                      310                      315                      320
Lys Val Ile Glu Glu Phe Lys Ile Asn Gly Phe Ser Gln Lys Asp Val
      325                      330                      335
Ile Leu Arg Pro Gly Tyr Arg Met Gln Tyr Met Gly Gln Leu Asn Asp
      340                      345                      350
Leu Glu Ile Thr Ser Pro Val Ser Lys Ala Ala Ser Val Ala Asp Trp
      355                      360                      365
Glu Glu Ile Val Lys Glu Tyr Glu Lys Thr Tyr Ala Arg Val Tyr Ser
      370                      375                      380
Glu Ser Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile
      385                      390                      395                      400
Met Arg Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys
      405                      410                      415
Glu His Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys
      420                      425                      430
Phe Tyr Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu
      435                      440                      445
Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser
      450                      455                      460
Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp
      465                      470                      475                      480
Lys His Arg Leu Phe His Leu Lys Glu Ile Lys
      485                      490

```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

```

GCG TGT TCT CCA GAG CTT GGT TTT AGC GTG ACT GGC GTG ATC ATG CGT      1256
Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile Met Arg
          390                      395                      400

GGT GTT GTG GCT ACG CAA AAA CCT GTG ATT CCG GTT GAA AAA GAG CAT      1304
Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys Glu His
          405                      410                      415

GGT GCT ACG CCC CCA AAA GAA GCC AAA ATA GGC GTT AGA AAA TTC TAT      1352
Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys Phe Tyr
          420                      425                      430

CGG CAT AAA AAA TGG GTG GAT GCA GAT GTG TGG CAA ATG GAA AAA TTA      1400
Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu Lys Leu
          435                      440                      445                      450

CTG CCT GGA AAT GAA GTC ATA GGA CCT GCG ATC GTG GAA TCA GAT GCG      1448
Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser Asp Ala
          455                      460                      465

ACC ACT TTC GTG ATA CCC AAA GGC TTT GCG ACA AGA CTA GAC AAA CAC      1496
Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp Lys His
          470                      475                      480

CGA TTG TTC CAC TTG AAA GAA ATT AAA TAAAGGAGTT CAAAATGGCA AATTTAT      1550
Arg Leu Phe His Leu Lys Glu Ile Lys
          485                      490

TGAAAAACGG CAAAACTTTA AAACAA                                         1576

```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```

Met Asn Thr Thr Ile Leu Glu Ala Tyr Ala Ala Glu Pro Ser Arg Gln
 1              5              10              15
Thr Leu Ser Lys Val Ser Asn Arg Phe Lys Glu His Gly Ala Lys Phe
          20              25              30
Asp Leu Arg Val Met Ala Thr His Gly Gly Thr Ile Ser Trp Lys Ala
          35              40              45
Lys Glu Leu Ala Arg Thr Ile Val Ser Gly Pro Ile Gly Gly Val Ile
          50              55              60
Gly Ser Lys Leu Leu Gly Glu Thr Leu Gly Tyr Asp Asn Ile Ala Cys
          65              70              75              80
Ser Asp Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser
          85              90              95

```

GTA	ACC	GAT	TGC	CAT	ATT	GTT	TTA	GGC	TAT	TTG	AAC	CCG	GAT	AAT	TTC	584
Val	Thr	Asp	Cys	His	Ile	Val	Leu	Gly	Tyr	Leu	Asn	Pro	Asp	Asn	Phe	
		165						170				175				
TTA	GGC	GGT	TTG	ATC	AAA	TTA	GAT	GTG	GAT	AGG	GCT	AAA	AAA	CAC	ATT	632
Leu	Gly	Gly	Leu	Ile	Lys	Leu	Asp	Val	Asp	Arg	Ala	Lys	Lys	His	Ile	
		180						185				190				
AAA	GAA	CAA	ATC	GCT	GAT	CCG	CTA	GGC	ATT	AGC	GTA	GAA	GAT	GCG	GCT	680
Lys	Glu	Gln	Ile	Ala	Asp	Pro	Leu	Gly	Ile	Ser	Val	Glu	Asp	Ala	Ala	
		195				200				205					210	
GCT	GGT	GTG	ATT	GAA	TTG	CTT	GAT	TTG	GAG	CTT	AAA	GAA	TAC	TTG	CGA	728
Ala	Gly	Val	Ile	Glu	Leu	Leu	Asp	Leu	Glu	Leu	Lys	Glu	Tyr	Leu	Arg	
				215					220					225		
TCC	AAC	ATT	AGC	GCT	AAA	GGG	TAT	AGC	CCA	TCT	GAT	TTT	GTG	TGC	TTT	776
Ser	Asn	Ile	Ser	Ala	Lys	Gly	Tyr	Ser	Pro	Ser	Asp	Phe	Val	Cys	Phe	
			230					235					240			
TCA	TAT	GGT	GGC	GCA	GGA	CCT	GTG	CAT	ACC	TAT	GGC	TAT	ACA	GAA	GGA	824
Ser	Tyr	Gly	Gly	Ala	Gly	Pro	Val	His	Thr	Tyr	Gly	Tyr	Thr	Glu	Gly	
		245						250				255				
TTA	GGG	TTT	AAG	GAT	GTG	GTA	GTG	CCT	GCG	TGG	GCG	GCT	GGA	TTT	AGC	872
Leu	Gly	Phe	Lys	Asp	Val	Val	Val	Pro	Ala	Trp	Ala	Ala	Gly	Phe	Ser	
		260						265				270				
GCT	TTT	GGT	TGT	GCT	TGC	GCT	GAT	TTT	GAA	TAC	AGA	TAC	GAC	AAG	AGC	920
Ala	Phe	Gly	Cys	Ala	Cys	Ala	Asp	Phe	Glu	Tyr	Arg	Tyr	Asp	Lys	Ser	
		275				280				285					290	
GTG	GAT	ATT	GCC	ATT	CCG	CAG	TAT	TCT	TCA	GAC	AAG	TCA	AAA	ATA	GAC	968
Val	Asp	Ile	Ala	Ile	Pro	Gln	Tyr	Ser	Ser	Asp	Lys	Ser	Lys	Ile	Asp	
				295					300					305		
GCA	TGC	AAA	ATC	ATT	CAA	GAC	GCA	TGG	GAT	GAA	TTG	ACT	TTG	AAA	GTG	1016
Ala	Cys	Lys	Ile	Ile	Gln	Asp	Ala	Trp	Asp	Glu	Leu	Thr	Leu	Lys	Val	
			310					315					320			
ATT	GAA	GAG	TTC	AAG	ATC	AAT	GGA	TTT	TCT	CAA	AAA	GAT	GTG	ATC	TTA	1064
Ile	Glu	Glu	Phe	Lys	Ile	Asn	Gly	Phe	Ser	Gln	Lys	Asp	Val	Ile	Leu	
		325					330					335				
AGA	CCT	GGA	TAC	AGG	ATG	CAG	TAT	ATG	GGG	CAA	TTG	AAT	GAT	TTA	GAG	1112
Arg	Pro	Gly	Tyr	Arg	Met	Gln	Tyr	Met	Gly	Gln	Leu	Asn	Asp	Leu	Glu	
		340				345					350					
ATC	ACT	TCT	CCT	GTG	TCA	AAA	GCT	GCA	AGC	GTG	GCT	GAT	TGG	GAA	GAG	1160
Ile	Thr	Ser	Pro	Val	Ser	Lys	Ala	Ala	Ser	Val	Ala	Asp	Trp	Glu	Glu	
		355				360				365				370		
ATT	GTC	AAA	GAA	TAT	GAA	AAA	ACC	TAC	GCT	CGC	GTT	TAT	TCT	GAA	TCA	1208
Ile	Val	Lys	Glu	Tyr	Glu	Lys	Thr	Tyr	Ala	Arg	Val	Tyr	Ser	Glu	Ser	
				375					380					385		

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1523
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CTGTATTTCGC TTCTGTGGAT TACTACCCTC AAAGAAAAGA AAGCCACAGA ATG AAC	56
Met Asn	
1	
ACC ACC ATC TTA GAA GCT TAT GCG GCT GAG CCA AGC AGG CAA ACC CTC	104
Thr Thr Ile Leu Glu Ala Tyr Ala Ala Glu Pro Ser Arg Gln Thr Leu	
5 10 15	
TCT AAA GTC AGC AAC CGA TTC AAA GAG CAT GGC GCT AAA TTT GAT CTT	152
Ser Lys Val Ser Asn Arg Phe Lys Glu His Gly Ala Lys Phe Asp Leu	
20 25 30	
CGT GTG ATG GCA ACG CAT GGA GGC ACC ATT AGT TGG AAA GCT AAA GAA	200
Arg Val Met Ala Thr His Gly Gly Thr Ile Ser Trp Lys Ala Lys Glu	
35 40 45 50	
CTC GCT AGG ACT ATT GTG AGC GGC CCT ATT GGA GGC GTG ATT GGA TCT	248
Leu Ala Arg Thr Ile Val Ser Gly Pro Ile Gly Gly Val Ile Gly Ser	
55 60 65	
AAA TTG CTA GGC GAA ACG CTT GGT TAT GAC AAT ATT GCA TGC AGT GAT	296
Lys Leu Leu Gly Glu Thr Leu Gly Tyr Asp Asn Ile Ala Cys Ser Asp	
70 75 80	
ATT GGK GGC ACG AGC TTT GAT ATG GCG CTT ATC GTT AAG AGC AAT TTT	344
Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser Asn Phe	
85 90 95	
AAC ATC GCT TCT GAC CCT GAT ATG GCA CGC CTT GTT TTA TCT CTA CCG	392
Asn Ile Ala Ser Asp Pro Asp Met Ala Arg Leu Val Leu Ser Leu Pro	
100 105 110	
CTT GTG GCT ATG GAT TCT GTT GGC GCA GGT GCT GGG AGT TTT GTG CGC	440
Leu Val Ala Met Asp Ser Val Gly Ala Gly Ala Gly Ser Phe Val Arg	
115 120 125 130	
ATT GAT CCA CAC AGC CGA TCT GTC AAA CTA GGG CCT GAC AGC GCG GGG	488
Ile Asp Pro His Ser Arg Ser Val Lys Leu Gly Pro Asp Ser Ala Gly	
135 140 145	
TAT AGA GTT GGC ACT TGT TGG AAA GAC AGC GGG TTA GAC ACG GTT TCA	536
Tyr Arg Val Gly Thr Cys Trp Lys Asp Ser Gly Leu Asp Thr Val Ser	
150 155 160	

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...161
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

GCATTGCTAA TTTGGGAATA CTTGTTTATG CCA GTGAAAT AGGAGCGGCT ATG ATG      56
                                   Met Met
                                   1

TGG CGT AGT CTC ARG GTG GCT TTT ACG ATC ACT GAT ATT AGT AAA ACC      104
Trp Arg Ser Leu Xaa Val Ala Phe Thr Ile Thr Asp Ile Ser Lys Thr
      5              10              15

TTT CAA TCC CAG CCT AAG CAC CAT CAA ATC GGC ACT TTA GAA TTG AAT      152
Phe Gln Ser Gln Pro Lys His His Gln Ile Gly Thr Leu Glu Leu Asn
      20              25              30

TTC GCC TTT TGATTTAATA TCAGTTTAAT ATTTTCTTC CTATATGATA TTTATATGA      210
Phe Ala Phe
35

TATT                                                                214
  
```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

Met Met Trp Arg Ser Leu Xaa Val Ala Phe Thr Ile Thr Asp Ile Ser
  1              5              10              15
Lys Thr Phe Gln Ser Gln Pro Lys His His Gln Ile Gly Thr Leu Glu
      20              25              30
Leu Asn Phe Ala Phe
35
  
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

GAT CAT ATC GCT TTA GAA TGT ATC GCT GAA CTT TCT TAT AAG GGT TTT T 585
Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys Gly Phe
165 170 175

GAATTGGTTT TTGTTTTTCT TTTTAAATGC GTTAATGAAG AAACAAGCCT GA 637

(2) INFORMATION FOR SEO ID NO:124:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEO ID NO:124:

[illegible]

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...584

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAAAGTTCGG GGGCGGATTC TATGATTAAT GGCTATGGTT ATACCAAAGA ATG AGT	56
Met Ser	
1	
CAA AAA ATC CTA ATT CTA GGT ATT GGC AAT ATC CTT TTT GGC GAT GAA	104
Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly Asp Glu	
5 10 15	
GGG ATT GGG GTG CAT TTA GCC CAC TAC CTC AAA AAA AAT TTT TCT TTT	152
Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe Ser Phe	
20 25 30	
TTC CCT AGC GTG GAT ATT ATA GAT GGG GGG ACA ATG GCC CAG CAG CTC	200
Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln Gln Leu	
35 40 45 50	
ATT CCT TTA ATC ACT TCG TAT GAA AAG GTT TTG ATT TTG GAT TGC GTG	248
Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp Cys Val	
55 60 65	
AGC GCT GAA GGC GTT GAG ATA GGA TCA GTC TAT GCT TTT GAT TTT AAG	296
Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp Phe Lys	
70 75 80	
GAC GCT CCT AAA GAA ATC ACA TGG GCT GGG AGC GCT CAT GAA GTG GAA	344
Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu Val Glu	
85 90 95	
ATG CTA CAC ACT TTA AGG CTC ACG GAG TTT TTA GGG GAT TTG CCT AAA	392
Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu Pro Lys	
100 105 110	
ACT TTT ATC GTG GGG CTT GTG CCT TTT GTG ATA GGG AGC GAG ACC ACT	440
Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu Thr Thr	
115 120 125 130	
TTC AAG CTT TCA AGC AAA ATT TTA AAC GCT TTA GAA ACC GCC TTA AAA	488
Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala Leu Lys	
135 140 145	
GCC ATA GAA ACC CAA CTC AAC GCA TGG GGG GTT AAA ATG CAA CGC ACC	536
Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln Arg Thr	
150 155 160	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```

Met Thr Leu Asn Thr Phe Leu Asp Thr Cys Phe Leu Leu Phe Ile Ser
 1           5           10           15
Ile Leu Phe Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val
          20           25           30
Val Pro Gln Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln
          35           40           45
Gly Val Asp Met Asn Ala Leu Asp Leu Leu Phe Leu Arg Leu Met Gly
          50           55           60
Met Pro Lys Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys
65           70           75           80
Gly Asp Phe Leu Val Arg Leu Ile Lys Ala Lys Ala Ala Gln Lys Ser
          85           90           95
Ala Thr Leu Ile Pro Gly Glu Ser Arg Tyr Phe Phe Thr Gln Ile Leu
          100          105          110
Ser Glu Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu
          115          120          125
Ser Ile Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile
          130          135          140
Trp Pro Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile
          145          150          155          160
Met Gln Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser
          165          170          175
Lys Gln Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile
          180          185          190
Ile Leu Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met
          195          200          205
Pro Leu Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro
          210          215          220
Leu Gln Met Asp Gly Ala Leu Asn Tyr Gln Glu Phe Ser His Ala Lys
          225          230          235          240
Val Thr Lys Glu Arg Ile Lys Thr Asp Asn Thr Pro Tyr Asn Thr Tyr
          245          250          255
Lys Phe Lys Gly Leu Pro Lys Asn Pro Val Gly Ser Val Ser Leu Glu
          260          265          270
Ala Ile Arg Ala Val Ile Phe Pro Lys Lys Thr Asp Phe Leu Tyr Phe
          275          280          285
Val Lys Met Pro Asp Lys Lys His Ala Phe Ser Ala Thr Tyr Lys Glu
          290          295          300
His Leu Lys Asn Ile Asn Leu Ser Asn Asn His Phe
          305          310          315

```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 637 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

Ala	Pro	Arg	Leu	Asn	Gly	Glu	Val	Ile	Glu	Asp	Gly	Val	Ile	Trp	Pro		
				135					140					145			
GAC	ACT	TAT	CAT	TTG	CCT	TTA	GGG	GAG	GAC	GCT	TTT	AAA	ATC	ATG	CAA	536	
Asp	Thr	Tyr	His	Leu	Pro	Leu	Gly	Glu	Asp	Ala	Phe	Lys	Ile	Met	Gln		
			150					155					160				
ACT	TTG	ATT	GGT	CAA	TCC	ATG	AAA	AAA	CAC	GAA	GCC	TTA	AGC	AAA	CAA	584	
Thr	Leu	Ile	Gly	Gln	Ser	Met	Lys	Lys	His	Glu	Ala	Leu	Ser	Lys	Gln		
		165					170					175					
TGG	CTT	GGA	TAC	TAC	CAT	AAA	GAA	GAG	TGG	TTT	GAA	AAA	ATC	ATT	CTC	632	
Trp	Leu	Gly	Tyr	Tyr	His	Lys	Glu	Glu	Trp	Phe	Glu	Lys	Ile	Ile	Leu		
	180					185					190						
GCT	TCT	ATT	GTG	CAA	AAA	GAA	GCC	GCT	AAT	GTT	GAA	GAA	ATG	CCC	TTG	680	
Ala	Ser	Ile	Val	Gln	Lys	Glu	Ala	Ala	Asn	Val	Glu	Glu	Met	Pro	Leu		
195					200					205					210		
ATT	GCG	AGC	GTG	ATT	TTT	AAC	CGC	TTG	AAA	AAA	GGC	ATG	CCT	TTA	CAA	728	
Ile	Ala	Ser	Val	Ile	Phe	Asn	Arg	Leu	Lys	Lys	Gly	Met	Pro	Leu	Gln		
			215						220					225			
ATG	GAT	GGG	GCT	TTG	AAT	TAT	CAG	GAA	TTT	TCA	CAC	GCT	AAA	GTA	ACC	776	
Met	Asp	Gly	Ala	Leu	Asn	Tyr	Gln	Glu	Phe	Ser	His	Ala	Lys	Val	Thr		
			230					235					240				
AAA	GAG	CGC	ATT	AAA	ACC	GAT	AAC	ACC	CCC	TAC	AAT	ACC	TAT	AAA	TTT	824	
Lys	Glu	Arg	Ile	Lys	Thr	Asp	Asn	Thr	Pro	Tyr	Asn	Thr	Tyr	Lys	Phe		
		245					250					255					
AAG	GGT	TTG	CCT	AAA	AAT	CCT	GTA	GGG	AGC	GTG	AGC	CTA	GAA	GCG	ATT	872	
Lys	Gly	Leu	Pro	Lys	Asn	Pro	Val	Gly	Ser	Val	Ser	Leu	Glu	Ala	Ile		
	260					265					270						
AGA	GCC	GTG	ATC	TTC	CCT	AAA	AAA	ACG	GAT	TTC	TTG	TAT	TTT	GTG	AAA	920	
Arg	Ala	Val	Ile	Phe	Pro	Lys	Lys	Thr	Asp	Phe	Leu	Tyr	Phe	Val	Lys		
275					280					285					290		
ATG	CCG	GAT	AAA	AAA	CAT	GCT	TTC	AGC	GCG	ACT	TAT	AAA	GAG	CAT	TTA	968	
Met	Pro	Asp	Lys	Lys	His	Ala	Phe	Ser	Ala	Thr	Tyr	Lys	Glu	His	Leu		
			295					300					305				
AAA	AAC	ATT	AAT	CTT	TCT	AAT	AAT	CAT	TTT	TAAGATTAAG	GTAAATGGGG	CGT	1021				
Lys	Asn	Ile	Asn	Leu	Ser	Asn	Asn	His	Phe								
			310					315									
TTTTTCTTTT	GAATTGAGTA	AAAAGTGTTT														1051	

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...998
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```

GGGTTTTGTG AATGACGACT AAAAGAGTGA ATACTGCCAC AAACAAGATA ATG ACA      56
                                   Met Thr
                                   1

TTA AAT ACT TTC TTG GAT ACA TGT TTT CTT TTA TTC ATC AGT ATT CTT      104
Leu Asn Thr Phe Leu Asp Thr Cys Phe Leu Leu Phe Ile Ser Ile Leu
      5                      10                      15

TTT TAT TTA AGT ATA CCA ATT TAT CCT AAC AAA GTG GTG GTT GTC CCG      152
Phe Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val Val Pro
      20                      25                      30

CAA GGT TCG CTC AAA AAA GTG TTT TTT TCT TTA AAA GAG CAA GGC GTG      200
Gln Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln Gly Val
      35                      40                      45                      50

GAT ATG AAC GCT TTG GAT TTG CTT TTT TTA CGC CTG ATG GGC ATG CCT      248
Asp Met Asn Ala Leu Asp Leu Leu Phe Leu Arg Leu Met Gly Met Pro
                        55                      60                      65

AAA AAA GGT TAT ATT GAT ATG GGC GAT GGG GCT TTA AGG AAG GGG GAT      296
Lys Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys Gly Asp
                        70                      75                      80

TTT TTA GTC CGT TTG ATT AAG GCA AAA GCG GCA CAA AAA AGT GCG ACT      344
Phe Leu Val Arg Leu Ile Lys Ala Lys Ala Ala Gln Lys Ser Ala Thr
      85                      90                      95

CTA ATC CCT GGG GAA AGC CGC TAT TTT TTC ACG CAA ATT TTG AGC GAG      392
Leu Ile Pro Gly Glu Ser Arg Tyr Phe Phe Thr Gln Ile Leu Ser Glu
      100                      105                      110

ACT TAC CAA CTA GAA ACA AGC GAT CTC AAT CAG GCT TAT GAA AGC ATC      440
Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu Ser Ile
      115                      120                      125                      130

GCT CCA CGA TTG AAT GGC GAA GTG ATA GAA GAT GGG GTG ATA TGG CCA      488

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```

CCCCACAAAT CCTAGCGATA GTGAAATGCC CTAATTCATG GACAAAGATT AAAAACGCCA      60
GCATCAAAAC CGCTAC AAT GAA CAT CAT ACC CCT GCA GGC TCT TTG GTG TTA      112
      Asn Glu His His Thr Pro Ala Gly Ser Leu Val Leu
        1             5             10

GGA TCT TTT ATC ATC GGC TCT TTT AAA GGC GTG GGT GCT ATA GGG GGC      160
Gly Ser Phe Ile Ile Gly Ser Phe Lys Gly Val Gly Ala Ile Gly Gly
      15             20             25

GTG GGT GCT GTG GTT TTT GGG ATT TCT TTA TTT TCT TTT GGG GGT TTT      208
Val Gly Ala Val Val Phe Gly Ile Ser Leu Phe Ser Phe Gly Gly Phe
      30             35             40

TGC CAC AAC TCT GTC AAA GCC GCC GCT TTT TTA GGA TCC ATT TTG GCT      256
Cys His Asn Ser Val Lys Ala Ala Ala Phe Leu Gly Ser Ile Leu Ala
      45             50             55             60

AAA ATT TTA CCG AGT TCT TGG GGT TTT AGC GCC ATT AAA ATT TCT AAT      304
Lys Ile Leu Pro Ser Ser Trp Gly Phe Ser Ala Ile Lys Ile Ser Asn
      65             70             75

GCG TTT TGAGTGGGTA AATTTTCTAA AATCAGAGCC GATTTAGAAT CTTTCATTT      359
Ala Phe

```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```

Asn Glu His His Thr Pro Ala Gly Ser Leu Val Leu Gly Ser Phe Ile
  1             5             10             15
Ile Gly Ser Phe Lys Gly Val Gly Ala Ile Gly Gly Val Gly Ala Val
      20             25             30
Val Phe Gly Ile Ser Leu Phe Ser Phe Gly Gly Phe Cys His Asn Ser
      35             40             45
Val Lys Ala Ala Ala Phe Leu Gly Ser Ile Leu Ala Lys Ile Leu Pro
      50             55             60
Ser Ser Trp Gly Phe Ser Ala Ile Lys Ile Ser Asn Ala Phe
      65             70             75

```

(2) INFORMATION FOR SEQ ID NO:121:

TCT GGG GCG TCT TCG CGC AGT AAA AAA TAGCCAAACC CTATAGCGTA TAGGGCA 543
 Ser Gly Ala Ser Ser Arg Ser Lys Lys
 150

AAAGAGATTA AAAAGCTAAC ACTCGT

569

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala	Ser	Glu	Val	Ala	Pro	Ser	Glu	Val	Leu	Leu	Asp	Ser	Ser	Cys	Leu	1	5	10	15
Ser	Phe	Ser	Leu	Thr	Ile	Ser	Leu	Val	Val	Thr	Cys	Leu	Gly	Ala	Leu	20	25	30	
Phe	Ser	Leu	Ala	Ser	Ser	Leu	Ala	Ser	Ser	Phe	Leu	Gly	Ser	Ser	Leu	35	40	45	
Gly	Ser	Ser	Phe	Leu	Thr	Ser	Ser	Thr	Leu	Gly	Ser	Gly	Leu	Gly	Ser	50	55	60	
Gly	Phe	Gly	Ser	Gly	Leu	Gly	Ser	Gly	Leu	Gly	Phe	Gly	Phe	Gly	Phe	65	70	75	80
Gly	Leu	Gly	Leu	Gly	Leu	Gly	Leu	Gly	Phe	Val	Thr	Ser	Phe	Leu	Gly	85	90	95	
Ser	Ser	Phe	Phe	Gly	Ser	Ser	Phe	Leu	Gly	Phe	Ser	Leu	Gly	Ser	Ser	100	105	110	
Leu	Gly	Leu	Ala	Asp	Ser	Ala	Leu	Val	Phe	Val	Leu	Glu	Leu	Val	Leu	115	120	125	
Met	Leu	Ala	Lys	Leu	Met	Val	Thr	Leu	Val	Val	Pro	Ala	Cys	Ala	Lys	130	135	140	
Gly	Ser	Gly	Ala	Ser	Ser	Arg	Ser	Lys	Lys							145	150		

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 77...310
- (D) OTHER INFORMATION:

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 55...516
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCGGTTTGGG	TCTTCATTAA	AAATTCGTTG	CTCACCCCTG	GGTTATAAGC	TTGA	GCT	57
						Ala	
						1	
TCA GAA GTG GCC CCC TCA GAG GTT TTG TTG GAT TCT TCT TGC TTG TCT	105						
Ser Glu Val Ala Pro Ser Glu Val Leu Leu Asp Ser Ser Cys Leu Ser							
5 10 15							
TTT TCT TTG ACT ATA TCC TTA GTT GTT ACT TGT TTA GGA GCG CTT TTT	153						
Phe Ser Leu Thr Ile Ser Leu Val Val Thr Cys Leu Gly Ala Leu Phe							
20 25 30							
TCT TTA GCT TCC TCT TTA GCT TCT TCT TTT TTG GGC TCT TCT TTA GGC	201						
Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu Gly							
35 40 45							
TCT TCT TTT TTA ACC TCT TCA ACT TTA GGC TCA GGC TTA GGC TCG GGT	249						
Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser Gly							
50 55 60 65							
TTT GGT TCA GGT TTG GGT TCA GGC TTA GGT TTT GGT TTT GGC TTT GGC	297						
Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe Gly							
70 75 80							
TTG GGT TTA GGC TTA GGT TTA GGC TTT GTA ACC TCC TTT TTG GGT TCT	345						
Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly Ser							
85 90 95							
TCT TTT TTT GGC TCT TCT TTC TTG GGT TTT TCT TTA GGC TCT TCT TTG	393						
Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser Leu							
100 105 110							
GGT TTA GCC GAC TCA GCA TTA GTC TTT GTA TTG GAA TTA GTG TTG ATG	441						
Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu Met							
115 120 125							
CTG GCT AAA CTC ATG GTA ACC TTA GTG GTC CCG GCT TGC GCT AAA GGC	489						
Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys Gly							
130 135 140 145							

```

AAA GAT ATT CTT CTC ATC GCT TCG CAA ATT CTC AAA GAA AGA CTT TTT      152
Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu Phe
      20              25              30

GCC CAC AAA AAT GAG ATT TTC TTT TGC CCT AGA AAT AGC TAC ATT CAA      200
Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile Gln
      35              40              45

GCG TTT AGA ATC TAT CAA GAA AGA AAG ATT ACC ATA AGT TTT CAC GGT      248
Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His Gly
      50              55              60              65

GGA ATA AAT AAT AAT ATC TGC CTT CTC GCC TTG AAA GGC ATC CAC AGT      296
Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His Ser
      70              75              80

GTC TAT TTT GAG CTC ATC AAA ATT CTT GAA GCC GTA TTT TTC CAC TTC T      345
Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His Phe
      85              90              95

GATCGCAAGC ATCTTTTGTG GGCATTATAA GGTGTGATAA T      386

```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

Met Ile Ile Phe Gly Lys Asp Tyr Leu Ser Thr Asp Leu Gln Asn Ser
  1              5              10              15
Ala Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu
      20              25              30
Phe Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile
      35              40              45
Gln Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His
      50              55              60
Gly Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His
      65              70              75              80
Ser Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His
      85              90              95
Phe

```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid

ACATTTAAAA TCTTA

367

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

Met Ile Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu
 1             5             10             15
Leu Val Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe
             20             25             30
Asn Gln Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu
             35             40             45
Asp Met Ala Pro Ile His Ile Ser Ile Gly His Asp Asn Asp Phe Met
             50             55             60
Ile Ala Gln Ser Phe Tyr Ile Lys Thr Leu Leu Asn Ala Ala Pro Lys
65             70             75             80
Ser Arg Asp His Val Phe Asn Phe Phe
             85

```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 54...344
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

TAAAAAGCAC TTTAGAGAGA TTTACGAAAG TGTTTTGAAG CGAAGAATGT CTG ATG      56
                                     Met
                                     1

ATT ATC TTT GGA AAA GAT TAC CTA TCT ACA GAC TTG CAA AAT AGC GCT      104
Ile Ile Phe Gly Lys Asp Tyr Leu Ser Thr Asp Leu Gln Asn Ser Ala
 5             10             15

```

50	55	60
Ala Tyr Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val		
65	70	75
Gly Ile Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser		80
	85	90
Gln Trp Leu Phe		95
100		

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...318
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTTGCCAATC CCTTCAATAT CCACCGAATT GATGCCATGC TCAATTAAAA A ATG ATC	57
Met Ile	
1	
CAA AGC GAC GCT GTC TTT AAG ATA AAT TTC TGT CTT GCC CTT CTT GTA	105
Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu Leu Val	
5 10 15	
TTT GTA AAG AGG GGC TTG AGC GAT ATA AAC ATG CCC TTG TTC AAT CAG	153
Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe Asn Gln	
20 25 30	
CGG GCG CAA ATA ACG ATA GAA AAA AGT CAT CAG CAA GGT TTG GAT ATG	201
Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu Asp Met	
35 40 45 50	
GCT CCC ATC CAC ATC AGC ATC GGT CAT GAT AAT GAT TTT ATG ATA GCG	249
Ala Pro Ile His Ile Ser Ile Gly His Asp Asn Asp Phe Met Ile Ala	
55 60 65	
CAA TCT TTC TAT ATC AAA ACT CTC TTG AAT GCC GCA CCC AAA AGC CGT	297
Gln Ser Phe Tyr Ile Lys Thr Leu Leu Asn Ala Ala Pro Lys Ser Arg	
70 75 80	
GAT CAT GTT TTT AAT TTC TTC TGATTTTAGG ATTTTGTATA AATGGCTTTT TTCC	352
Asp His Val Phe Asn Phe Phe	
85	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

CTAATTCTGT CTATTACACC AACAATCAAT CTCAAAACAA AGGACATGAAAG ATG AAA      58
                                     Met Lys
                                     1

ACA AAA CAT AAA GGA ATA AGA ATG TTT AAG CAA ATT CGT AGA ATG ATG      106
Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg Met Met
      5                      10                      15

AGT TTG GCA ATA TTA ATG CCT AGT TTT TTA TTG GCG GCA CCA GAT TAC      154
Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro Asp Tyr
      20                      25                      30

AAA CAA AAA TTC ACT CAA ATA TTG GAT TTC ATA AGC AAT GAC TTT ATC      202
Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp Phe Ile
      35                      40                      45                      50

AAG GCT ATT GGT GGT CTA ATC ATT GTT GGG ACT TGC ATT TAC GCC TAT      250
Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr Ala Tyr
                        55                      60                      65

AAA AAT TGG GAC AGG CTT GGA GAA ATT GGT TGG AAA TGC GTT GGG ATT      298
Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val Gly Ile
                        70                      75                      80

ATC ATT ATA ACC GCT GCT ATT TCT AAT GCT AAA ACT TTA AGT CAA TGG      346
Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser Gln Trp
      85                      90                      95

TTA TTT TAGATGGCAT TGCATATTGT TTGTGTTGAA AGTATCAACA TTAGA      397
Leu Phe
      100

```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Lys Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg
1                      5                      10                      15
Met Met Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro
      20                      25                      30
Asp Tyr Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp
      35                      40                      45
Phe Ile Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr

```

```

Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser Asp Thr Thr Leu Thr
225                230                235                240
Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser Glu Tyr Leu Phe Ser
                245                250                255
Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu Ile Pro Asn Leu Ala
                260                265                270
Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys Gly Ser Leu Thr Leu
                275                280                285
Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu Lys Val Ser Gly His
                290                295                300
Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr Leu Leu Asn Lys Asp
305                310                315                320
Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu Lys Ala Leu Asp Leu
                325                330                335
Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala Asp Ala Asn Leu Asp
                340                345                350
Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys Ala Arg Leu Lys Asn
                355                360                365
Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe Leu Tyr Ser Ile Ser
                370                375                380
Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp Ala Asn Leu Val Ser
385                390                395                400
Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu Ser Leu Lys Ser Pro
                405                410                415
Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu Asp Leu Asn Thr Lys
                420                425                430
Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu Lys Phe Ile Phe Lys
                435                440                445
Met Lys Leu Gln Gly Asn Met His Gln Pro Lys Phe Ser Leu Ile Leu
                450                455                460
Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile
465                470                475                480
Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp
                485                490                495
Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe
                500                505                510

```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...352
- (D) OTHER INFORMATION:

GGC TTG AAA GAA ATC TTA AAA AAC GAC ACC CTT AAA AAA GGT TTA GAT 1551
 Gly Leu Lys Glu Ile Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp
 480 485 490

CAT TTG CTT AAA GAT GAT AAG CTC AAA GAA AAG CTT GAA AAA GGG CTT 1599
 His Leu Leu Lys Asp Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu
 495 500 505

AAG GGG CTT TTT TAAATTTTA AAGGATAGAA ATGGCGCACA TTTTAGTTAG CGGGG 1656
 Lys Gly Leu Phe
 510

CGACT 1661

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu Leu Leu Ile Gly Leu
 1 5 10 15
 Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp Gly Asn Lys Ile Ile
 20 25 30
 Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn Glu His Tyr Leu Ser
 35 40 45
 Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu Asp Phe Lys Ala Gln
 50 55 60
 Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly Asp Phe Ser Leu Leu
 65 70 75 80
 Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp Ile Lys Asp Leu Arg
 85 90 95
 Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg Gly Ala Val Ile Thr
 100 105 110
 Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu Met Ile Gln Gly Val
 115 120 125
 Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn Ala Leu Leu Asp Asp
 130 135 140
 Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln Asp Ala Asn Leu Glu
 145 150 155 160
 Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr Ala Asn Ala Lys Val
 165 170 175
 Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro Leu Glu Gly His Leu
 180 185 190
 Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn Ala Leu Ile Asn Gln
 195 200 205
 Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val Phe Ser Leu Ser His
 210 215 220

GAA TAC CTT TTC TCT ATT TTA AAA CTC AAC GCC CCC TAC ACT TTA GAA	879
Glu Tyr Leu Phe Ser Ile Leu Lys Leu Asn Ala Pro Tyr Thr Leu Glu	
255 260 265	
ATC CCC AAT CTA GCC AAA CTC TAT AAC ATT ACC AAC CAC CCC TTA AAA	927
Ile Pro Asn Leu Ala Lys Leu Tyr Asn Ile Thr Asn His Pro Leu Lys	
270 275 280	
GGG AGC TTG ACT TTA AAA GGC GCT ATA GAA CAA AGC CCC AAA CTT TTA	975
Gly Ser Leu Thr Leu Lys Gly Ala Ile Glu Gln Ser Pro Lys Leu Leu	
285 290 295	
AAA GTC AGC GGC CAT TCA AAT TTA CTA GAC GGC GCG CTG GAT TTC ACG	1023
Lys Val Ser Gly His Ser Asn Leu Leu Asp Gly Ala Leu Asp Phe Thr	
300 305 310 315	
CTT TTA AAT AAA GAT TTG AAA GGG CGT TTT TCC AAT ATT TCC ACT TTA	1071
Leu Leu Asn Lys Asp Leu Lys Gly Arg Phe Ser Asn Ile Ser Thr Leu	
320 325 330	
AAA GCT TTA GAT TTA TTC CAT TAC CCT AAG TTT TTC CAA TCC GTT GCA	1119
Lys Ala Leu Asp Leu Phe His Tyr Pro Lys Phe Phe Gln Ser Val Ala	
335 340 345	
GAC GCT AAT TTG GAT TAT GAT CTT ATC GCT AAG CAA GGC GTA TTG AAA	1167
Asp Ala Asn Leu Asp Tyr Asp Leu Ile Ala Lys Gln Gly Val Leu Lys	
350 355 360	
GCC CGC CTA AAA AAC GCA AGA TTC CTC AAA AAT GCA TTC AGC GAT TTT	1215
Ala Arg Leu Lys Asn Ala Arg Phe Leu Lys Asn Ala Phe Ser Asp Phe	
365 370 375	
CTC TAC TCC ATT TCT AAA TTT GAT ATT ACA AAA GAA ATT TAT AAC GAT	1263
Leu Tyr Ser Ile Ser Lys Phe Asp Ile Thr Lys Glu Ile Tyr Asn Asp	
380 385 390 395	
GCC AAT CTG GTA AGC CAA ATC AAC CAG CAA CGC CTG CTC TCT GAT CTG	1311
Ala Asn Leu Val Ser Gln Ile Asn Gln Gln Arg Leu Leu Ser Asp Leu	
400 405 410	
AGT TTA AAA AGC CCC AAA ACC CAA TTG AAA ATC CAT AAC GGT TTG TTG	1359
Ser Leu Lys Ser Pro Lys Thr Gln Leu Lys Ile His Asn Gly Leu Leu	
415 420 425	
GAT TTA AAC ACC AAA CAA ATG AAC ATG CTC ATG GAT GCG GAA ATT TTA	1407
Asp Leu Asn Thr Lys Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu	
430 435 440	
AAA TTC ATT TTT AAA ATG AAA CTT CAA GGC AAC ATG CAC CAG CCA AAA	1455
Lys Phe Ile Phe Lys Met Lys Leu Gln Gly Asn Met His Gln Pro Lys	
445 450 455	
TTT TCT CTC ATT TTA AAC GAA AAA GCC ATT CAG CAA AAC TTG CAA CAA	1503
Phe Ser Leu Ile Leu Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln	
460 465 470 475	

GGG AAT AAG ATC ATC GCT TCG TAT ATA GAG AAA AAA ATC AAC CCG AAC	207
Gly Asn Lys Ile Ile Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn	
30 35 40	
GAG CAC TAC TTG AGC GTT AAA ACC TTT AAA TTG AGA TTC AAC TCT TTG	255
Glu His Tyr Leu Ser Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu	
45 50 55	
GAT TTT AAA GCT CAA GCC AAC GAT GAT TCC ACG CTC ATT CTT AAG GGG	303
Asp Phe Lys Ala Gln Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly	
60 65 70 75	
GAT TTT TCA CTT TTA AAG CAA AGC GTA AAT TTG AAT TAC CAT ATA GAT	351
Asp Phe Ser Leu Leu Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp	
80 85 90	
ATT AAA GAT TTA CGC TCT TTC AAA GAA TGG ATA CCC TAC CCT TTA AGG	399
Ile Lys Asp Leu Arg Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg	
95 100 105	
GGG GCT GTT ATC ACT TCT GGG AAT ATT AAA GGG CAT AGA AAA GCC CTT	447
Gly Ala Val Ile Thr Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu	
110 115 120	
ATG ATT CAA GGC GTC TCT AAT GTG GCT CAA TCC CAC ACT GCC TAC AAT	495
Met Ile Gln Gly Val Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn	
125 130 135	
GCC CTT TTA GAT GAT TTC AAG CTT TCT CGC TTA AAT TTG AAC GCA CAA	543
Ala Leu Leu Asp Asp Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln	
140 145 150 155	
GAC GCC AAT TTA GAA GAT TTG CTT TAT TTA ATC AAT CGC CCC GCT TAT	591
Asp Ala Asn Leu Glu Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr	
160 165 170	
GCG AAC GCA AAA GTG TCC TTA CAG GCG GAT TTT AAC TCT CTA AAG CCT	639
Ala Asn Ala Lys Val Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro	
175 180 185	
TTA GAG GGG CAT TTG ATC CTA ACA GCT AAT AAC GCT TTA ATC AAT AAC	687
Leu Glu Gly His Leu Ile Leu Thr Ala Asn Asn Ala Leu Ile Asn Asn	
190 195 200	
GCC CTA ATC AAT CAA ATT TTT CAT TTA AAC CTT AAA GAC ACG CTT GTT	735
Ala Leu Ile Asn Gln Ile Phe His Leu Asn Leu Lys Asp Thr Leu Val	
205 210 215	
TTC AGC CTC TCG CAT TCA AGC GAC TTT AAA GGA AAC AAA GCC ATC AGC	783
Phe Ser Leu Ser His Ser Ser Asp Phe Lys Gly Asn Lys Ala Ile Ser	
220 225 230 235	
GAT ACC ACC CTG ACT AGC CCT TTA GCC AAT TTC AAA GCC CTA AAA AGC	831
Asp Thr Thr Leu Thr Ser Pro Leu Ala Asn Phe Lys Ala Leu Lys Ser	
240 245 250	

```

      50              55              60
Ile Ala Pro Asn Phe Arg Val Val Ser Ile Ile Ala Asn Asn Gln Arg
65              70              75              80
Asn Phe Gln Ala Leu Arg Pro Ile Asn His Ile Ser Phe Ile Pro Arg
      85              90              95
Ile Pro Thr Phe Asn Arg Ala Pro Arg Gln Asp Phe Ala Val Phe Leu
      100             105             110
His Asp Leu Thr Leu Ile Ile Asp Lys Asn Gln Ser Val Ile Gly Ile
      115             120             125
Leu Phe Gly Leu Leu Val Phe Phe Pro Cys Gln Arg Glu His Ser Pro
      130             135             140
Asn Leu Val Phe Leu Thr Ser Phe Ser Lys Asp Arg Gly Phe Phe Ser
145             150             155             160
Arg Asn Ala Cys Gly Cys Ile Lys His Phe Leu Ser Val Ile His Asn
      165             170             175
Pro Met Arg Ala Val Phe Arg Glu Asn Asn Gln Ile Gln Pro Arg Gln
      180             185             190
Thr Leu Phe Asp Pro Thr Asn His Leu Ser Asp Ile Ala Thr Ile Phe
      195             200             205
Gln His Leu Ile Leu Ser Val Glu Ser Arg His Leu Ile Ile Asn Tyr
      210             215             220
Arg Tyr Thr His Ser Ile Trp Ala Ala Thr Asn Ile Ser Met Ser His
225             230             235             240
Ile Met Phe Leu Val Phe
      245

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...1611
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

GGCTTTATAA AAAATGTTAG AAACCCTTAC AAAACAAGCT AATATATTCT ATTCAATTTG      60
CCTCAAGGAC AAACAAAC ATG AAA AAA CTT CTT TAT ACC ATA CTC GCG CTT      111
      Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu
              1              5              10

CTT TTA ATC GGC CTT TTA ACA ATC TAT CTC ATC CTT TTT ACA GAA TGG      159
Leu Leu Ile Gly Leu Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp
      15              20              25

```

ATA GGG ATT CTT TTT GGC TTG CTC GTG TTT TTC CCC TGT CAA AGA GAA	795
Ile Gly Ile Leu Phe Gly Leu Leu Val Phe Phe Pro Cys Gln Arg Glu	
130 135 140	
CAC TCC CCA AAC CTT GTT TTT CTT ACA AGC TTC AGC AAA GAT CGC GGT	843
His Ser Pro Asn Leu Val Phe Leu Thr Ser Phe Ser Lys Asp Arg Gly	
145 150 155	
TTC TTC TCC AGG AAC GCT TGC GGC TGT ATC AAA CAT TTC TTG TCT GTC	891
Phe Phe Ser Arg Asn Ala Cys Gly Cys Ile Lys His Phe Leu Ser Val	
160 165 170	
ATA CAT AAT CCC ATG CGT GCT GTA TTC AGG GAA AAT AAT CAG ATC CAA	939
Ile His Asn Pro Met Arg Ala Val Phe Arg Glu Asn Asn Gln Ile Gln	
175 180 185	
CCC AGG CAA ACC CTG TTT GAC CCC ACC AAT CAC CTT AGC GAT ATT GCG	987
Pro Arg Gln Thr Leu Phe Asp Pro Thr Asn His Leu Ser Asp Ile Ala	
190 195 200 205	
ACA ATT TTC CAA CAC CTC ATT CTT AGT GTG GAG TCT AGG CAT CTT ATA	1035
Thr Ile Phe Gln His Leu Ile Leu Ser Val Glu Ser Arg His Leu Ile	
210 215 220	
ATT AAC TAC CGC TAC ACC CAC AGT ATC TGG GCT GCT ACT AAT ATC TCC	1083
Ile Asn Tyr Arg Tyr Thr His Ser Ile Trp Ala Ala Thr Asn Ile Ser	
225 230 235	
ATG TCT CAT ATT ATG TTC CTT GTT TTT TGATGAGAGT TCCTACAAAC CCTCTAC	1137
Met Ser His Ile Met Phe Leu Val Phe	
240 245	
TTGAATTTAT AAAATAATTG TGT	1160

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Pro Val Lys Thr Asn Asn Ala Arg Met Pro Lys Ile Gly Ile His	
1 5 10 15	
Pro Ile Lys Thr Gly Arg Ile Arg Tyr Arg Tyr Ile Thr Leu Ile Gly	
20 25 30	
Pro Arg His Ser Phe Tyr Tyr Cys Asn Leu Leu Leu Leu Ser Arg Ile	
35 40 45	
His Val Thr Leu Thr Ala His Asn Glu Phe Cys Pro Thr His Arg Ala	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 373...1110
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

GAGATATTAA AAAGAGATAT TAAAATGGCT TTTAAGCTTC TATGAAGCCC CCCCCCTCC      60
TCCTTTTGGC CTTTATTTTCG TGGGCAAATC GCCCACAGGA CAAGCGGCCA CACCCACGCT      120
TGGGCGGGTG ATTTTCTCTA CATTTTCTTG AGCTTTTGTG GGGTCATTCA CCCAAGTTTT      180
ATAGAACTCA AAAGGGCATT CCGCCACACC CTTATCCCCA TCGCCACTAG CAAAAACCCC      240
ACTATAACCT CTGTGCAAGA GTTTGAAGAG TTGGTTTGTG CTTTGGTCGT ATTTTCTCGC      300
ATCACGGATT TGTGTCACAG AAAGTTGAGC GTATTGAAGA CCATTTTCTT CTTCCCCGCA      360
TTCGCCCAAA GT ATG CCC GTC AAA ACC AAT AAT GCT AGA ATG CCC AAA ATA      411
      Met Pro Val Lys Thr Asn Asn Ala Arg Met Pro Lys Ile
              1              5              10

GGA ATA CAC CCC ATC AAA ACC GGT CGC ATT CGC TAC CGC TAC ATA ACA      459
Gly Ile His Pro Ile Lys Thr Gly Arg Ile Arg Tyr Arg Tyr Ile Thr
      15              20              25

TTG ATT GGC CCA CGC CAT AGC TTT TAC TAT TGC AAT TTG TTG CTC CTT      507
Leu Ile Gly Pro Arg His Ser Phe Tyr Tyr Cys Asn Leu Leu Leu Leu
      30              35              40              45

AGC CGG ATA CAT GTA ACC TTG ACA GCG CAC AAT GAG TTC TGC CCC ACG      555
Ser Arg Ile His Val Thr Leu Thr Ala His Asn Glu Phe Cys Pro Thr
              50              55              60

CAT CGC GCA ATC GCG CCA AAT TTC AGG GTA GTT TCC ATC ATC GCA AAT      603
His Arg Ala Ile Ala Pro Asn Phe Arg Val Val Ser Ile Ile Ala Asn
              65              70              75

AAT CAA AGA AAC TTT CAA GCC CTT AGG CCC ATC AAC CAC ATA AGT TTT      651
Asn Gln Arg Asn Phe Gln Ala Leu Arg Pro Ile Asn His Ile Ser Phe
              80              85              90

ATC CCC AGG ATA CCA ACA TTC AAT AGG GCA CCA AGG CAA GAT TTT GCG      699
Ile Pro Arg Ile Pro Thr Phe Asn Arg Ala Pro Arg Gln Asp Phe Ala
              95              100              105

GTA TTT TTG CAC GAT CTC ACC CTT ATC ATT GAC AAG AAT CAA AGT GTT      747
Val Phe Leu His Asp Leu Thr Leu Ile Ile Asp Lys Asn Gln Ser Val
      110              115              120              125

```

TTT AAA GAA GAA ATC AGC CTG GCC TTT AGC GCC ATT AGC AAA ATC TTT T 828
Phe Lys Glu Glu Ile Ser Leu Ala Phe Ser Ala Ile Ser Lys Ile Phe
240 245 250 255

AAAGGATAAA CATGATTAGT TTAAAGAAG CTCTAAAAT CCATTCT 875

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asp | Phe | Ile | Gln | Glu | Leu | Ser | Thr | Pro | His | Val | Arg | Asp | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Leu | Phe | Leu | Arg | Val | Ser | Gly | Val | Leu | Ser | Phe | Phe | Pro | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Glu | Asn | His | Leu | Val | Pro | Leu | Ser | Val | Arg | Gly | Ala | Leu | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Val | Ser | Ala | Ile | Phe | Tyr | Pro | Thr | Leu | Glu | Phe | Ser | Asn | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Thr | Pro | Glu | Gly | Phe | Ile | Ile | Ala | Cys | Leu | Cys | Glu | Leu | Phe | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Gly | Val | Cys | Ala | Ser | Val | Phe | Leu | Gln | Ile | Val | Phe | Ala | Ser | Leu | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Ala | Thr | Asp | Ser | Ile | Ser | Phe | Ser | Met | Gly | Leu | Thr | Met | Ala | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Tyr | Asp | Pro | Ile | Ser | Gly | Ser | Gln | Lys | Pro | Ile | Val | Gly | Gln | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Leu | Leu | Ala | Ile | Leu | Ile | Leu | Leu | Asp | Leu | Ser | Phe | His | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Ile | Ile | Leu | Phe | Val | Asp | His | Ser | Leu | Lys | Ala | Val | Pro | Leu | Gly |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Phe | Val | Phe | Glu | Pro | Ala | Leu | Ala | Lys | Asn | Ile | Val | Lys | Ala | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | His | Leu | Phe | Val | Ile | Gly | Phe | Ser | Met | Ala | Phe | Pro | Ile | Leu | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Val | Leu | Leu | Ser | Asp | Ile | Ile | Phe | Gly | Met | Ile | Met | Lys | Thr | His |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Pro | Gln | Phe | Asn | Leu | Leu | Ala | Ile | Gly | Phe | Pro | Val | Lys | Ile | Ala | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Phe | Val | Gly | Ile | Ile | Leu | Ile | Ala | Ser | Ala | Ile | Met | Gly | Arg | Phe |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Lys | Glu | Glu | Ile | Ser | Leu | Ala | Phe | Ser | Ala | Ile | Ser | Lys | Ile | Phe |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |

(2) INFORMATION FOR SEQ ID NO:107:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Phe | Leu | Leu | Phe | Leu | Arg | Val | Ser | Gly | Val | Leu | Ser | Phe | Phe | Pro |     |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| TTT | TTT | GAA | AAC | CAT | TTA | GTG | CCT | TTG | TCG | GTG | CGT | GGG | GCT | TTG | AGT | 203 |  |
| Phe | Phe | Glu | Asn | His | Leu | Val | Pro | Leu | Ser | Val | Arg | Gly | Ala | Leu | Ser |     |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| TTG | TAT | GTG | AGC | GCG | ATT | TTT | TAC | CCC | ACT | TTA | GAA | TTT | TCA | AAC | GCC | 251 |  |
| Leu | Tyr | Val | Ser | Ala | Ile | Phe | Tyr | Pro | Thr | Leu | Glu | Phe | Ser | Asn | Ala |     |  |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| GCT | TAC | ACG | CCA | GAG | GGT | TTT | ATC | ATT | GCT | TGC | TTG | TGC | GAA | TTG | TTT | 299 |  |
| Ala | Tyr | Thr | Pro | Glu | Gly | Phe | Ile | Ile | Ala | Cys | Leu | Cys | Glu | Leu | Phe |     |  |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |  |
| TTA | GGG | GTG | TGC | GCG | TCT | GTC | TTT | TTA | CAA | ATC | GTC | TTT | GCA | AGC | TTA | 347 |  |
| Leu | Gly | Val | Cys | Ala | Ser | Val | Phe | Leu | Gln | Ile | Val | Phe | Ala | Ser | Leu |     |  |
| 80  |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| GTG | TTT | GCA | ACC | GAT | AGC | ATC | AGC | TTT | TCT | ATG | GGG | CTT | ACG | ATG | GCG | 395 |  |
| Val | Phe | Ala | Thr | Asp | Ser | Ile | Ser | Phe | Ser | Met | Gly | Leu | Thr | Met | Ala |     |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| AGC | GCG | TAT | GAT | CCT | ATT | TCA | GGA | TCG | CAA | AAA | CCC | ATT | GTG | GGG | CAA | 443 |  |
| Ser | Ala | Tyr | Asp | Pro | Ile | Ser | Gly | Ser | Gln | Lys | Pro | Ile | Val | Gly | Gln |     |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| GCC | CTT | TTA | TTG | TTA | GCG | ATT | TTA | ATT | TTA | TTG | GAT | TTA | TCG | TTC | CAC | 491 |  |
| Ala | Leu | Leu | Leu | Leu | Ala | Ile | Leu | Ile | Leu | Leu | Asp | Leu | Ser | Phe | His |     |  |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| CAT | CAA | ATC | ATT | TTG | TTT | GTG | GAT | CAC | AGC | TTA | AAA | GCC | GTC | CCT | TTA | 539 |  |
| His | Gln | Ile | Ile | Leu | Phe | Val | Asp | His | Ser | Leu | Lys | Ala | Val | Pro | Leu |     |  |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |  |
| GGG | CAA | TTT | GTC | TTT | GAG | CCA | GCG | TTG | GCT | AAA | AAC | ATC | GTT | AAA | GCC | 587 |  |
| Gly | Gln | Phe | Val | Phe | Glu | Pro | Ala | Leu | Ala | Lys | Asn | Ile | Val | Lys | Ala |     |  |
| 160 |     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| TTT | TCG | CAC | CTC | TTT | GTC | ATA | GGG | TTT | TCT | ATG | GCG | TTC | CCT | ATT | TTA | 635 |  |
| Phe | Ser | His | Leu | Phe | Val | Ile | Gly | Phe | Ser | Met | Ala | Phe | Pro | Ile | Leu |     |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |  |
| TGC | TTG | GTG | TTA | TTG | AGC | GAT | ATT | ATT | TTT | GGC | ATG | ATC | ATG | AAA | ACC | 683 |  |
| Cys | Leu | Val | Leu | Leu | Ser | Asp | Ile | Ile | Phe | Gly | Met | Ile | Met | Lys | Thr |     |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| CAC | CCT | CAG | TTC | AAC | CTG | CTC | GCT | ATT | GGG | TTT | CCG | GTT | AAA | ATT | GCG | 731 |  |
| His | Pro | Gln | Phe | Asn | Leu | Leu | Ala | Ile | Gly | Phe | Pro | Val | Lys | Ile | Ala |     |  |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| ATC | GGG | TTT | GTG | GGC | ATT | ATC | TTA | ATC | GCT | TCG | GCT | ATC | ATG | GGG | CGT | 779 |  |
| Ile | Gly | Phe | Val | Gly | Ile | Ile | Leu | Ile | Ala | Ser | Ala | Ile | Met | Gly | Arg |     |  |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |  |

```

Lys Glu Phe Val Leu Ala Ile Trp Leu Thr Leu Pro Val Leu Val Phe
 195 200 205
Ala Phe Asp His Ser Pro Ile Ile Ser Thr Phe Thr Gln Asn Val Gly
 210 215 220
Lys Glu Tyr Gly Val Phe Lys Glu Tyr Lys Leu Asn Gln Ile Glu Leu
 225 230 235 240
Gly Thr Ser Leu Met Leu Leu Gly Phe Val Met Phe Phe Val Phe Ser
 245 250 255
Cys Val Met Cys Leu Asn Ala Asp Asp Phe Val Lys Ala Arg Glu Gln
 260 265 270
Asn Ile Pro Ile Leu Ser Tyr Leu Ala Asn Thr Leu Asn Asn Pro Leu
 275 280 285
Ile Asn Tyr Ala Gly Pro Val Val Ala Phe Leu Ala Ile Phe Ser Ser
 290 295 300
Phe Phe Gly His Tyr Tyr Gly Ala Lys Glu Gly Leu Glu Gly Ile Ile
 305 310 315 320
Ile Gln Ser Leu Lys Leu Lys Lys Ala Ser Lys Pro Leu Ser Val Ser
 325 330 335
Val Thr Ile Phe Leu Trp Leu Thr Ile Thr Leu Val Ala Tyr Ile Asn
 340 345 350
Pro Asn Ile Leu Asp Phe Ile Glu Asn Leu Gly Gly Pro Ile Ile Ala
 355 360 365
Leu Ile Leu Phe Val Met Pro Met Ile Ala Phe Tyr Ser Val Ser Ser
 370 375 380
Leu Lys Arg Phe Arg Asn Phe Lys Val Asp Ile Phe Val Phe Val Phe
 385 390 395 400
Gly Ser Leu Thr Ala Leu Ser Val Phe Leu Gly Leu Phe
 405 410

```

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 63...827
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

TTTGCCACCT TATTGCAAAC CCTAATGCTA ACGCACTACT TTTTATCTT TAAAGAGAAA 60
GA ATG CTA GAT TTT ATT CAA GAG CTT AGC ACC CCC CAT GTT AGG GAT 107
Met Leu Asp Phe Ile Gln Glu Leu Ser Thr Pro His Val Arg Asp
 1 5 10 15

TTT TTC TTG TTG TTT TTA AGG GTT AGC GGC GTG CTG TCT TTC TTC CCT 155

```

AAT TTA GGC GGC CCC ATT ATC GCG CTC ATT CTG TTT GTG ATG CCC ATG 1218  
 Asn Leu Gly Gly Pro Ile Ile Ala Leu Ile Leu Phe Val Met Pro Met  
                   365                                  370                                  375

ATA GCT TTT TAT AGT GTT TCT AGT TTG AAG CGT TTT AGA AAT TTC AAA 1266  
 Ile Ala Phe Tyr Ser Val Ser Ser Leu Lys Arg Phe Arg Asn Phe Lys  
                   380                                  385                                  390

GTG GAT ATT TTT GTG TTT GTC TTT GGG AGC TTG ACG GCT TTG AGC GTG 1314  
 Val Asp Ile Phe Val Phe Val Phe Gly Ser Leu Thr Ala Leu Ser Val  
                   395                                  400                                  405

TTT TTA GGA CTA TTT TAATGGCTAG TTTTCTATT TTATCTATTT TTAAAATCGG C 1370  
 Phe Leu Gly Leu Phe  
                   410

GTGGGGCCTA GC 1382

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Ala Gln Glu Lys Ala Val Pro Arg Asp Pro Lys Lys Leu Asn Ala  
 1                  5                  10                  15  
 Phe Asp Leu Arg Trp Met Val Ser Leu Phe Gly Thr Ala Val Gly Ala  
                   20                  25                  30  
 Gly Ile Leu Phe Leu Pro Ile Arg Ala Gly Gly His Gly Val Trp Ala  
                   35                  40                  45  
 Ile Val Val Met Ser Ala Ile Ile Phe Pro Leu Thr Tyr Leu Gly His  
                   50                  55                  60  
 Arg Ala Leu Ala Tyr Phe Ile Gly Ser Lys Asp Lys Glu Asp Ile Thr  
 65                  70                  75                  80  
 Met Val Val Arg Ser His Phe Gly Ala Gln Trp Gly Phe Leu Ile Thr  
                   85                  90                  95  
 Leu Leu Tyr Phe Leu Ala Ile Tyr Pro Ile Cys Leu Val Tyr Gly Val  
                   100                  105                  110  
 Gly Ile Thr Asn Val Phe Asp His Phe Phe Thr Asn Gln Leu His Leu  
                   115                  120                  125  
 Ala Pro Phe His Arg Gly Leu Ala Val Ala Leu Val Ser Leu Met  
                   130                  135                  140  
 Met Leu Val Met Val Phe Asn Ala Thr Ile Val Thr Arg Ile Cys Asn  
 145                  150                  155                  160  
 Ala Leu Val Tyr Pro Leu Cys Leu Ile Leu Leu Phe Ser Leu Tyr  
                   165                  170                  175  
 Leu Ile Pro Tyr Trp Gln Gly Ala Asn Leu Phe Val Val Pro Ser Phe  
                   180                  185                  190



|                                                                 |      |
|-----------------------------------------------------------------|------|
| Ala Val Ala Leu Val Ser Leu Met Met Leu Val Met Val Phe Asn Ala |      |
| 140 145 150                                                     |      |
| ACG ATT GTT ACG CGC ATT TGT AAC GCT TTA GTG TAT CCT TTA TGC TTG | 594  |
| Thr Ile Val Thr Arg Ile Cys Asn Ala Leu Val Tyr Pro Leu Cys Leu |      |
| 155 160 165                                                     |      |
| ATT TTA TTG CTT TTT TCT TTG TAT CTT ATC CCT TAT TGG CAA GGC GCT | 642  |
| Ile Leu Leu Leu Phe Ser Leu Tyr Leu Ile Pro Tyr Trp Gln Gly Ala |      |
| 170 175 180                                                     |      |
| AAT CTT TTT GTG GTG CCG AGT TTT AAA GAA TTT GTG TTA GCG ATT TGG | 690  |
| Asn Leu Phe Val Val Pro Ser Phe Lys Glu Phe Val Leu Ala Ile Trp |      |
| 185 190 195 200                                                 |      |
| CTA ACC TTA CCG GTG CTT GTG TTT GCA TTC GAC CAT AGC CCC ATC ATT | 738  |
| Leu Thr Leu Pro Val Leu Val Phe Ala Phe Asp His Ser Pro Ile Ile |      |
| 205 210 215                                                     |      |
| TCA ACC TTC ACT CAA AAT GTG GGA AAA GAA TAC GGC GTT TTC AAA GAA | 786  |
| Ser Thr Phe Thr Gln Asn Val Gly Lys Glu Tyr Gly Val Phe Lys Glu |      |
| 220 225 230                                                     |      |
| TAC AAA CTC AAT CAA ATT GAA TTA GGG ACA TCG CTG ATG CTT TTA GGG | 834  |
| Tyr Lys Leu Asn Gln Ile Glu Leu Gly Thr Ser Leu Met Leu Leu Gly |      |
| 235 240 245                                                     |      |
| TTT GTG ATG TTT TTT GTG TTT TCG TGC GTC ATG TGC TTG AAT GCT GAT | 882  |
| Phe Val Met Phe Phe Val Phe Ser Cys Val Met Cys Leu Asn Ala Asp |      |
| 250 255 260                                                     |      |
| GAT TTT GTG AAA GCA AGG GAA CAA AAT ATC CCC ATT TTA AGC TAT TTG | 930  |
| Asp Phe Val Lys Ala Arg Glu Gln Asn Ile Pro Ile Leu Ser Tyr Leu |      |
| 265 270 275 280                                                 |      |
| GCT AAC ACT TTA AAC AAC CCT TTA ATC AAT TAT GCG GGG CCT GTG GTG | 978  |
| Ala Asn Thr Leu Asn Asn Pro Leu Ile Asn Tyr Ala Gly Pro Val Val |      |
| 285 290 295                                                     |      |
| GCT TTT TTA GCG ATT TTT TCA TCT TTT TTT GGG CAT TAT TAT GGG GCT | 1026 |
| Ala Phe Leu Ala Ile Phe Ser Ser Phe Phe Gly His Tyr Tyr Gly Ala |      |
| 300 305 310                                                     |      |
| AAG GAG GGT TTA GAA GGC ATT ATT ATT CAA AGC TTA AAA TTG AAA AAA | 1074 |
| Lys Glu Gly Leu Glu Gly Ile Ile Ile Gln Ser Leu Lys Leu Lys Lys |      |
| 315 320 325                                                     |      |
| GCT TCT AAA CCC TTG AGC GTT AGC GTA ACG ATT TTT TTA TGG CTG ACT | 1122 |
| Ala Ser Lys Pro Leu Ser Val Ser Val Thr Ile Phe Leu Trp Leu Thr |      |
| 330 335 340                                                     |      |
| ATC ACG CTT GTG GCT TAT ATT AAC CCC AAT ATC TTG GAT TTT ATT GAA | 1170 |
| Ile Thr Leu Val Ala Tyr Ile Asn Pro Asn Ile Leu Asp Phe Ile Glu |      |
| 345 350 355 360                                                 |      |

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 91...1329
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

ACCACCCCTT AATCTCAAAA AACCCCAATC ATAAAAAGCT TTATGCTACA ATGAAAGCTC 60
TTTAACACGA TAAAAGGGCG GTTTAATAGC ATG GCA CAA GAA AAA GCA GTT CCA 114
 Met Ala Gln Glu Lys Ala Val Pro
 1 5

AGA GAT CCT AAA AAA CTC AAT GCG TTT GAT TTG CGT TGG ATG GTG TCC 162
Arg Asp Pro Lys Lys Leu Asn Ala Phe Asp Leu Arg Trp Met Val Ser
 10 15 20

TTA TTT GGC ACG GCG GTG GGG GCT GGG ATT TTA TTT TTG CCT ATT AGA 210
Leu Phe Gly Thr Ala Val Gly Ala Gly Ile Leu Phe Leu Pro Ile Arg
 25 30 35 40

GCC GGT GGG CAT GGG GTA TGG GCT ATT GTG GTA ATG AGC GCG ATC ATT 258
Ala Gly Gly His Gly Val Trp Ala Ile Val Val Met Ser Ala Ile Ile
 45 50 55

TTC CCT TTA ACT TAT CTA GGG CAT AGA GCT TTA GCT TAT TTC ATA GGA 306
Phe Pro Leu Thr Tyr Leu Gly His Arg Ala Leu Ala Tyr Phe Ile Gly
 60 65 70

TCT AAA GAC AAA GAA GAC ATT ACC ATG GTC GTT CGC TCT CAT TTT GGC 354
Ser Lys Asp Lys Glu Asp Ile Thr Met Val Val Arg Ser His Phe Gly
 75 80 85

GCT CAA TGG GGT TTT CTT ATC ACT TTG CTT TAT TTC TTA GCG ATT TAT 402
Ala Gln Trp Gly Phe Leu Ile Thr Leu Leu Tyr Phe Leu Ala Ile Tyr
 90 95 100

CCT ATT TGC TTG GTT TAT GGG GTG GGT ATC ACT AAC GTG TTT GAT CAT 450
Pro Ile Cys Leu Val Tyr Gly Val Gly Ile Thr Asn Val Phe Asp His
 105 110 115 120

TTT TTC ACT AAC CAG TTG CAT TTA GCG CCT TTT CAT CGG GGA TTA TTG 498
Phe Phe Thr Asn Gln Leu His Leu Ala Pro Phe His Arg Gly Leu Leu
 125 130 135

GCT GTA GCG TTA GTT TCT TTA ATG ATG TTG GTG ATG GTT TTT AAC GCT 546

```

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 59...196
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

AACAAATTCTT TTTTAAGCAA AAACAAAACA AAATTAAGGC ATAATCACTC TTTTTAAA 58

ATG AAA GGT CGC GTA GCT CAG TTG GTA GAG CAC TAC CTT GAC ATG GTA 106
Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val
 1 5 10 15

GTG GCC GCT GGT TCA AGT CCA GTC GTG GCC ACC ATT ATC ACT CCA ATT 154
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile
 20 25 30

TTA ATT CTC ATT TTT TTG CGA GTT TTT GAT CTT TAT AAA TTC TAAAGGGGTA 206
Leu Ile Leu Ile Phe Leu Arg Val Phe Asp Leu Tyr Lys Phe
 35 40 45

TTAAACGCAC TTCTAATAAC GATTTTATAG CGCT 240

```

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val
 1 5 10 15
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile
 20 25 30
Leu Ile Leu Ile Phe Leu Arg Val Phe Asp Leu Tyr Lys Phe
 35 40 45

```

(2) INFORMATION FOR SEQ ID NO:103:

ATTACAAGGG AATGA

1010

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Met Lys Thr Ser Lys Thr Lys Thr Pro Lys Ser Val Leu Ile Ala Gly
 1 5 10 15
Pro Cys Val Ile Glu Ser Leu Glu Asn Leu Arg Ser Ile Ala Thr Lys
 20 25 30
Leu Gln Pro Leu Ala Asn Asn Glu Arg Leu Asp Phe Tyr Phe Lys Ala
 35 40 45
Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg Gly Pro
 50 55 60
Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Glu Glu Phe
 65 70 75 80
Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala Ser Val
 85 90 95
Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu Cys Arg
 100 105 110
Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile Val Asn
 115 120 125
Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr Ser Val
 130 135 140
Leu Lys Ala Leu Lys Thr Arg Asp Lys Ser Ile Gln Ser Pro Thr Tyr
 145 150 155 160
Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly Ser Ser
 165 170 175
Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys Ile Met
 180 185 190
Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val Gln Met
 195 200 205
Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe Ala Pro
 210 215 220
Ile Leu Ala Arg Ala Ala Ala Ala Val Gly Ile Asp Gly Leu Phe Ala
 225 230 235 240
Glu Thr His Val Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala Asn Met
 245 250 255
Leu Lys Pro Asp Glu Leu Glu Gln Leu Val Thr Asp Met Leu Lys Ile
 260 265 270
Gln Asn Leu Phe
 275

```

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGG CCT GGT TTA GAA AAA GGC CTA GAA ATG TTA CAA ACG ATC AAA GAG   | 363 |
| Gly Pro Gly Leu Glu Lys Gly Leu Glu Met Leu Gln Thr Ile Lys Glu   |     |
| 65 70 75                                                          |     |
| GAA TTT GGT TAT AAA ATC TTA ACC GAT GTG CAT GAG AGT TAT CAA GCA   | 411 |
| Glu Phe Gly Tyr Lys Ile Leu Thr Asp Val His Glu Ser Tyr Gln Ala   |     |
| 80 85 90                                                          |     |
| AGC GTG GCA GCC AAA GTG GCG GAT ATT TTA CAA ATC CCG GCG TTT TTG   | 459 |
| Ser Val Ala Ala Lys Val Ala Asp Ile Leu Gln Ile Pro Ala Phe Leu   |     |
| 95 100 105 110                                                    |     |
| TGC CGC CAA ACG GAT CTG ATT GTA GAA GTG AGC CAG ACT AAC GCT ATT   | 507 |
| Cys Arg Gln Thr Asp Leu Ile Val Glu Val Ser Gln Thr Asn Ala Ile   |     |
| 115 120 125                                                       |     |
| GTC AAT ATC AAA AAA GGG CAA TTC ATG AAC CCA AAA GAC ATG CAA TAT   | 555 |
| Val Asn Ile Lys Lys Gly Gln Phe Met Asn Pro Lys Asp Met Gln Tyr   |     |
| 130 135 140                                                       |     |
| TCT GTT CTA AAG GCC CTT AAA ACG AGA GAT AAA AGC ATT CAA AGC CCC   | 603 |
| Ser Val Leu Lys Ala Leu Lys Thr Arg Asp Lys Ser Ile Gln Ser Pro   |     |
| 145 150 155                                                       |     |
| ACT TAT GAA ACA GCG TTA AAA AAT GGC GTG TGG CTG TGT GAA AGG GGG   | 651 |
| Thr Tyr Glu Thr Ala Leu Lys Asn Gly Val Trp Leu Cys Glu Arg Gly   |     |
| 160 165 170                                                       |     |
| AGC AGC TTT GGG TAT GGG AAT TTA GTG GTG GAT ATG CGC TCT TTA AAA   | 699 |
| Ser Ser Phe Gly Tyr Gly Asn Leu Val Val Asp Met Arg Ser Leu Lys   |     |
| 175 180 185 190                                                   |     |
| ATC ATG CGA GAA TTT GCC CCT GTG ATT TTT GAC GCT ACC CAT AGC GTG   | 747 |
| Ile Met Arg Glu Phe Ala Pro Val Ile Phe Asp Ala Thr His Ser Val   |     |
| 195 200 205                                                       |     |
| CAA ATG CCA GGG GGA GCG AAC GGG AAA AGT TCA GGA GAC AGC TCT TTT   | 795 |
| Gln Met Pro Gly Gly Ala Asn Gly Lys Ser Ser Gly Asp Ser Ser Phe   |     |
| 210 215 220                                                       |     |
| GCC CCT ATT TTA GCG AGA GCT GCG GCG GCG GTG GGG ATT GAT GGG TTG   | 843 |
| Ala Pro Ile Leu Ala Arg Ala Ala Ala Ala Val Gly Ile Asp Gly Leu   |     |
| 225 230 235                                                       |     |
| TTT GCT GAA ACG CAT GTT GAT CCT AAA AAC GCC CTA AGC GAT GGA GCA   | 891 |
| Phe Ala Glu Thr His Val Asp Pro Lys Asn Ala Leu Ser Asp Gly Ala   |     |
| 240 245 250                                                       |     |
| AAC ATG CTA AAA CCT GAC GAG CTA GAA CAA TTA GTA ACC GAC ATG TTA   | 939 |
| Asn Met Leu Lys Pro Asp Glu Leu Glu Gln Leu Val Thr Asp Met Leu   |     |
| 255 260 265 270                                                   |     |
| AAA ATC CAA AAT TTA TTT TAAAGGAATT TCATGCAAAT CATAGAAGGG AAATTGCA | 995 |
| Lys Ile Gln Asn Leu Phe                                           |     |
| 275                                                               |     |

```

Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val Glu
 85 90 95
Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn Gly
 100 105 110
Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr Gly
 115 120 125
Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe Ile
 130 135 140
Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr Ser
 145 150 155 160
His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu Phe
 165 170 175
Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro Thr
 180 185 190
Phe Lys Gly Gly Phe
 195

```

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 130...957
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

AAGCGAGCAA GAATGAATTA AAAATTTTTTG GTTGGCACTA CATCATAGAA ACAGGCAGGA 60
TTTATAATTA TAATTTTGAA AGCCATTTTTT TTGAGCCGAT TGGAGAAACC ATTAAACAAA 120
GGAAAAGTC ATG AAA ACT TCT AAA ACA AAA ACC CCT AAA TCC GTT TTA ATC 171
 Met Lys Thr Ser Lys Thr Lys Thr Pro Lys Ser Val Leu Ile
 1 5 10

GCT GGG CCA TGC GTC ATT GAG AGC TTA GAA AAT CTA AGA AGT ATC GCC 219
Ala Gly Pro Cys Val Ile Glu Ser Leu Glu Asn Leu Arg Ser Ile Ala
 15 20 25 30

ACT AAA TTG CAA CCC CTA GCC AAC AAC GAG CGG TTG GAT TTT TAT TTT 267
Thr Lys Leu Gln Pro Leu Ala Asn Asn Glu Arg Leu Asp Phe Tyr Phe
 35 40 45

AAA GCG AGT TTT GAT AAG GCG AAC CGC ACG AGT TTA GAG AGT TAC AGA 315
Lys Ala Ser Phe Asp Lys Ala Asn Arg Thr Ser Leu Glu Ser Tyr Arg
 50 55 60

```

| 80                                                                  | 85 | 90  | 95  |     |
|---------------------------------------------------------------------|----|-----|-----|-----|
| GAG TCT CCT AAG GCC AAA CGG CAG CAG GAT TTG TAT TTC TTC CCT AAT     |    |     |     | 396 |
| Glu Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn     |    |     |     |     |
| 100                                                                 |    | 105 | 110 |     |
| GGG GTT ACT TAT AAA AGA AGC GAT GAT TCC AGT TTT TGG AGT GAA ACA     |    |     |     | 444 |
| Gly Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr     |    |     |     |     |
| 115                                                                 |    | 120 | 125 |     |
| GGG ATT TAT AAC CAT AAG GAG CAA AAT TTT AAA GGC AAG GGC CGT TTC     |    |     |     | 492 |
| Gly Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe     |    |     |     |     |
| 130                                                                 |    | 135 | 140 |     |
| ATT CTC ACT TCA AAG GAC AGC AAG ATT GAA GGG CTT GAC ATT TCT TAT     |    |     |     | 540 |
| Ile Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr     |    |     |     |     |
| 145                                                                 |    | 150 | 155 |     |
| TCG CAT GCA TTA GCT ATT ATT GAA GCT CAA AGC ATT CAA GCG CAT TTA     |    |     |     | 588 |
| Ser His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu     |    |     |     |     |
| 160                                                                 |    | 165 | 170 | 175 |
| TTC TTA GAT GAA ATC AAA CAA AGC CAA AAA GAA AAG AAA AAA TTC CCC     |    |     |     | 636 |
| Phe Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro     |    |     |     |     |
| 180                                                                 |    | 185 | 190 |     |
| ACT TTC AAA GGA GGT TTT TAATGCGTTG GTGGTGT TTTT TTGGTGTGTT GTTTTGGT |    |     |     | 692 |
| Thr Phe Lys Gly Gly Phe                                             |    |     |     |     |
| 195                                                                 |    |     |     |     |
| ATTTTAAGCG TGAT                                                     |    |     |     | 706 |

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Ser | Ser | Phe | Thr | Ser | Asn | Ser | Val | Leu | Asn | Phe | Phe | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Leu | Ser | Phe | Ile | Thr | Ile | Gly | Leu | Val | Phe | Phe | Phe | Leu | Arg | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gln | Pro | Thr | Ser | Val | Val | Ser | Lys | Glu | Asn | Ile | Pro | Lys | Ile | Glu | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Asn | Phe | Lys | Ala | Phe | Gln | Ile | Asn | Asp | Lys | Ile | Leu | Asp | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Glu | Gly | Lys | Lys | Ala | Leu | Gln | Tyr | Asp | Asp | His | Glu | Ile | Phe | Phe |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 435                                                             | 440 | 445 |
| Asn Ala Ser Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala |     |     |
| 450                                                             | 455 | 460 |
| Ser Val Leu Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala |     |     |
| 465                                                             | 470 | 475 |
| Leu Thr Thr Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Val |     |     |
|                                                                 | 485 | 490 |
| Gly Thr Gln Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Thr Gln Thr |     |     |
|                                                                 | 500 | 505 |
| Lys Ser Leu Tyr Phe Trp Phe Gly Val Asn Lys Arg Ala             |     |     |
| 515                                                             | 520 | 525 |

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 64...654
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CAGGGGGCAA GGGGGCTGTT AGGGAAGCGA TTGATTATCT TTAAACATTA GAAGGCTTGC | 60  |
| AAG ATG AAG CGC TCA AGC TTT ACC TCT AAT AGC GTT TTA AAC TTT TTT   | 108 |
| Met Lys Arg Ser Ser Phe Thr Ser Asn Ser Val Leu Asn Phe Phe       |     |
| 1 5 10 15                                                         |     |
| GTA GTT TTG TCT TTC ATT ACG ATA GGA TTA GTG TTT TTC TTT TTG CGT   | 156 |
| Val Val Leu Ser Phe Ile Thr Ile Gly Leu Val Phe Phe Phe Leu Arg   |     |
| 20 25 30                                                          |     |
| TCC CAA CCC ACT AGC GTA GTT TCT AAA GAA AAT ATC CCT AAA ATT GAA   | 204 |
| Ser Gln Pro Thr Ser Val Val Ser Lys Glu Asn Ile Pro Lys Ile Glu   |     |
| 35 40 45                                                          |     |
| TTA GAA AAT TTT AAA GCG TTT CAA ATC AAC GAT AAA ATC CTT GAT CTG   | 252 |
| Leu Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu   |     |
| 50 55 60                                                          |     |
| TCC ATA GAG GGC AAA AAA GCC CTA CAA TAC GAT GAT CAT GAA ATC TTT   | 300 |
| Ser Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe   |     |
| 65 70 75                                                          |     |
| TTT GAT TCC AAA ATC AAG CGC TAT GAT GAA GAC ACC ATT GAA AGC GTT   | 348 |
| Phe Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val   |     |



Met Lys Leu Phe Asn Ala Arg Leu Ile Val Phe Ile Gly Ala Leu Leu  
 1 5 10 15  
 Leu Gly Val Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro  
 20 25 30  
 Lys Ile Thr Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu  
 35 40 45  
 Gly Val Gln Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala  
 50 55 60  
 Ser Ala Leu Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp  
 65 70 75 80  
 Ile Lys Ser Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp  
 85 90 95  
 Glu Ala Lys Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser  
 100 105 110  
 Gln Phe Glu Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr  
 115 120 125  
 Pro Leu Glu Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile  
 130 135 140  
 Gly Ile Ile Arg Asn Arg Leu Asp Gln Phe Gly Leu Ala Glu Pro Val  
 145 150 155 160  
 Val Ile Gln Gln Gly Lys Glu Glu Ile Ser Val Gln Leu Pro Gly Ile  
 165 170 175  
 Lys Thr Leu Glu Glu Glu Arg Arg Ala Lys Asp Leu Ile Ser Arg Ser  
 180 185 190  
 Ala His Leu Gln Met Met Ala Val Asp Glu Glu His Asn Lys Asp Ala  
 195 200 205  
 Met Lys Met Thr Asp Leu Glu Ala Gln Lys Leu Gly Ser Val Leu Leu  
 210 215 220  
 Ser Asp Val Glu Met Gly Gly Lys Ile Leu Leu Lys Ala Ile Pro Ile  
 225 230 235 240  
 Leu Asp Gly Glu Met Leu Thr Asp Ala Lys Val Val Tyr Asp Gln Asn  
 245 250 255  
 Asn Gln Pro Val Val Ser Phe Thr Leu Asp Ala Gln Gly Ala Lys Ile  
 260 265 270  
 Phe Gly Asp Phe Ser Gly Ala Asn Val Gly Lys Arg Met Ala Ile Val  
 275 280 285  
 Leu Asp Asn Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly  
 290 295 300  
 Gly Gly Ser Gly Gln Ile Ser Gly Asn Phe Ser Val Ala Gln Ala Ser  
 305 310 315 320  
 Asp Leu Ala Ile Ala Leu Arg Ser Gly Ala Met Ser Ala Pro Ile Gln  
 325 330 335  
 Val Leu Glu Lys Arg Ile Ile Gly Pro Ser Leu Gly Lys Asp Ser Val  
 340 345 350  
 Lys Thr Ser Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly  
 355 360 365  
 Phe Met Val Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Leu Ala  
 370 375 380  
 Leu Val Val Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly  
 385 390 395 400  
 Ala Thr Leu Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly  
 405 410 415  
 Ile Ala Val Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val  
 420 425 430  
 Leu Arg Glu Asn Glu Gly Ile Ala Lys Ala Ile His Leu Gly Tyr Ile

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CTT TAT TAC TCT ATG GCG GGG GTG ATC GCT TGT TTG GCG TTA GTG GTC   | 1210 |
| Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Leu Ala Leu Val Val   |      |
| 375 380 385                                                       |      |
| AAT CTT TTT TTG ATT GTG GCG GTC ATG GCG ATT TTT GGA GCG ACG CTG   | 1258 |
| Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly Ala Thr Leu   |      |
| 390 395 400                                                       |      |
| ACT TTA CCG GGA ATG GCG GGG ATT GTT TTA ACC GTG GGG ATT GCC GTG   | 1306 |
| Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly Ile Ala Val   |      |
| 405 410 415                                                       |      |
| GAT GCT AAT ATC ATC ATC AAC GAG CGC ATT AGA GAA GTC TTA AGA GAG   | 1354 |
| Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val Leu Arg Glu   |      |
| 420 425 430 435                                                   |      |
| AAT GAG GGC ATC GCT AAA GCG ATC CAT TTA GGC TAT ATC AAT GCG AGC   | 1402 |
| Asn Glu Gly Ile Ala Lys Ala Ile His Leu Gly Tyr Ile Asn Ala Ser   |      |
| 440 445 450                                                       |      |
| CGG GCG ATT TTT GAT TCT AAT ATC ACT TCT TTG ATC GCT TCA GTG TTA   | 1450 |
| Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala Ser Val Leu   |      |
| 455 460 465                                                       |      |
| TTA TAC GCT TAT GGC ACA GGA GCG ATT AAA GGC TTT GCC CTA ACT ACA   | 1498 |
| Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala Leu Thr Thr   |      |
| 470 475 480                                                       |      |
| GGC ATT GGG ATT TTA GCC TCT ATT ATC ACC GCT ATT GTT GGC ACG CAA   | 1546 |
| Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Val Gly Thr Gln   |      |
| 485 490 495                                                       |      |
| GGG ATT TAT CAA GCC CTT TTA CCT AAA CTC ACT CAA ACA AAA AGC CTT   | 1594 |
| Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Thr Gln Thr Lys Ser Leu   |      |
| 500 505 510 515                                                   |      |
| TAC TTT TGG TTT GGC GTG AAT AAA AGA GCT TAGGAGGTTT TATGGAATTA TTC | 1647 |
| Tyr Phe Trp Phe Gly Val Asn Lys Arg Ala                           |      |
| 520 525                                                           |      |
| AAACGAACTA GAATCTTAAG CTTC                                        | 1671 |

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

|                                                                 |      |
|-----------------------------------------------------------------|------|
| CGT AAC CGC TTG GAT CAA TTT GGT TTG GCA GAG CCT GTA GTC ATT CAG | 538  |
| Arg Asn Arg Leu Asp Gln Phe Gly Leu Ala Glu Pro Val Val Ile Gln |      |
| 150 155 160                                                     |      |
| CAA GGT AAA GAA GAA ATT TCG GTG CAA TTG CCT GGC ATT AAG ACT TTA | 586  |
| Gln Gly Lys Glu Glu Ile Ser Val Gln Leu Pro Gly Ile Lys Thr Leu |      |
| 165 170 175                                                     |      |
| GAA GAA GAA CGG CGC GCT AAA GAC TTG ATT TCA AGA TCC GCT CAT TTG | 634  |
| Glu Glu Glu Arg Arg Ala Lys Asp Leu Ile Ser Arg Ser Ala His Leu |      |
| 180 185 190 195                                                 |      |
| CAG ATG ATG GCG GTG GAT GAA GAA CAC AAT AAA GAT GCG ATG AAA ATG | 682  |
| Gln Met Met Ala Val Asp Glu Glu His Asn Lys Asp Ala Met Lys Met |      |
| 200 205 210                                                     |      |
| ACG GAT TTA GAG GCT CAA AAA TTA GGC AGC GTG TTG TTG TCT GAT GTG | 730  |
| Thr Asp Leu Glu Ala Gln Lys Leu Gly Ser Val Leu Leu Ser Asp Val |      |
| 215 220 225                                                     |      |
| GAA ATG GGG GGT AAA ATC TTG CTC AAA GCG ATC CCC ATT TTA GAT GGC | 778  |
| Glu Met Gly Gly Lys Ile Leu Leu Lys Ala Ile Pro Ile Leu Asp Gly |      |
| 230 235 240                                                     |      |
| GAA ATG CTT ACA GAT GCG AAA GTG GTG TAT GAC CAA AAC AAC CAG CCG | 826  |
| Glu Met Leu Thr Asp Ala Lys Val Val Tyr Asp Gln Asn Asn Gln Pro |      |
| 245 250 255                                                     |      |
| GTG GTG AGC TTC ACG CTG GAT GCG CAA GGG GCT AAG ATT TTT GGG GAT | 874  |
| Val Val Ser Phe Thr Leu Asp Ala Gln Gly Ala Lys Ile Phe Gly Asp |      |
| 260 265 270 275                                                 |      |
| TTC TCA GGT GCG AAT GTG GGC AAA CGC ATG GCG ATT GTT TTA GAC AAT | 922  |
| Phe Ser Gly Ala Asn Val Gly Lys Arg Met Ala Ile Val Leu Asp Asn |      |
| 280 285 290                                                     |      |
| AAG GTC TAT TCA GCC CCG GTG ATT AGG GAG CGT ATC GGT GGG GGG AGC | 970  |
| Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly Gly Gly Ser |      |
| 295 300 305                                                     |      |
| GGG CAG ATT AGC GGG AAT TTT AGC GTG GCT CAA GCG AGC GAT TTA GCG | 1018 |
| Gly Gln Ile Ser Gly Asn Phe Ser Val Ala Gln Ala Ser Asp Leu Ala |      |
| 310 315 320                                                     |      |
| ATC GCT TTA AGG AGT GGG GCG ATG AGC GCT CCC ATT CAG GTT TTA GAA | 1066 |
| Ile Ala Leu Arg Ser Gly Ala Met Ser Ala Pro Ile Gln Val Leu Glu |      |
| 325 330 335                                                     |      |
| AAA AGA ATT ATA GGC CCA AGT TTA GGG AAA GAC AGC GTT AAA ACT TCC | 1114 |
| Lys Arg Ile Ile Gly Pro Ser Leu Gly Lys Asp Ser Val Lys Thr Ser |      |
| 340 345 350 355                                                 |      |
| ATT ATC GCT CTA GTT GGG GGC TTT ATT TTA GTG ATG GGC TTT ATG GTG | 1162 |
| Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly Phe Met Val |      |
| 360 365 370                                                     |      |

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 50...1624  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CAAAATTATC TGGTGCTAAG ACTTTGAAAC AACGCCAAAT AACAACTGA ATG AAA CTT | 58  |
| Met Lys Leu                                                       |     |
| 1                                                                 |     |
| TTT AAC GCT CGT TTA ATC GTT TTT ATT GGC GCG CTT CTT TTA GGG GTA   | 106 |
| Phe Asn Ala Arg Leu Ile Val Phe Ile Gly Ala Leu Leu Leu Gly Val   |     |
| 5 10 15                                                           |     |
| GGG TTT TCT GTG CCT TCT TTA CTA GAA ACT AAA GGC CCT AAA ATC ACT   | 154 |
| Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro Lys Ile Thr   |     |
| 20 25 30 35                                                       |     |
| TTA GGT TTG GAT TTA AGG GGG GGG TTG AAC ATG CTT TTA GGG GTA CAA   | 202 |
| Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu Gly Val Gln   |     |
| 40 45 50                                                          |     |
| ACC GAT GAG GCT TTA AAA AAC AAG TAT TTA AGC TTG GCG TCC GCT TTA   | 250 |
| Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala Ser Ala Leu   |     |
| 55 60 65                                                          |     |
| GAA TAC AAC GCT AAA AAG CAA AAT ATC TTG CTT AAA GAT ATT AAA TCC   | 298 |
| Glu Tyr Asn Ala Lys Lys Gln Asn Ile Leu Leu Lys Asp Ile Lys Ser   |     |
| 70 75 80                                                          |     |
| AAT TTA GAA GGG ATC AGT TTT GAG CTT TTA GAT GAA GAT GAA GCG AAA   | 346 |
| Asn Leu Glu Gly Ile Ser Phe Glu Leu Leu Asp Glu Asp Glu Ala Lys   |     |
| 85 90 95                                                          |     |
| AAA TTA GAC GCG CTT TTA TTG GAA TTG CAA GGC CAT AGC CAG TTT GAA   | 394 |
| Lys Leu Asp Ala Leu Leu Leu Glu Leu Gln Gly His Ser Gln Phe Glu   |     |
| 100 105 110 115                                                   |     |
| ATC AAA AAG GAA GCG GGG TTT TAT AGC GTG AAT CTC ACC CCT TTA GAG   | 442 |
| Ile Lys Lys Glu Ala Gly Phe Tyr Ser Val Asn Leu Thr Pro Leu Glu   |     |
| 120 125 130                                                       |     |
| CAA GAA GAA TTG CGT AAA AAC ACG ATT TTG CAA GTG ATA GGG ATC ATT   | 490 |
| Gln Glu Glu Leu Arg Lys Asn Thr Ile Leu Gln Val Ile Gly Ile Ile   |     |
| 135 140 145                                                       |     |

Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu  
 100 105 110

CTG GAA AAA GAC CCC ACA AGG AGA AAC GCA AGG TTT TAT CGC GTG TTT 443  
 Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe  
 115 120 125

AAT GAG GCG CCA ACG ATT TTA ATG ATC CTC ATT GTG ATT TTA GTG GTT 491  
 Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val  
 130 135 140

GTC AAG CCT TTT TAAAGACAAG CCATGAAAAA AGAAAAGTCA TGAAAAAAGA AAAGCA 549  
 Val Lys Pro Phe  
 145

TCTCAAGC 557

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val  
 1 5 10 15  
 Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu  
 20 25 30  
 Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val  
 35 40 45  
 Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala  
 50 55 60  
 Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro  
 65 70 75 80  
 Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val  
 85 90 95  
 Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu  
 100 105 110  
 Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe  
 115 120 125  
 Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val  
 130 135 140  
 Val Lys Pro Phe  
 145

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs

```

Phe Glu Val Lys Gly Asp Thr Glu Ser Ile Gly Arg Leu Thr Thr Ile
 340 345 350
Ser Val Val Asn Ala Leu Phe Trp Ile Ile Phe Leu Asp Ala Ile Phe
 355 360 365
Ser Ile Ile Phe Ser Lys Leu Asn Ile
 370 375

```

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...503
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

CACAAAGAGAA AATTTGCAAG CGTTTTTACA ACAAATAAG ATAAATTAGG GAGAGTGGT 59

ATG GGA TTT TTG AAT GGG TAT TTT TTA TGG GTT AAG GCT TTC CAT GTG 107
Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val
 1 5 10 15

ATA GCG GTC ATT TCG TGG ATG GCA GCG TTG TTT TAT TTG CCG CGC CTT 155
Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
 20 25 30

TTT GTC TAT CAT GCA GAA AAC GCG CAT AAA AAA GAG TTT GTA GGA GTG 203
Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
 35 40 45

GTT CAA ATC CAA GAA AAA AAG CTT TAT TCC TTT ATC GCT TCA CCG GCT 251
Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
 50 55 60

ATG GGT TTT ACG CTT ATT ACA GGG ATT TTA ATG CTG TTG ATA GAG CCT 299
Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro
 65 70 75 80

ACG CTC TTT AAA AGT GGG GGT TGG TTG CAT GCT AAA TTG GCT TTA GTG 347
Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
 85 90 95

GTT TTA CTT TTA GCC TAT CAT TTT TAT TGC AAA AAA TGC ATG CGC GAG 395

```

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Met Lys Thr Glu Lys Gln Lys Phe Leu Glu Met Arg Lys Asp Gly Ala
 1 5 10 15
Asn Ser Val Leu Ile Leu Arg Gly Asp Trp Asp Phe Lys Thr Ser Val
 20 25 30
Phe Arg Leu Asp Glu Leu Lys Lys Asn Leu Leu Asp His Gln Gly Pro
 35 40 45
Leu Lys Met Asp Phe Ser Gly Cys Gln Lys Val Asp Phe Val Phe Gly
 50 55 60
Met Phe Leu Phe Asp Leu Val Lys Glu Arg Ser Leu Asn Ile Glu Leu
65 70 75 80
Cys Asn Val Ser Glu Asn Asn Ala Cys Ala Leu Lys Val Val Lys Asp
 85 90 95
Trp Leu Glu Lys Glu Glu Asp Leu Glu Ser Lys Lys Ala Gly Lys His
 100 105 110
Tyr Glu Leu Leu Ile Thr Lys Leu Gly Lys Ser Ile Val Glu Thr Tyr
 115 120 125
Asn Thr Phe Leu Asn Ala Phe Asn Phe Cys Gly Met Ile Leu Phe Tyr
 130 135 140
Phe Ile Lys Ser Val Phe Asn Pro Lys Arg Phe Cys Ile Thr Pro Leu
145 150 155 160
Leu Tyr His Ile Asn Glu Ser Gly Phe Lys Val Leu Pro Val Ser Ile
 165 170 175
Leu Thr Val Phe Ile Val Gly Phe Ala Val Ala Leu Gln Gly Ala Leu
 180 185 190
Gln Leu Gln Asp Met Gly Ala Pro Leu Met Ser Val Glu Met Thr Ala
 195 200 205
Lys Leu Ala Leu Arg Glu Ile Gly Pro Phe Ile Leu Thr Leu Val Val
 210 215 220
Ala Gly Arg Ser Ala Ser Ser Phe Thr Ala Gln Ile Gly Val Met Lys
225 230 235 240
Ile Thr Glu Glu Leu Asp Ala Met Lys Thr Met Gly Phe Asn Pro Phe
 245 250 255
Glu Phe Leu Val Leu Pro Arg Val Leu Ala Leu Val Ile Val Leu Pro
 260 265 270
Leu Leu Val Phe Ile Ala Asp Ala Phe Ala Ile Leu Gly Gly Met Phe
 275 280 285
Ala Ile Lys Tyr Gln Leu Asp Leu Gly Phe Pro Ser Tyr Ile Asp Arg
 290 295 300
Phe His Asp Thr Val Gly Trp Asn His Phe Leu Val Gly Ile Val Lys
305 310 315 320
Ala Pro Phe Trp Gly Phe Ala Ile Ala Met Val Gly Cys Met Arg Gly
 325 330 335

```

| 155                                                               | 160 | 165 | 170 |      |
|-------------------------------------------------------------------|-----|-----|-----|------|
| GTT TTG CCA GTG AGT ATT TTA ACG GTG TTT ATC GTG GGG TTT GCC GTT   |     |     |     | 641  |
| Val Leu Pro Val Ser Ile Leu Thr Val Phe Ile Val Gly Phe Ala Val   |     |     |     |      |
|                                                                   | 175 | 180 | 185 |      |
| GCT TTA CAA GGG GCT TTA CAA TTA CAA GAC ATG GGC GCG CCT TTA ATG   |     |     |     | 689  |
| Ala Leu Gln Gly Ala Leu Gln Leu Gln Asp Met Gly Ala Pro Leu Met   |     |     |     |      |
|                                                                   | 190 | 195 | 200 |      |
| TCG GTG GAA ATG ACG GCT AAA CTC GCT TTA AGA GAA ATC GGC CCT TTT   |     |     |     | 737  |
| Ser Val Glu Met Thr Ala Lys Leu Ala Leu Arg Glu Ile Gly Pro Phe   |     |     |     |      |
|                                                                   | 205 | 210 | 215 |      |
| ATT TTA ACC CTT GTG GTG GCC GGG AGG AGC GCG AGC AGT TTT ACC GCG   |     |     |     | 785  |
| Ile Leu Thr Leu Val Val Ala Gly Arg Ser Ala Ser Ser Phe Thr Ala   |     |     |     |      |
|                                                                   | 220 | 225 | 230 |      |
| CAA ATT GGG GTG ATG AAG ATC ACT GAG GAA TTA GAC GCG ATG AAA ACC   |     |     |     | 833  |
| Gln Ile Gly Val Met Lys Ile Thr Glu Glu Leu Asp Ala Met Lys Thr   |     |     |     |      |
|                                                                   | 235 | 240 | 245 | 250  |
| ATG GGC TTT AAC CCT TTT GAA TTT TTA GTG TTG CCT AGG GTG TTA GCC   |     |     |     | 881  |
| Met Gly Phe Asn Pro Phe Glu Phe Leu Val Leu Pro Arg Val Leu Ala   |     |     |     |      |
|                                                                   | 255 | 260 | 265 |      |
| TTA GTG ATT GTT TTG CCT TTA TTG GTG TTT ATT GCC GAT GCG TTC GCC   |     |     |     | 929  |
| Leu Val Ile Val Leu Pro Leu Leu Val Phe Ile Ala Asp Ala Phe Ala   |     |     |     |      |
|                                                                   | 270 | 275 | 280 |      |
| ATT CTT GGG GGC ATG TTT GCG ATT AAA TAC CAA TTG GAT TTA GGC TTC   |     |     |     | 977  |
| Ile Leu Gly Gly Met Phe Ala Ile Lys Tyr Gln Leu Asp Leu Gly Phe   |     |     |     |      |
|                                                                   | 285 | 290 | 295 |      |
| CCG AGC TAT ATT GAC AGA TTC CAT GAC ACA GTG GGT TGG AAC CAT TTT   |     |     |     | 1025 |
| Pro Ser Tyr Ile Asp Arg Phe His Asp Thr Val Gly Trp Asn His Phe   |     |     |     |      |
|                                                                   | 300 | 305 | 310 |      |
| TTG GTA GGG ATT GTC AAA GCC CCT TTT TGG GGG TTT GCG ATT GCG ATG   |     |     |     | 1073 |
| Leu Val Gly Ile Val Lys Ala Pro Phe Trp Gly Phe Ala Ile Ala Met   |     |     |     |      |
|                                                                   | 315 | 320 | 325 | 330  |
| GTA GGG TGC ATG CGC GGG TTT GAA GTC AAG GGG GAT ACT GAG AGC ATT   |     |     |     | 1121 |
| Val Gly Cys Met Arg Gly Phe Glu Val Lys Gly Asp Thr Glu Ser Ile   |     |     |     |      |
|                                                                   | 335 | 340 | 345 |      |
| GGG CGC TTG ACC ACT ATT AGC GTC GTG AAC GCT TTG TTT TGG ATC ATT   |     |     |     | 1169 |
| Gly Arg Leu Thr Thr Ile Ser Val Val Asn Ala Leu Phe Trp Ile Ile   |     |     |     |      |
|                                                                   | 350 | 355 | 360 |      |
| TTC TTA GAC GCT ATT TTT TCT ATC ATC TTT TCT AAG TTG AAC ATA TAATG |     |     |     | 1219 |
| Phe Leu Asp Ala Ile Phe Ser Ile Ile Phe Ser Lys Leu Asn Ile       |     |     |     |      |
|                                                                   | 365 | 370 | 375 |      |
| AACGCTACTA ACAATCAAGT CTTAATTGAA GTGAAGGATC TCCATAGCGC            |     |     |     | 1269 |



(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 84...1214  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTATCATTGT GTTAAAATAG TCGTTTAAAC AAACAAAATT TTGTTAATAG ATTTTACCTA | 60  |
| ATCTGAGAGA GAATTATATT TTA ATG AAG ACA GAG AAA CAA AAA TTT TTA GAG | 113 |
| Met Lys Thr Glu Lys Gln Lys Phe Leu Glu                           |     |
| 1 5 10                                                            |     |
| ATG CGT AAA GAT GGG GCG AAC TCT GTG CTG ATT TTA AGA GGG GAT TGG   | 161 |
| Met Arg Lys Asp Gly Ala Asn Ser Val Leu Ile Leu Arg Gly Asp Trp   |     |
| 15 20 25                                                          |     |
| GAT TTT AAA ACG AGC GTG TTT CGT TTA GAT GAG TTG AAA AAA AAT TTA   | 209 |
| Asp Phe Lys Thr Ser Val Phe Arg Leu Asp Glu Leu Lys Lys Asn Leu   |     |
| 30 35 40                                                          |     |
| TTA GAT CAT CAA GGG CCT TTA AAA ATG GAT TTT TCA GGG TGC CAA AAA   | 257 |
| Leu Asp His Gln Gly Pro Leu Lys Met Asp Phe Ser Gly Cys Gln Lys   |     |
| 45 50 55                                                          |     |
| GTG GAT TTT GTT TTT GGC ATG TTT TTA TTT GAT TTA GTT AAG GAG CGT   | 305 |
| Val Asp Phe Val Phe Gly Met Phe Leu Phe Asp Leu Val Lys Glu Arg   |     |
| 60 65 70                                                          |     |
| TCT TTA AAC ATT GAA TTG TGT AAC GTG AGT GAG AAT AAC GCA TGC GCT   | 353 |
| Ser Leu Asn Ile Glu Leu Cys Asn Val Ser Glu Asn Asn Ala Cys Ala   |     |
| 75 80 85 90                                                       |     |
| TTG AAA GTG GTT AAA GAC TGG CTT GAA AAA GAA GAG GAT TTA GAG TCT   | 401 |
| Leu Lys Val Val Lys Asp Trp Leu Glu Lys Glu Glu Asp Leu Glu Ser   |     |
| 95 100 105                                                        |     |
| AAA AAA GCG GGC AAA CAC TAC GAA CTT TTG ATC ACT AAA TTG GGT AAG   | 449 |
| Lys Lys Ala Gly Lys His Tyr Glu Leu Leu Ile Thr Lys Leu Gly Lys   |     |
| 110 115 120                                                       |     |
| AGT ATC GTA GAG ACT TAT AAT ACC TTT TTA AAC GCA TTC AAT TTT TGC   | 497 |
| Ser Ile Val Glu Thr Tyr Asn Thr Phe Leu Asn Ala Phe Asn Phe Cys   |     |
| 125 130 135                                                       |     |
| GGC ATG ATT TTA TTC TAC TTC ATT AAA AGC GTT TTC AAC CCC AAA CGC   | 545 |
| Gly Met Ile Leu Phe Tyr Phe Ile Lys Ser Val Phe Asn Pro Lys Arg   |     |
| 140 145 150                                                       |     |
| TTT TGT ATC ACT CCT TTG CTC TAT CAT ATC AAT GAA TCC GGG TTT AAG   | 593 |
| Phe Cys Ile Thr Pro Leu Leu Tyr His Ile Asn Glu Ser Gly Phe Lys   |     |

ATG TTT TAAATTTATA TTTGAAAGGA TGAACAATGA AAAATCAAGT TAAAAAAATT TT 740  
 Met Phe  
 210

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Lys | Thr | Lys | Leu | Lys | Ile | Ile | Ser | Ser | Val | Ile | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Leu | Leu | Trp | Val | Gly | Cys | Ser | Ser | Glu | Met | Ala | Thr | Tyr | Gln | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asn | Asp | Ala | Thr | Lys | Asn | Thr | Thr | Ala | Ser | Ile | Asn | Ser | Thr | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Leu | Thr | Ala | Asn | Ala | Met | Leu | Asp | Ser | Met | Phe | Ser | Asp | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Phe | Glu | Gln | Leu | Lys | Gly | Lys | His | Leu | Ile | Glu | Val | Ser | Asp | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Asn | Asp | Thr | Thr | Gln | Pro | Asn | Leu | Asp | Met | Asn | Leu | Leu | Thr | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Ile | Ala | Arg | Gln | Leu | Arg | Leu | Arg | Ser | Asn | Gly | Arg | Phe | Asn | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Arg | Ala | Ser | Gly | Gly | Ser | Gly | Ile | Ala | Ala | Asp | Ser | Arg | Met | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Gln | Arg | Glu | Lys | Glu | Arg | Glu | Ser | Glu | Glu | Tyr | Asn | Gln | Asp | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Thr | Val | Glu | Lys | Gly | Thr | Leu | Lys | Ala | Ala | Asp | Leu | Ser | Leu | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Val | Ser | Ser | Ile | Ala | Ala | Ser | Ile | Ser | Ser | Ser | Arg | Gln | Arg | Leu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asp | Tyr | Asp | Phe | Thr | Leu | Ser | Leu | Thr | Asn | Arg | Lys | Thr | Gly | Glu | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Trp | Ser | Asp | Val | Lys | Pro | Ile | Val | Lys | Asn | Ala | Ser | Asn | Lys | Arg |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Met | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 210 |

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

TTTAAATTA GAAACAGATG TATCTGTTTT AAATTTTGAA TAGGGAGTTT CTATCATT 58

ATG TTA TTG AAA ACA AAA TTA AAA ATT ATA AGC TCG GTG ATT TTG AGC 106  
Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser  
1 5 10 15

GCT TTA TTG TGG GTG GGT TGC TCA AGC GAA ATG GCA ACT TAT CAA AAC 154  
Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn  
20 25 30

GTG AAT GAT GCC ACT AAA AAT ACG ACT GCA AGC ATT AAT AGC ACG GAT 202  
Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp  
35 40 45

TTA TTG CTA ACC GCT AAC GCG ATG TTA GAT TCC ATG TTT AGC GAC CCT 250  
Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro  
50 55 60

AAT TTT GAG CAA CTC AAG GGC AAG CAT TTG ATT GAA GTT TCA GAT GTG 298  
Asn Phe Glu Gln Leu Lys Gly Lys His Leu Ile Glu Val Ser Asp Val  
65 70 75 80

ATT AAC GAC ACC ACG CAG CCC AAT TTG GAC ATG AAT CTT TTG ACG ACT 346  
Ile Asn Asp Thr Thr Gln Pro Asn Leu Asp Met Asn Leu Leu Thr Thr  
85 90 95

GAA ATC GCG CGG CAG TTG CGG TTG CGA TCT AAT GGG AGG TTC AAT ATC 394  
Glu Ile Ala Arg Gln Leu Arg Leu Arg Ser Asn Gly Arg Phe Asn Ile  
100 105 110

ACA AGG GCG AGC GGA GGG AGT GGC ATT GCA GCC GAT AGC AGA ATG GTG 442  
Thr Arg Ala Ser Gly Gly Ser Gly Ile Ala Ala Asp Ser Arg Met Val  
115 120 125

AAA CAG CGC GAA AAA GAA CGA GAG AGC GAA GAG TAT AAT CAA GAC ACC 490  
Lys Gln Arg Glu Lys Glu Arg Glu Ser Glu Glu Tyr Asn Gln Asp Thr  
130 135 140

ACT GTA GAA AAA GGC ACT TTA AAA GCC GCT GAT TTA TCT TTA AGT GGT 538  
Thr Val Glu Lys Gly Thr Leu Lys Ala Ala Asp Leu Ser Leu Ser Gly  
145 150 155 160

AAA GTA TCT AGT ATC GCA GCC TCT ATT AGT AGT TCT AGG CAG CGC TTG 586  
Lys Val Ser Ser Ile Ala Ala Ser Ile Ser Ser Ser Arg Gln Arg Leu  
165 170 175

GAC TAT GAC TTC ACC CTA AGC CTT ACC AAC AGG AAA ACG GGT GAA GAG 634  
Asp Tyr Asp Phe Thr Leu Ser Leu Thr Asn Arg Lys Thr Gly Glu Glu  
180 185 190

GTA TGG AGC GAT GTT AAG CCT ATT GTG AAG AAC GCT AGC AAT AAG CGT 682  
Val Trp Ser Asp Val Lys Pro Ile Val Lys Asn Ala Ser Asn Lys Arg  
195 200 205

GAC GCT CCC ATA AGA AGC GGT AAA ATA AAA TAC GGA TCC ATG ATG GAT 357  
Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser Met Met Asp  
70 75 80

AAA TCA TGAATCCATA AGATCCACTC TGAGCTTTTC AATTCCACAG CGTTATAAAG CA 415  
Lys Ser  
85

CTCTATAA 423

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

[illegible]

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 59...688  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

BNSDOCID: <WO\_\_9843478A1\_I\_>

```

AAC AAG CGC ATC ATG AAT TAC ATT CCT ATT AAG TTG AAT TTA AGT GGG 825
Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn Leu Ser Gly
 245 250 255

GTG ATC CCC CCT ATT TTC GCT TCA GCT TTG CTC GTG TTC CCT TCT ACG 873
Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe Pro Ser Thr
 260 265 270 275

ATT TTG CAG CAA GCC ACA AGC AAC AAA ACC TTG CAA GCG GTT GCG NAT 921
Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala Val Ala Xaa
 280 285 290

TTT TTA AGC CCG CAA GGT ATG CGT ATA ATA TTT TGATGTTCTT GCTCATCATC 974
Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe
 295 300

TTTTTTGCTT ACTTTTATTC TTCTATTGTG TTCAATTCTA AGGATATTGC GGATAATTTG 1034
AGGCGTAATG GCGGGTATAT TCCAGGGCTT AGGCCTGGAG AGGGGAC 1081

```

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Met Asn Lys Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu
 1 5 10 15
Phe Leu Tyr Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu
 20 25 30
Ala Ala Ile Lys Ala Phe Phe Asp Ser Asn Ser Asn Asn Ala Leu Gly
 35 40 45
Leu Phe Asn Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile
 50 55 60
Ser Leu Gly Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu
 65 70 75 80
Leu Ser Ala Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp
 85 90 95
Gly Met Gln Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile
 100 105 110
Thr Leu Ile Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser
 115 120 125
Gly Gly Ala Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile
 130 135 140
Val Ser Ala Phe Ser Met Leu Thr Gly Thr Met Leu Leu Met Trp Ile
 145 150 155 160
Gly Glu Gln Ile Thr Gln Arg Gly Val Gly Asn Gly Ile Ser Leu Ile
 165 170 175
Ile Phe Ala Gly Ile Val Ser Gly Ile Pro Ser Ala Ile Ser Gly Thr

```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu Ala Ala Ile |     |
| 20 25 30 35                                                     |     |
| AAG GCT TTT TTT GAC AGC AAT TCC AAC AAC GCT TTG GGG TTG TTT AAT | 201 |
| Lys Ala Phe Phe Asp Ser Asn Ser Asn Asn Ala Leu Gly Leu Phe Asn |     |
| 40 45 50                                                        |     |
| ATG TTT AGC GGG AAT GCG GTT TCT CGC TTG AGC ATC ATC TCG TTG GGT | 249 |
| Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile Ser Leu Gly |     |
| 55 60 65                                                        |     |
| ATC ATG CCC TAT ATC ACT TCT TCA ATT ATC ATG GAG CTT TTG AGC GCG | 297 |
| Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu Leu Ser Ala |     |
| 70 75 80                                                        |     |
| ACT TTC CCT AAC CTG GCT AAA ATG AAA AAA GAG CGG GAT GGC ATG CAA | 345 |
| Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp Gly Met Gln |     |
| 85 90 95                                                        |     |
| AAA TAC ATG CAA ATC GTG CGT TAT TTG ACC ATT TTA ATC ACC CTA ATC | 393 |
| Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile Thr Leu Ile |     |
| 100 105 110 115                                                 |     |
| CAA GCG GTG AGC GTT TCA GTA GGC TTA AGG AGC ATT AGT GGA GGA GCC | 441 |
| Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser Gly Gly Ala |     |
| 120 125 130                                                     |     |
| AAT GGG GCG ATC ATG ATT GAT ATG CAA GTT TTT ATG ATC GTT TCA GCG | 489 |
| Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile Val Ser Ala |     |
| 135 140 145                                                     |     |
| TTT TCT ATG CTT ACA GGA ACG ATG CTA CTC ATG TGG ATA GGG GAG CAA | 537 |
| Phe Ser Met Leu Thr Gly Thr Met Leu Leu Met Trp Ile Gly Glu Gln |     |
| 150 155 160                                                     |     |
| ATC ACG CAA AGG GGC GTG GGG AAT GGG ATC AGT CTC ATT ATT TTT GCC | 585 |
| Ile Thr Gln Arg Gly Val Gly Asn Gly Ile Ser Leu Ile Ile Phe Ala |     |
| 165 170 175                                                     |     |
| GGG ATT GTT TCA GGG ATC CCA TCA GCT ATT TCA GGC ACA TTC AAT TTG | 633 |
| Gly Ile Val Ser Gly Ile Pro Ser Ala Ile Ser Gly Thr Phe Asn Leu |     |
| 180 185 190 195                                                 |     |
| GTC AAT ACG GGC GTT ATT AAT ATC TTA ATG CTC ATT GGT ATT GTG CTG | 681 |
| Val Asn Thr Gly Val Ile Asn Ile Leu Met Leu Ile Gly Ile Val Leu |     |
| 200 205 210                                                     |     |
| ATT GTT TTA GCG ACT ATT TTT GCG ATT ATC TAT GTG GAA TTA GCT GAG | 729 |
| Ile Val Leu Ala Thr Ile Phe Ala Ile Ile Tyr Val Glu Leu Ala Glu |     |
| 215 220 225                                                     |     |
| CGC AGG ATC CCT ATT TCT TAT GCG CGT AAA GTG GTG ATG CAA AAC CAA | 777 |
| Arg Arg Ile Pro Ile Ser Tyr Ala Arg Lys Val Val Met Gln Asn Gln |     |
| 230 235 240                                                     |     |

```

Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys Asn Phe
65 70 75 80
Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro Ile Gly
 85 90 95
Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp Gly Phe
 100 105 110
Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile Ala Asp
 115 120 125
Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln Lys His
 130 135 140
Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser Lys Asp
 145 150 155 160
Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala Leu Ala
 165 170 175
Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp Ser Ser
 180 185 190
Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala Leu Leu
 195 200 205
Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys Gly Met
 210 215 220
Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile Ile Glu
 225 230 235 240
Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys Gly Phe
 245 250 255
Ile Gly Gly Met Ile Phe
 260

```

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...954
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

AAGTAATGCC CCTGTTGTAT CAGCTTGATT TAAGAGGAAT AAGTTATT ATG AAT AAA 57
 Met Asn Lys
 1

GCT ATT GCT AGT AAG ATA CTC ATC ACT TTG GGT TTT TTA TTT CTC TAC 105
Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu Phe Leu Tyr
 5 10 15

AGA GTC TTA GCT TAT ATC CCC ATT CCT GGC GTA GAT TTA GCA GCG ATC 153

```



|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAA CAC CAA ATC AAG CAA ATC TTT ATC GCC AGC CCC AAT GCG AGC AGT  | 540 |
| Lys His Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser  |     |
| 145 150 155                                                      |     |
| AAA GAT TTA GAA CAA GTC GCT ACG CAT TCG CAA GGC TAT ATC TAC GCT  | 588 |
| Lys Asp Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala  |     |
| 160 165 170                                                      |     |
| TTA GCC AGG AGT GGG GTT ACA GGG GCG AGC CGT ATT TTA GAG AAT GAT  | 636 |
| Leu Ala Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp  |     |
| 175 180 185 190                                                  |     |
| TCG AGT GCT ATT ATT AAA ACC TTA AAA GCT TTT AGC CCT ACC CCA GCC  | 684 |
| Ser Ser Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala  |     |
| 195 200 205                                                      |     |
| TTA CTG GGC TTT GGC ATT TCC AAA AAA GAA CAC ATC ACA AAC GCT AAA  | 732 |
| Leu Leu Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys  |     |
| 210 215 220                                                      |     |
| GGC ATG GGT GCT GAT GGC GTG ATT TGC GGA TCA GCG TTA GTC AAA ATC  | 780 |
| Gly Met Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile  |     |
| 225 230 235                                                      |     |
| ATA GAA GAA AAT TTA AAC AAT GAA AAC GCC ATG CTG GAA AAA ATT AAA  | 828 |
| Ile Glu Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys  |     |
| 240 245 250                                                      |     |
| GGG TTT ATA GGA GGA ATG ATT TTT TAAGGCTTTT AGGCTTTGTT GCGTTAAAAA | 882 |
| Gly Phe Ile Gly Gly Met Ile Phe                                  |     |
| 255 260                                                          |     |
| TTAAAGATCA CAGATTAAC                                             | 901 |

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu Lys Met |  |
| 1 5 10 15                                                       |  |
| Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu Leu Ser |  |
| 20 25 30                                                        |  |
| Phe Glu Ile Ile Lys Thr Leu Ile Ser Gly Val Ser Ala Leu Glu     |  |
| 35 40 45                                                        |  |
| Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr Ile Gln |  |
| 50 55 60                                                        |  |

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...852
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

GAATTTAAGC GGCAGAGGGG ATAAGGATTT AAGCACCGTT TATAACGCTT TAAAAGGAGG 60
TTTAAA ATG AGG TAT CAA AAC ATG TTT GAA ACC TTA AAA AAA CAC GAA 108
 Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu
 1 5 10

AAA ATG GCG TTT ATC CCG TTT GTA ACC TTG GGC GAT CCT AAT TAT GAA 156
Lys Met Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu
 15 20 25 30

TTG AGT TTT GAA ATC ATT AAA ACC CTA ATT ATT AGC GGG GTG AGC GCT 204
Leu Ser Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala
 35 40 45

TTA GAA TTG GGT CTT GCT TTT TCT GAT CCT GTG GCG GAT GGC ATT ACC 252
Leu Glu Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr
 50 55 60

ATA CAA GCG AGC CAT TTA AGG GCG TTA AAA CAC GCT AGC ATG GCT AAA 300
Ile Gln Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys
 65 70 75

AAT TTC CAG CTT TTA AAA AAG ATT AGA GAT TAC AAC CAC AAT ATT CCC 348
Asn Phe Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro
 80 85 90

ATA GGG CTT TTA GCG TAT GCG AAT TTA ATT TTT TCT TAT GGC GTT GAT 396
Ile Gly Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp
 95 100 105 110

GGC TTT TAC GCT CAA GCT AAA GAA TGC GGT ATA GAT AGC GTT TTA ATA 444
Gly Phe Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile
 115 120 125

GCG GAC ATG CCC CTA ATA GAA AAA GAA TTA GTC ATC AAA TCC GCT CAA 492
Ala Asp Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln
 130 135 140

```

| 85                                                                | 90  | 95  |     |
|-------------------------------------------------------------------|-----|-----|-----|
| TTT AGG ATT AAG ATT ATT GAT ATT TAT TTG GCA GAT TGC CCC AGT AGG   |     |     | 393 |
| Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys Pro Ser Arg   |     |     |     |
| 100                                                               | 105 | 110 | 115 |
|                                                                   |     |     |     |
| GCT ATT TTA TTG AAG CGT TTA GGG TTA AAG ATC GTG GTT TTT CTA TGC   |     |     | 441 |
| Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val Phe Leu Cys   |     |     |     |
|                                                                   | 120 | 125 | 130 |
|                                                                   |     |     |     |
| CCC TTT TTA TGG TTT GTT GCG TTT AAA AAC CCC TAT CAT AGG GCG TGG   |     |     | 489 |
| Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His Arg Ala Trp   |     |     |     |
|                                                                   | 135 | 140 | 145 |
|                                                                   |     |     |     |
| CAT GAA GAA AAA AGC AAA AGT CTT TTG GTA TTG TTT TAATCATGAT TTATTG |     |     | 541 |
| His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe                   |     |     |     |
|                                                                   | 150 | 155 |     |
|                                                                   |     |     |     |
| GTTGTATTTG GCGGTCTTTT TTTTGTGAG CGCATTAGAC                        |     |     | 581 |

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| Met His Ser Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr |     |     |     |
| 1                                                               | 5   | 10  | 15  |
| Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe     |     |     |     |
|                                                                 | 145 | 150 | 155 |

## (2) INFORMATION FOR SEQ ID NO:83:

```

Thr Lys Lys Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu
945 950 955 960
Glu Glu Lys Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met
 965 970 975
Leu Asn Arg Glu Glu Leu Leu Arg Val Thr Arg Ser Phe Leu Lys Arg
 980 985 990
Phe

```

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...525
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

AGGTTAAAGT TTAAGACAAA CCAAAGAGTT TGTCTTGTTT GTTTTTGA ATG CAC TCT 57
 Met His Ser
 1

CCA AAT TTA GAA AAA GAA GAA ACC GAA ATC ATA GAA ACA CTC CTT ATG 105
Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr Leu Leu Met
 5 10 15

CGT GAA AAA ATG CGT TTA TGC CCC TTG TAT TGG CGC ATC TTA GCG TTT 153
Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile Leu Ala Phe
20 25 30 35

TTA ACC GAT GGT TTG TTA GTG GCG TTT TTA TTG AGC GAT CTT TTA GAC 201
Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp Leu Leu Asp
 40 45 50

GCA TGC GAT TTC TTG CAT TCT TTA TAT TGG CTA GCT AAC CCT ATT TAT 249
Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn Pro Ile Tyr
 55 60 65

CAC AGC GCA TTT GTT GCG ATG GGT TTT ATC ATC TTG TAT GGC GTT TAT 297
His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr Gly Val Tyr
 70 75 80

GAA ATC TTT TTT GTG TGT TTG TGC AAG ATG AGC TTG GCT AAA CTG GTT 345
Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala Lys Leu Val

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 500 |     |     |     |     | 505 |     |     |     | 510 |     |     |     |  |  |
| Thr | Ser | Thr | Ile | Met | Glu | Phe | Phe | Met | Gly | Gly | Gln | Leu | Ser | Gln | Phe |  |  |
|     |     | 515 |     |     |     |     |     | 520 |     |     |     | 525 |     |     |     |  |  |
| Met | Asp | Gln | Thr | Asn | Pro | Leu | Ser | Glu | Val | Thr | His | Lys | Arg | Arg | Leu |  |  |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |
| Ser | Ala | Leu | Gly | Glu | Gly | Gly | Leu | Val | Lys | Asp | Arg | Val | Gly | Phe | Glu |  |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |  |
| Ala | Arg | Asp | Val | His | Pro | Thr | His | Tyr | Gly | Arg | Ile | Cys | Pro | Ile | Glu |  |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |  |
| Thr | Pro | Glu | Gly | Gln | Asn | Ile | Gly | Leu | Ile | Asn | Thr | Leu | Ser | Thr | Phe |  |  |
|     |     | 580 |     |     |     |     |     | 585 |     |     |     |     |     | 590 |     |  |  |
| Thr | Arg | Val | Asn | Asp | Leu | Gly | Phe | Ile | Glu | Ala | Pro | Tyr | Lys | Lys | Val |  |  |
|     | 595 |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |  |  |
| Val | Asp | Gly | Lys | Val | Val | Gly | Glu | Thr | Ile | Tyr | Leu | Thr | Ala | Ile | Gln |  |  |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |  |  |
| Glu | Asp | Ser | His | Ile | Ile | Ala | Pro | Ala | Ser | Thr | Pro | Ile | Asp | Glu | Glu |  |  |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |  |  |
| Gly | Asn | Ile | Leu | Gly | Asp | Leu | Ile | Glu | Thr | Arg | Val | Glu | Gly | Glu | Ile |  |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |  |  |
| Val | Leu | Asn | Glu | Lys | Ser | Lys | Val | Thr | Leu | Met | Asp | Leu | Ser | Ser | Ser |  |  |
|     |     | 660 |     |     |     |     |     | 665 |     |     |     | 670 |     |     |     |  |  |
| Met | Leu | Val | Gly | Val | Ala | Ala | Ser | Leu | Ile | Pro | Phe | Leu | Glu | His | Asp |  |  |
|     | 675 |     |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |  |  |
| Asp | Ala | Asn | Arg | Ala | Leu | Met | Gly | Thr | Asn | Met | Gln | Arg | Gln | Ala | Val |  |  |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |  |  |
| Pro | Leu | Leu | Arg | Ser | Asp | Ala | Pro | Ile | Val | Gly | Thr | Gly | Ile | Glu | Lys |  |  |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |  |  |
| Ile | Ile | Ala | Arg | Asp | Ser | Trp | Gly | Ala | Ile | Lys | Ala | Asn | Arg | Ala | Gly |  |  |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |  |  |
| Val | Val | Glu | Lys | Ile | Asp | Ser | Lys | Asn | Ile | Tyr | Ile | Leu | Gly | Glu | Ser |  |  |
|     |     | 740 |     |     |     |     |     | 745 |     |     |     | 750 |     |     |     |  |  |
| Lys | Glu | Glu | Ala | Tyr | Ile | Asp | Ala | Tyr | Ser | Leu | Gln | Lys | Asn | Leu | Arg |  |  |
|     | 755 |     |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |  |  |
| Thr | Asn | Gln | Asn | Thr | Ser | Phe | Asn | Gln | Val | Pro | Ile | Val | Lys | Val | Gly |  |  |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |  |  |
| Asp | Lys | Val | Gly | Ala | Gly | Gln | Ile | Ile | Ala | Asp | Gly | Pro | Ser | Met | Asp |  |  |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |  |  |
| Arg | Gly | Glu | Leu | Ala | Leu | Gly | Lys | Asn | Val | Arg | Val | Ala | Phe | Met | Pro |  |  |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |  |  |
| Trp | Asn | Gly | Tyr | Asn | Phe | Glu | Asp | Ala | Ile | Val | Val | Ser | Glu | Cys | Ile |  |  |
|     |     | 820 |     |     |     |     |     | 825 |     |     |     | 830 |     |     |     |  |  |
| Thr | Lys | Asp | Asp | Ile | Phe | Thr | Ser | Thr | His | Ile | Tyr | Glu | Lys | Glu | Val |  |  |
|     | 835 |     |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |  |  |
| Asp | Ala | Arg | Glu | Leu | Lys | His | Gly | Val | Glu | Glu | Phe | Thr | Ala | Asp | Ile |  |  |
|     | 850 |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |  |  |
| Pro | Asp | Val | Lys | Glu | Glu | Ala | Leu | Ala | His | Leu | Asp | Glu | Ser | Gly | Ile |  |  |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     | 880 |  |  |
| Val | Lys | Val | Gly | Thr | Tyr | Val | Ser | Ala | Gly | Met | Ile | Leu | Val | Gly | Lys |  |  |
|     |     |     |     | 885 |     |     |     |     | 890 |     |     |     |     | 895 |     |  |  |
| Thr | Ser | Pro | Lys | Gly | Glu | Ile | Lys | Ser | Thr | Pro | Glu | Glu | Arg | Leu | Leu |  |  |
|     |     | 900 |     |     |     |     |     | 905 |     |     |     |     |     | 910 |     |  |  |
| Arg | Ala | Ile | Phe | Gly | Asp | Lys | Ala | Gly | His | Val | Val | Asn | Lys | Ser | Leu |  |  |
|     | 915 |     |     |     |     |     | 920 |     |     |     |     | 925 |     |     |     |  |  |
| Tyr | Cys | Pro | Pro | Ser | Leu | Glu | Gly | Thr | Val | Ile | Asp | Val | Lys | Val | Phe |  |  |
|     | 930 |     |     |     |     | 935 |     |     |     |     | 940 |     |     |     |     |  |  |

Arg Ile Thr Leu Glu Tyr Ala Gly Cys Glu Phe Gly Lys Ser Lys Tyr  
 65 70 75 80  
 Thr Val Arg Glu Ala Met Glu Arg Gly Ile Thr Tyr Ser Ile Pro Leu  
 85 90 95  
 Lys Ile Lys Val Arg Leu Ile Leu Trp Glu Lys Asp Thr Lys Ser Gly  
 100 105 110  
 Glu Lys Asn Gly Ile Lys Asp Ile Lys Glu Gln Ser Ile Phe Ile Arg  
 115 120 125  
 Glu Ile Pro Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val  
 130 135 140  
 Glu Arg Val Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe  
 145 150 155 160  
 Lys Glu Glu Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly  
 165 170 175  
 Gln Ile Ile Pro Asp Arg Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser  
 180 185 190  
 Lys Asp Val Leu Tyr Ala Arg Ile Asn Lys Arg Arg Lys Val Pro Val  
 195 200 205  
 Thr Ile Leu Phe Arg Ala Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys  
 210 215 220  
 Met Phe Tyr Pro Leu Val Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu  
 225 230 235 240  
 Ile Pro Phe Ala Ser Leu Asp Ala Asn Gln Arg Met Glu Phe Asp Leu  
 245 250 255  
 Lys Asp Pro Gln Gly Lys Val Ile Leu Leu Ala Gly Lys Lys Leu Thr  
 260 265 270  
 Ser Arg Lys Ile Lys Glu Leu Lys Glu Asn His Leu Glu Trp Val Glu  
 275 280 285  
 Tyr Pro Met Asp Ile Leu Leu Asn Arg His Leu Ala Glu Pro Val Met  
 290 295 300  
 Val Gly Lys Glu Val Leu Leu Asp Met Leu Thr Gln Leu Asp Lys Asn  
 305 310 315 320  
 Lys Leu Glu Lys Ile His Asp Leu Gly Val Gln Glu Phe Val Ile Ile  
 325 330 335  
 Asn Asp Leu Ala Leu Gly His Asp Ala Ser Ile Ile Gln Ser Phe Ser  
 340 345 350  
 Ala Asp Ser Glu Ser Leu Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp  
 355 360 365  
 Asp Glu Asn Ala Leu Ala Ala Ile Arg Ile His Lys Val Met Lys Pro  
 370 375 380  
 Gly Asp Pro Val Thr Thr Glu Val Ala Lys Gln Phe Val Lys Lys Leu  
 385 390 395 400  
 Phe Phe Asp Pro Glu Arg Tyr Asp Leu Thr Met Val Gly Arg Met Lys  
 405 410 415  
 Met Asn His Lys Leu Gly Leu His Val Pro Asp Tyr Ile Thr Thr Leu  
 420 425 430  
 Thr His Glu Asp Ile Ile Thr Thr Val Lys Tyr Leu Met Lys Ile Lys  
 435 440 445  
 Asn Asn Gln Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg  
 450 455 460  
 Ile Arg Ala Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu  
 465 470 475 480  
 Val Lys Met Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly  
 485 490 495  
 Ala Phe Asp Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile

```

AAA GAA GAA GCG CTC GCT CAT CTT GAT GAA AGC GGG ATC GTT AAA GTC 2697
Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile Val Lys Val
 870 875 880

GGT ACT TAT GTG AGC GCT GGC ATG ATT TTG GTG GGC AAA ACT TCT CCT 2745
Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys Thr Ser Pro
 885 890 895

AAA GGC GAG ATT AAA AGC ACG CCT GAA GAG CGG CTT TTA AGG GCT ATT 2793
Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile
 900 905 910 915

TTT GGG GAT AAA GCC GGG CAT GTG GTC AAT AAG AGT TTG TAT TGC CCT 2841
Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu Tyr Cys Pro
 920 925 930

CCC AGT TTG GAA GGC ACG GTG ATT GAT GTG AAA GTC TTC ACT AAA AAA 2889
Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe Thr Lys Lys
 935 940 945

GGC TAT GAG AAA GAC GCG CGA GTT TTG AGC GCG TAT GAA GAA GAA AAA 2937
Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu Glu Glu Lys
 950 955 960

GCC AAG CTT GAT ATG GAG CAT TTT GAT CGC TTG ACC ATG CTC AAT AGA 2985
Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met Leu Asn Arg
 965 970 975

GAA GAA TTG TTG CGC GTT ACT CGC TCC TTT CTC AAG CGA TTT TAGAAGAGC 3036
Glu Glu Leu Leu Arg Val Thr Arg Ser Phe Leu Lys Arg Phe
 980 985 990

CTTTCAGCCA TAACGGCAAG GATTATAAAG AAGGCGATCA AATCCCTA 3084

```

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Met Ser Lys Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr
 1 5 10 15
Lys Thr Pro Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg
 20 25 30
Asp Ser Tyr Asp Ser Phe Leu Tyr Ser Lys Glu Gly Lys Glu Ser Gly
 35 40 45
Ile Glu Lys Val Phe Lys Ser Ile Phe Pro Ile Gln Asp Glu His Asn
 50 55 60

```

|                                                                 |      |
|-----------------------------------------------------------------|------|
| TTG GGC GAT TTG ATT GAA ACG CGC GTG GAA GGC GAG ATC GTT TTA AAC | 2025 |
| Leu Gly Asp Leu Ile Glu Thr Arg Val Glu Gly Glu Ile Val Leu Asn |      |
| 645 650 655                                                     |      |
| GAA AAA AGC AAA GTA ACC TTA ATG GAT TTA AGC TCT AGC ATG CTA GTG | 2073 |
| Glu Lys Ser Lys Val Thr Leu Met Asp Leu Ser Ser Ser Met Leu Val |      |
| 660 665 670 675                                                 |      |
| GGG GTA GCC GCA TCG CTC ATT CCT TTC TTA GAG CAT GAT GAC GCC AAC | 2121 |
| Gly Val Ala Ala Ser Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn |      |
| 680 685 690                                                     |      |
| CGT GCC TTA ATG GGG ACT AAC ATG CAG CGC CAA GCG GTG CCC TTA TTA | 2169 |
| Arg Ala Leu Met Gly Thr Asn Met Gln Arg Gln Ala Val Pro Leu Leu |      |
| 695 700 705                                                     |      |
| AGA AGC GAC GCT CCC ATT GTA GGC ACG GGG ATT GAA AAA ATT ATT GCT | 2217 |
| Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys Ile Ile Ala |      |
| 710 715 720                                                     |      |
| AGG GAT TCT TGG GGA GCG ATC AAA GCC AAT CGC GCA GGC GTT GTA GAA | 2265 |
| Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly Val Val Glu |      |
| 725 730 735                                                     |      |
| AAA ATT GAT TCT AAA AAT ATT TAT ATT TTA GGC GAA AGC AAA GAA GAA | 2313 |
| Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser Lys Glu Glu |      |
| 740 745 750 755                                                 |      |
| GCC TAT ATT GAT GCG TAT TCT TTG CAA AAA AAC TTG CGC ACC AAC CAA | 2361 |
| Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg Thr Asn Gln |      |
| 760 765 770                                                     |      |
| AAC ACC AGT TTC AAT CAA GTC CCT ATC GTT AAA GTG GGC GAT AAA GTG | 2409 |
| Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly Asp Lys Val |      |
| 775 780 785                                                     |      |
| GGA GCC GGG CAA ATC ATC GCT GAT GGC CCT AGC ATG GAT AGA GGC GAG | 2457 |
| Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp Arg Gly Glu |      |
| 790 795 800                                                     |      |
| TTG GCG TTA GGG AAA AAT GTG CGC GTG GCG TTC ATG CCT TGG AAT GGC | 2505 |
| Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro Trp Asn Gly |      |
| 805 810 815                                                     |      |
| TAT AAC TTT GAA GAC GCG ATC GTG GTG AGT GAG TGC ATC ACT AAA GAT | 2553 |
| Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile Thr Lys Asp |      |
| 820 825 830 835                                                 |      |
| GAT ATT TTC ACT TCC ACC CAC ATT TAT GAA AAA GAA GTG GAT GCT AGG | 2601 |
| Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val Asp Ala Arg |      |
| 840 845 850                                                     |      |
| GAG CTT AAG CAT GGT GTG GAA GAA TTT ACC GCT GAT ATT CCT GAT GTG | 2649 |
| Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile Pro Asp Val |      |
| 855 860 865                                                     |      |



|                                                                 |      |
|-----------------------------------------------------------------|------|
| AAG TTA GGC TTG CAT GTG CCT GAT TAC ATT ACG ACT TTA ACG CAT GAA | 1353 |
| Lys Leu Gly Leu His Val Pro Asp Tyr Ile Thr Thr Leu Thr His Glu |      |
| 420 425 430 435                                                 |      |
| GAT ATT ATC ACC ACC GTT AAA TAC CTC ATG AAG ATC AAA AAC AAT CAA | 1401 |
| Asp Ile Ile Thr Thr Val Lys Tyr Leu Met Lys Ile Lys Asn Asn Gln |      |
| 440 445 450                                                     |      |
| GGC AAG ATT GAT GAC AGG GAC CAC TTG GGC AAT CGT AGG ATT AGG GCG | 1449 |
| Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg Ile Arg Ala |      |
| 455 460 465                                                     |      |
| GTA GGG GAA TTG TTG GCC AAT GAA TTG CAT TCA GGT TTA GTG AAA ATG | 1497 |
| Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu Val Lys Met |      |
| 470 475 480                                                     |      |
| CAA AAG ACC ATT AAA GAC AAG CTC ACT ACC ATG AGC GGG GCT TTT GAT | 1545 |
| Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly Ala Phe Asp |      |
| 485 490 495                                                     |      |
| TCG CTC ATG CCC CAT GAC TTG GTC AAT TCT AAA ATG ATC ACA AGC ACC | 1593 |
| Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile Thr Ser Thr |      |
| 500 505 510 515                                                 |      |
| ATC ATG GAA TTT TTC ATG GGC GGT CAG CTC TCG CAA TTT ATG GAT CAA | 1641 |
| Ile Met Glu Phe Phe Met Gly Gly Gln Leu Ser Gln Phe Met Asp Gln |      |
| 520 525 530                                                     |      |
| ACG AAT CCC TTG AGT GAG GTT ACG CAC AAG CGC CGC CTT TCA GCG CTC | 1689 |
| Thr Asn Pro Leu Ser Glu Val Thr His Lys Arg Arg Leu Ser Ala Leu |      |
| 535 540 545                                                     |      |
| GGC GAA GGG GGG TTG GTG AAA GAC AGA GTG GGG TTT GAA GCC AGG GAT | 1737 |
| Gly Glu Gly Gly Leu Val Lys Asp Arg Val Gly Phe Glu Ala Arg Asp |      |
| 550 555 560                                                     |      |
| GTG CAC CCC ACG CAT TAT GGC CGA ATT TGT CCC ATT GAG ACC CCA GAA | 1785 |
| Val His Pro Thr His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu |      |
| 565 570 575                                                     |      |
| GGT CAA AAT ATC GGT CTG ATC AAC ACC CTT TCC ACT TTC ACA AGA GTG | 1833 |
| Gly Gln Asn Ile Gly Leu Ile Asn Thr Leu Ser Thr Phe Thr Arg Val |      |
| 580 585 590 595                                                 |      |
| AAT GAT TTA GGC TTT ATT GAA GCC CCT TAT AAA AAG GTT GTG GAT GGC | 1881 |
| Asn Asp Leu Gly Phe Ile Glu Ala Pro Tyr Lys Lys Val Val Asp Gly |      |
| 600 605 610                                                     |      |
| AAG GTC GTG GGT GAG ACG ATT TAT TTG ACC GCT ATT CAA GAA GAC AGC | 1929 |
| Lys Val Val Gly Glu Thr Ile Tyr Leu Thr Ala Ile Gln Glu Asp Ser |      |
| 615 620 625                                                     |      |
| CAC ATC ATC GCT CCC GCA AGC ACC CCC ATT GAT GAA GAG GGG AAT ATT | 1977 |
| His Ile Ile Ala Pro Ala Ser Thr Pro Ile Asp Glu Glu Gly Asn Ile |      |
| 630 635 640                                                     |      |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| Leu Tyr Ala Arg Ile Asn Lys Arg Arg Lys Val Pro Val Thr Ile Leu |      |
| 200 205 210                                                     |      |
| TTC AGG GCG ATG GAT TAT CAA AAA CAA GAC ATC ATC AAA ATG TTC TAC | 729  |
| Phe Arg Ala Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys Met Phe Tyr |      |
| 215 220 225                                                     |      |
| CCG CTT GTT AAA GTG CGT TAT GAA AAC GAT AAA TAT TTG ATC CCG TTT | 777  |
| Pro Leu Val Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu Ile Pro Phe |      |
| 230 235 240                                                     |      |
| GCT TCA TTA GAC GCC AAT CAA AGA ATG GAA TTT GAC TTG AAA GAT CCT | 825  |
| Ala Ser Leu Asp Ala Asn Gln Arg Met Glu Phe Asp Leu Lys Asp Pro |      |
| 245 250 255                                                     |      |
| CAA GGC AAG GTT ATT CTT TTA GCG GGT AAA AAG CTC ACT TCA AGA AAG | 873  |
| Gln Gly Lys Val Ile Leu Leu Ala Gly Lys Lys Leu Thr Ser Arg Lys |      |
| 260 265 270 275                                                 |      |
| ATT AAA GAG CTT AAA GAA AAC CAT TTA GAA TGG GTG GAA TAC CCT ATG | 921  |
| Ile Lys Glu Leu Lys Glu Asn His Leu Glu Trp Val Glu Tyr Pro Met |      |
| 280 285 290                                                     |      |
| GAT ATT TTA CTC AAT CGC CAT TTA GCT GAG CCT GTT ATG GTA GGG AAA | 969  |
| Asp Ile Leu Leu Asn Arg His Leu Ala Glu Pro Val Met Val Gly Lys |      |
| 295 300 305                                                     |      |
| GAA GTC TTA TTG GAC ATG CTC ACT CAG CTA GAT AAA AAC AAA TTA GAA | 1017 |
| Glu Val Leu Leu Asp Met Leu Thr Gln Leu Asp Lys Asn Lys Leu Glu |      |
| 310 315 320                                                     |      |
| AAA ATC CAC GAT TTA GGC GTG CAA GAA TTT GTG ATC ATC AAC GAT CTG | 1065 |
| Lys Ile His Asp Leu Gly Val Gln Glu Phe Val Ile Ile Asn Asp Leu |      |
| 325 330 335                                                     |      |
| GCG TTA GGG CAT GAC GCT TCC ATT ATC CAA TCT TTT TCA GCC GAT TCT | 1113 |
| Ala Leu Gly His Asp Ala Ser Ile Ile Gln Ser Phe Ser Ala Asp Ser |      |
| 340 345 350 355                                                 |      |
| GAG TCT TTG AAA TTA CTC AAG CAA ACC GAA AAA ATT GAT GAT GAA AAC | 1161 |
| Glu Ser Leu Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp Asp Glu Asn |      |
| 360 365 370                                                     |      |
| GCT CTA GCG GCG ATT CGT ATC CAT AAG GTT ATG AAA CCA GGC GAT CCC | 1209 |
| Ala Leu Ala Ala Ile Arg Ile His Lys Val Met Lys Pro Gly Asp Pro |      |
| 375 380 385                                                     |      |
| GTT ACG ACT GAA GTG GCT AAG CAG TTT GTC AAA AAA CTT TTC TTT GAT | 1257 |
| Val Thr Thr Glu Val Ala Lys Gln Phe Val Lys Lys Leu Phe Phe Asp |      |
| 390 395 400                                                     |      |
| CCA GAA CGC TAT GAT TTG ACC ATG GTG GGC CGC ATG AAA ATG AAT CAC | 1305 |
| Pro Glu Arg Tyr Asp Leu Thr Met Val Gly Arg Met Lys Met Asn His |      |
| 405 410 415                                                     |      |

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GAATTAATGC ATTAAATAAC TCAAAATTTT TGATCAAAGG CTTGAAAT ATG TCA AAA | 57  |
| Met Ser Lys                                                      |     |
| 1                                                                |     |
| AAA ATT CCC CTA AAA AAC CGC TTG AGA GCT GAT TTT ACA AAA ACC CCA  | 105 |
| Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr Lys Thr Pro  |     |
| 5 10 15                                                          |     |
| ACA GAT TTA GAA GTC CCT AAT TTA TTA TTA TTA CAA CGA GAC AGC TAT  | 153 |
| Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg Asp Ser Tyr  |     |
| 20 25 30 35                                                      |     |
| GAT TCT TTC TTG TAT TCT AAA GAG GGT AAA GAG AGC GGG ATT GAA AAG  | 201 |
| Asp Ser Phe Leu Tyr Ser Lys Glu Gly Lys Glu Ser Gly Ile Glu Lys  |     |
| 40 45 50                                                         |     |
| GTT TTT AAA TCC ATT TTC CCT ATC CAA GAT GAG CAT AAC CGC ATC ACT  | 249 |
| Val Phe Lys Ser Ile Phe Pro Ile Gln Asp Glu His Asn Arg Ile Thr  |     |
| 55 60 65                                                         |     |
| TTA GAA TAC GCG GGT TGC GAA TTT GGC AAG TCT AAA TAC ACC GTT AGA  | 297 |
| Leu Glu Tyr Ala Gly Cys Glu Phe Gly Lys Ser Lys Tyr Thr Val Arg  |     |
| 70 75 80                                                         |     |
| GAA GCG ATG GAG AGG GGC ATT ACC TAC TCT ATC CCT CTC AAA ATT AAG  | 345 |
| Glu Ala Met Glu Arg Gly Ile Thr Tyr Ser Ile Pro Leu Lys Ile Lys  |     |
| 85 90 95                                                         |     |
| GTG CGC TTG ATC TTG TGG GAA AAA GAT ACC AAG AGT GGC GAA AAG AAC  | 393 |
| Val Arg Leu Ile Leu Trp Glu Lys Asp Thr Lys Ser Gly Glu Lys Asn  |     |
| 100 105 110 115                                                  |     |
| GGC ATT AAG GAT ATT AAA GAA CAA AGC ATT TTC ATT CGT GAG ATC CCT  | 441 |
| Gly Ile Lys Asp Ile Lys Glu Gln Ser Ile Phe Ile Arg Glu Ile Pro  |     |
| 120 125 130                                                      |     |
| TTG ATG ACA GAA CGC ACT TCA TTT ATT ATT AAT GGG GTG GAG CGC GTG  | 489 |
| Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val Glu Arg Val  |     |
| 135 140 145                                                      |     |
| GTG GTC AAT CAA CTC CAC AGA AGC CCC GGT GTG ATT TTC AAA GAA GAA  | 537 |
| Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe Lys Glu Glu  |     |
| 150 155 160                                                      |     |
| GAG TCT AGC ACT TCT TTA AAC AAG CTC ATT TAC ACA GGG CAA ATC ATT  | 585 |
| Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly Gln Ile Ile  |     |
| 165 170 175                                                      |     |
| CCT GAT AGG GGT TCG TGG TTG TAT TTT GAA TAC GAT TCT AAA GAT GTT  | 633 |
| Pro Asp Arg Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser Lys Asp Val  |     |
| 180 185 190 195                                                  |     |
| TTA TAC GCT CGT ATC AAT AAA CGC CGT AAA GTG CCT GTT ACC ATT TTA  | 681 |

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Met Gln Lys Thr Ser Asn Thr Leu Ala Leu Gly Ser Leu Thr Ala Leu
 1 5 10 15
Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro
 20 25 30
His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile
 35 40 45
Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly
 50 55 60
Asn Val Ile Ser Lys Ile Gly Tyr Pro Phe Gly Val Val Leu Gly Phe
65 70 75 80
Val Ile Thr Ala Thr Gly Cys Ala Leu Phe Tyr Pro Ala Ala His Phe
 85 90 95
Gly Ser Tyr Gly Phe Phe Leu Gly Ala Leu Phe Ile Leu Ala Ser Gly
 100 105 110
Ile Val Cys Leu Gln Thr Ala Gly Asn Pro Phe Val Thr Leu Leu Ser
 115 120 125
Lys Gly Lys Glu Ala Arg Asn Leu Val Leu Val Gln Ala Phe Asn Ser
 130 135 140
Leu Gly Thr Thr Leu Gly Pro Ile Phe Gly Ser Leu Leu Ile Phe Ser
145 150 155 160
Thr Thr Lys Met Gly Asp Asn Ala Ser Leu Ile Asp Lys Leu Ala Asp
 165 170 175
Ala Lys Ser Val Gln Met Pro Tyr Leu Gly Leu Ala Val Phe Ser Leu
 180 185 190
Leu Leu Ala Leu Ile Met Tyr Leu Leu Lys Leu Pro Asp Val Glu Lys
 195 200 205
Glu Met Pro Lys Glu Thr Thr Gln Lys Ser Leu Phe Ser His Lys His
 210 215 220
Phe Val Phe Gly Ala Trp Gly Ser Phe Phe Met Trp Gly Glu Xaa Trp
225 230 235 240
Arg Leu Ala His Ser Trp Cys
 245

```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3084 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...3027
- (D) OTHER INFORMATION:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTG ATC ACA GCG ACG GGG TGC GCG TTG TTT TAT CCG GCG GCG CAT TTT   | 408 |
| Val Ile Thr Ala Thr Gly Cys Ala Leu Phe Tyr Pro Ala Ala His Phe   |     |
| 85 90 95                                                          |     |
| GGA TCC TAT GGG TTT TTT TTA GGA GCG TTG TTT ATT TTA GCG AGC GGG   | 456 |
| Gly Ser Tyr Gly Phe Phe Leu Gly Ala Leu Phe Ile Leu Ala Ser Gly   |     |
| 100 105 110                                                       |     |
| ATT GTG TGC TTG CAA ACC GCT GGT AAT CCC TTT GTA ACC TTG CTT TCT   | 504 |
| Ile Val Cys Leu Gln Thr Ala Gly Asn Pro Phe Val Thr Leu Leu Ser   |     |
| 115 120 125                                                       |     |
| AAA GGT AAA GAA GCC AGA AAT TTG GTT TTA GTC CAG GCG TTC AAT TCG   | 552 |
| Lys Gly Lys Glu Ala Arg Asn Leu Val Leu Val Gln Ala Phe Asn Ser   |     |
| 130 135 140                                                       |     |
| CTT GGC ACA ACT TTA GGG CCT ATT TTT GGG AGC TTG TTG ATT TTT AGC   | 600 |
| Leu Gly Thr Thr Leu Gly Pro Ile Phe Gly Ser Leu Leu Ile Phe Ser   |     |
| 145 150 155 160                                                   |     |
| ACG ACT AAA ATG GGC GAT AAT GCA AGT TTG ATA GAT AAA TTA GCG GAC   | 648 |
| Thr Thr Lys Met Gly Asp Asn Ala Ser Leu Ile Asp Lys Leu Ala Asp   |     |
| 165 170 175                                                       |     |
| GCT AAA AGC GTT CAA ATG CCT TAT TTG GGC TTG GCG GTG TTT TCG CTT   | 696 |
| Ala Lys Ser Val Gln Met Pro Tyr Leu Gly Leu Ala Val Phe Ser Leu   |     |
| 180 185 190                                                       |     |
| CTT TTA GCG CTC ATC ATG TAT CTT TTG AAA TTG CCT GAT GTG GAA AAA   | 744 |
| Leu Leu Ala Leu Ile Met Tyr Leu Leu Lys Leu Pro Asp Val Glu Lys   |     |
| 195 200 205                                                       |     |
| GAA ATG CCC AAA GAG ACG ACT CAA AAA AGC TTG TTT TCG CAC AAA CAC   | 792 |
| Glu Met Pro Lys Glu Thr Thr Gln Lys Ser Leu Phe Ser His Lys His   |     |
| 210 215 220                                                       |     |
| TTT GTT TTT GGG GCT TGG GGA TCT TTT TTT ATG TGG GGG GAG AAN TGG   | 840 |
| Phe Val Phe Gly Ala Trp Gly Ser Phe Phe Met Trp Gly Glu Xaa Trp   |     |
| 225 230 235 240                                                   |     |
| CGA TTG GCT CAT TCT TGG TGC TAAGCTTTGA AAAGCTTTTG AATTTAGACT CTCA | 895 |
| Arg Leu Ala His Ser Trp Cys                                       |     |
| 245                                                               |     |
| ATCAAGCGCG CATTAC                                                 | 911 |

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     | 595 |     |     |     |     |     | 600 |     |     |     | 605 |     |     |     |     |  |
| Lys | Ser | Asp | Asn | Ser | Val | Leu | Asn | Asn | Val | Ser | His | Val | Ala | Gln | Met |  |
|     | 610 |     |     |     |     | 615 |     |     |     | 620 |     |     |     |     |     |  |
| Gln | Ile | Ile | Lys | Glu | Lys | Met | Ala | Thr | Thr | Thr | Asp | Glu | Lys | Ala | Leu |  |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |  |
| Lys | Thr | Leu | Gln | Lys | Ser | Phe | Phe | Asn | His | Ala | Ile | Asp | Ala | Ile | Leu |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |  |
| Cys | Val | Phe | Phe | Met | Leu | Val | Ala | Leu | Leu | Val | Leu | Ile | Val | Ser | Val |  |
|     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |     |  |
| Arg | Ile | Cys | Ser | Asn | Ala | Tyr | Phe | Lys | Asn | Lys | Ile | Tyr | Pro | Pro | Leu |  |
|     |     | 675 |     |     |     | 680 |     |     |     |     | 685 |     |     |     |     |  |
| Ala | Glu | Thr | Pro | Tyr | Ile | Lys | Ala | Ser |     |     |     |     |     |     |     |  |
|     | 690 |     |     |     |     | 695 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 121...861  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

|                                                                 |                                 |            |            |            |            |     |
|-----------------------------------------------------------------|---------------------------------|------------|------------|------------|------------|-----|
| TAAGGGGCTT                                                      | TGCATTTTT                       | ACTCATTTC  | TGCCTCTTT  | TCTTTATTTA | GACAGATTAT | 60  |
| TATCTTAAAA                                                      | TAATTGTAAT                      | ATCATTATTA | TTATATCAAC | TCAATAAAAA | AGGAGAAGGT | 120 |
| ATG CAA AAA ACT TCT AAC ACT CTG                                 | GCG CTG GGG AGT TTG ACA GCG CTA | 168        |            |            |            |     |
| Met Gln Lys Thr Ser Asn Thr Leu                                 | Ala Leu Gly Ser Leu Thr Ala Leu |            |            |            |            |     |
| 1                                                               | 5                               | 10         | 15         |            |            |     |
| TTC TTT CTA ATG GGT TTT ATC ACG GTT TTA AAC GAT ATT TTA ATC CCA | 216                             |            |            |            |            |     |
| Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro |                                 |            |            |            |            |     |
| 20                                                              | 25                              | 30         |            |            |            |     |
| CAC TTA AAG CCC ATT TTT GAC TTG ACC TAT TTT GAA GCT TCA CTC ATT | 264                             |            |            |            |            |     |
| His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile |                                 |            |            |            |            |     |
| 35                                                              | 40                              | 45         |            |            |            |     |
| CAA TTT TGC TTT TTT GGG GCG TAT TTC ATC ATG GGA GGA GTT TTT GGG | 312                             |            |            |            |            |     |
| Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly |                                 |            |            |            |            |     |
| 50                                                              | 55                              | 60         |            |            |            |     |
| AAT GTG ATC AGT AAA ATC GGC TAC CCT TTT GGC GTG GTG CTT GGT TTT | 360                             |            |            |            |            |     |
| Asn Val Ile Ser Lys Ile Gly Tyr Pro Phe Gly Val Val Leu Gly Phe |                                 |            |            |            |            |     |
| 65                                                              | 70                              | 75         | 80         |            |            |     |

Ile Lys Leu Glu Met Gly Gln Phe Val Gly Met Ile Ala Ser Leu Gly  
 165 170 175  
 Ile Leu Gly Ile Met Leu Ile Ile Ile Ala Ile Leu Ala Met Val Val  
 180 185 190  
 Val Lys Ala Leu Ala His Ser Pro Trp Gly Phe Phe Thr Ile Ala Met  
 195 200 205  
 Thr Ile Pro Ile Ala Ile Leu Met Gly Leu Tyr Met Arg Phe Phe Arg  
 210 215 220  
 Pro His Lys Ile Leu Glu Val Ser Val Ile Gly Phe Ile Leu Leu Ile  
 225 230 235 240  
 Ile Ala Ile Tyr Ala Gly Lys Tyr Val Ser Leu Asp Pro Lys Leu Ala  
 245 250 255  
 Ser Ile Phe Thr Phe Glu Ala Ser Ser Leu Ala Trp Met Ile Met Gly  
 260 265 270  
 Tyr Gly Phe Val Ala Ser Ile Leu Pro Val Trp Phe Leu Leu Ala Pro  
 275 280 285  
 Arg Asp Tyr Leu Ser Thr Phe Leu Lys Ile Gly Val Ile Gly Val Leu  
 290 295 300  
 Val Val Ala Ile Ile Phe Val Ala Pro Pro Leu Gln Ile Pro Lys Ile  
 305 310 315 320  
 Thr Pro Phe Val Asp Gly Ser Gly Pro Val Phe Ala Gly Ser Val Phe  
 325 330 335  
 Pro Phe Leu Phe Ile Thr Val Ala Cys Gly Thr Ile Ser Gly Phe His  
 340 345 350  
 Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Met Leu Ala Lys Glu Ser  
 355 360 365  
 Asp Ala Arg Leu Val Gly Tyr Gly Ser Met Val Met Glu Ser Val Val  
 370 375 380  
 Ala Leu Met Ala Leu Val Cys Ala Gly Ile Leu His Pro Gly Leu Tyr  
 385 390 395 400  
 Phe Ala Ile Asn Ser Pro Glu Val Ser Ile Gly Lys Asp Ile Ala Asp  
 405 410 415  
 Ala Ala Ser Val Ile Ser Ser Trp Gly Phe Asn Ile Ser Ala Glu Glu  
 420 425 430  
 Ile Arg Glu Met Thr Lys Asn Ile Gly Glu Ser Ser Ile Leu Ser Arg  
 435 440 445  
 Thr Gly Gly Ala Pro Thr Phe Ala Ile Gly Leu Ala Met Ile Val Tyr  
 450 455 460  
 His Ile Leu Gly Asp Pro Ser Val Met Ala Phe Trp Tyr His Phe Ala  
 465 470 475 480  
 Ile Leu Phe Glu Ala Leu Phe Ile Leu Thr Ala Val Asp Ala Gly Thr  
 485 490 495  
 Arg Thr Ala Arg Phe Met Ile Gln Asp Leu Leu Gly Asn Val Tyr Lys  
 500 505 510  
 Pro Leu Gly Asp Leu Ser Ser Tyr Lys Ala Gly Ile Phe Ala Thr Leu  
 515 520 525  
 Leu Cys Val Ala Gly Trp Gly Tyr Phe Leu Tyr Gln Gly Thr Ile Asp  
 530 535 540  
 Pro Lys Gly Gly Ile Tyr Thr Leu Trp Pro Leu Phe Gly Val Ser Asn  
 545 550 555 560  
 Gln Met Leu Ala Gly Met Ala Leu Leu Leu Val Thr Val Val Leu Phe  
 565 570 575  
 Lys Met Gly Arg Phe Lys Gly Ala Met Ile Ser Ala Leu Pro Ala Val  
 580 585 590  
 Leu Ile Leu Ser Ile Thr Phe Tyr Ser Gly Ile Leu Lys Val Val Pro

```

GTG GCG CAA ATG CAA ATC ATC AAA GAA AAA ATG GCT ACC ACT ACC GAT 1984
Val Ala Gln Met Gln Ile Ile Lys Glu Lys Met Ala Thr Thr Thr Asp
 625 630 635

GAA AAA GCG CTC AAA ACG CTC CAA AAA TCC TTT TTT AAC CAC GCT ATT 2032
Glu Lys Ala Leu Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile
 640 645 650

GAT GCG ATT TTG TGC GTG TTT TTC ATG CTT GTG GCG CTA TTG GTT TTA 2080
Asp Ala Ile Leu Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu
 655 660 665

ATC GTG AGC GTT AGG ATT TGC TCA AAC GCT TAT TTT AAA AAC AAA ATT 2128
Ile Val Ser Val Arg Ile Cys Ser Asn Ala Tyr Phe Lys Asn Lys Ile
 670 675 680

TAC CCA CCG CTG GCT GAA ACG CCC TAC ATC AAA GCC TCT TGAATAAAAA AG 2179
Tyr Pro Pro Leu Ala Glu Thr Pro Tyr Ile Lys Ala Ser
 685 690 695

GGGTTTTTAAC CCCCTTTTAA TCCATAGAAA AAAGTTTGA 2218

```

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Ile Lys Gln Ser Leu Asn Gly Glu Asp Met Gln Lys Ser Leu Val
 1 5 10 15
Ser Leu Ala Trp Val Phe Val Ala Ile Leu Gly Ala Ile Cys Leu Gly
 20 25 30
Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr Leu Trp Leu Val
 35 40 45
Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg Phe Tyr Ser His
 50 55 60
Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser Arg Ala Thr Pro
 65 70 75 80
Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro Thr Asp Lys Ala
 85 90 95
Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu
 100 105 110
Val Gly Pro Ile Leu Ala Ala Gln Met Gly Tyr Leu Pro Ser Ile Leu
 115 120 125
Trp Ile Leu Ile Gly Ser Val Leu Gly Gly Cys Val His Asp Phe Val
 130 135 140
Val Leu Phe Ala Ser Ile Arg Arg Asp Gly Lys Ser Leu Gly Glu Met
 145 150 155 160

```



|                                                                 |      |
|-----------------------------------------------------------------|------|
| CCA GGG CTT TAT TTC GCT ATC AAT TCG CCA GAA GTG AGC ATC GGT AAA | 1312 |
| Pro Gly Leu Tyr Phe Ala Ile Asn Ser Pro Glu Val Ser Ile Gly Lys |      |
| 400 405 410                                                     |      |
| GAT ATA GCT GAT GCG GCT TCA GTG ATT AGC TCA TGG GGG TTT AAT ATC | 1360 |
| Asp Ile Ala Asp Ala Ala Ser Val Ile Ser Ser Trp Gly Phe Asn Ile |      |
| 415 420 425                                                     |      |
| AGC GCT GAA GAA ATT CGT GAG ATG ACT AAA AAC ATC GGC GAA AGC TCC | 1408 |
| Ser Ala Glu Glu Ile Arg Glu Met Thr Lys Asn Ile Gly Glu Ser Ser |      |
| 430 435 440                                                     |      |
| ATT TTG AGC CGC ACC GGT GGG GCG CCC ACT TTT GCG ATC GGT TTA GCG | 1456 |
| Ile Leu Ser Arg Thr Gly Gly Ala Pro Thr Phe Ala Ile Gly Leu Ala |      |
| 445 450 455 460                                                 |      |
| ATG ATT GTG TAT CAC ATT TTA GGG GAT CCA AGC GTG ATG GCG TTT TGG | 1504 |
| Met Ile Val Tyr His Ile Leu Gly Asp Pro Ser Val Met Ala Phe Trp |      |
| 465 470 475                                                     |      |
| TAT CAT TTT GCG ATT TTG TTT GAA GCT TTG TTC ATT TTA ACC GCT GTG | 1552 |
| Tyr His Phe Ala Ile Leu Phe Glu Ala Leu Phe Ile Leu Thr Ala Val |      |
| 480 485 490                                                     |      |
| GAT GCT GGC ACA CGA ACC GCT CGT TTC ATG ATT CAA GAT TTG CTC GGT | 1600 |
| Asp Ala Gly Thr Arg Thr Ala Arg Phe Met Ile Gln Asp Leu Leu Gly |      |
| 495 500 505                                                     |      |
| AAT GTT TAT AAG CCT TTG GGC GAT CTT AGC TCT TAT AAG GCT GGG ATT | 1648 |
| Asn Val Tyr Lys Pro Leu Gly Asp Leu Ser Ser Tyr Lys Ala Gly Ile |      |
| 510 515 520                                                     |      |
| TTT GCC ACT CTT TTG TGC GTG GCA GGG TGG GGG TAT TTC TTG TAT CAA | 1696 |
| Phe Ala Thr Leu Leu Cys Val Ala Gly Trp Gly Tyr Phe Leu Tyr Gln |      |
| 525 530 535 540                                                 |      |
| GGC ACG ATT GAT CCT AAA GGG GGG ATT TAT ACG CTA TGG CCT TTA TTT | 1744 |
| Gly Thr Ile Asp Pro Lys Gly Gly Ile Tyr Thr Leu Trp Pro Leu Phe |      |
| 545 550 555                                                     |      |
| GGC GTG AGC AAT CAG ATG TTA GCG GGC ATG GCG TTG TTG TTG GTC ACG | 1792 |
| Gly Val Ser Asn Gln Met Leu Ala Gly Met Ala Leu Leu Leu Val Thr |      |
| 560 565 570                                                     |      |
| GTG GTG TTG TTT AAA ATG GGG CGT TTT AAG GGG GCG ATG ATA AGC GCC | 1840 |
| Val Val Leu Phe Lys Met Gly Arg Phe Lys Gly Ala Met Ile Ser Ala |      |
| 575 580 585                                                     |      |
| TTA CCG GCA GTT TTG ATT TTA TCC ATC ACT TTT TAT AGC GGT ATT TTA | 1888 |
| Leu Pro Ala Val Leu Ile Leu Ser Ile Thr Phe Tyr Ser Gly Ile Leu |      |
| 590 595 600                                                     |      |
| AAG GTG GTG CCA AAG AGC GAT AAC AGC GTG CTG AAT AAT GTT TCC CAT | 1936 |
| Lys Val Val Pro Lys Ser Asp Asn Ser Val Leu Asn Asn Val Ser His |      |
| 605 610 615 620                                                 |      |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GCA AGT CTG GGC ATT TTA GGG ATC ATG CTC ATT ATC ATT GCG ATT TTA<br>Ala Ser Leu Gly Ile Leu Gly Ile Met Leu Ile Ile Ile Ala Ile Leu<br>175 180 185     | 640  |
| GCG ATG GTG GTG GTG AAG GCT TTA GCG CAT TCG CCT TGG GGC TTT TTT<br>Ala Met Val Val Val Lys Ala Leu Ala His Ser Pro Trp Gly Phe Phe<br>190 195 200     | 688  |
| ACG ATC GCA ATG ACT ATT CCC ATT GCG ATT CTT ATG GGG CTT TAC ATG<br>Thr Ile Ala Met Thr Ile Pro Ile Ala Ile Leu Met Gly Leu Tyr Met<br>205 210 215 220 | 736  |
| CGG TTT TTC AGG CCA CAC AAG ATT TTA GAG GTT TCT GTT ATT GGC TTT<br>Arg Phe Phe Arg Pro His Lys Ile Leu Glu Val Ser Val Ile Gly Phe<br>225 230 235     | 784  |
| ATC CTA TTG ATT ATA GCG ATT TAT GCG GGT AAA TAC GTT TCT TTA GAT<br>Ile Leu Leu Ile Ile Ala Ile Tyr Ala Gly Lys Tyr Val Ser Leu Asp<br>240 245 250     | 832  |
| CCT AAA TTA GCG TCA ATA TTC ACT TTT GAG GCC AGT TCT TTA GCG TGG<br>Pro Lys Leu Ala Ser Ile Phe Thr Phe Glu Ala Ser Ser Leu Ala Trp<br>255 260 265     | 880  |
| ATG ATC ATG GGC TAT GGG TTT GTG GCT TCT ATT TTA CCG GTA TGG TTT<br>Met Ile Met Gly Tyr Gly Phe Val Ala Ser Ile Leu Pro Val Trp Phe<br>270 275 280     | 928  |
| TTA CTC GCT CCA CGA GAT TAT CTA AGC ACT TTT TTA AAA ATT GGC GTT<br>Leu Leu Ala Pro Arg Asp Tyr Leu Ser Thr Phe Leu Lys Ile Gly Val<br>285 290 295 300 | 976  |
| ATA GGG GTG TTG GTT GTG GCC ATT ATT TTT GTC GCT CCG CCT TTA CAA<br>Ile Gly Val Leu Val Val Ala Ile Ile Phe Val Ala Pro Pro Leu Gln<br>305 310 315     | 1024 |
| ATC CCT AAA ATC ACG CCC TTT GTA GAT GGC AGT GGG CCT GTG TTT GCA<br>Ile Pro Lys Ile Thr Pro Phe Val Asp Gly Ser Gly Pro Val Phe Ala<br>320 325 330     | 1072 |
| GGA AGC GTG TTC CCT TTC TTG TTT ATC ACG GTG GCT TGC GGG ACG ATT<br>Gly Ser Val Phe Pro Phe Leu Phe Ile Thr Val Ala Cys Gly Thr Ile<br>335 340 345     | 1120 |
| AGC GGA TTC CAT GCT TTA ATT TCT TCA GGC ACG ACC CCT AAA ATG CTC<br>Ser Gly Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Met Leu<br>350 355 360     | 1168 |
| GCT AAA GAA AGC GAC GCA AGG CTA GTG GGC TAT GGC TCT ATG GTG ATG<br>Ala Lys Glu Ser Asp Ala Arg Leu Val Gly Tyr Gly Ser Met Val Met<br>365 370 375 380 | 1216 |
| GAG AGC GTT GTG GCT CTT ATG GCG TTG GTG TGC GCA GGG ATC TTG CAC<br>Glu Ser Val Val Ala Leu Met Ala Leu Val Cys Ala Gly Ile Leu His<br>385 390 395     | 1264 |

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 77...2167  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

GAAGTTTATG AGCCGTTTTG CCACTATTCA AAGAAATTTT GGATTATAAT AAAAAAAGT 60
GCTGAAATTA ACAACA ATG ATT AAA CAA TCA TTA AAT GGA GAG GAC ATG CAA 112
 Met Ile Lys Gln Ser Leu Asn Gly Glu Asp Met Gln
 1 5 10

AAA AGT TTA GTT TCT TTG GCT TGG GTT TTT GTA GCT ATT TTA GGG GCG 160
Lys Ser Leu Val Ser Leu Ala Trp Val Phe Val Ala Ile Leu Gly Ala
 15 20 25

ATC TGT TTA GGG GTG TTA GCC TTA CAC AAG GGT GAG AGC ATT AAC ACG 208
Ile Cys Leu Gly Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr
 30 35 40

CTA TGG CTT GTA GTA GCG AGC GCT TGT ATT TAT AGC ATA GGC TAT CGT 256
Leu Trp Leu Val Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg
45 50 55 60

TTT TAT AGC CAT TTT ATC GCT TAT AAG GTG TTA AAG CTA GAT GAT AGC 304
Phe Tyr Ser His Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser
 65 70 75

AGA GCC ACG CCC GCA TGC GTA AGG AAT GAT GGC AAG GAT TTT GTG CCA 352
Arg Ala Thr Pro Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro
 80 85 90

ACC GAT AAA GCG ATC ACT TTT GGG CAC CAT TTC GCC GCT ATT GCT GGG 400
Thr Asp Lys Ala Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly
 95 100 105

GCT GGC CCT TTA GTA GGC CCG ATA CTA GCC GCT CAA ATG GGT TAC TTG 448
Ala Gly Pro Leu Val Gly Pro Ile Leu Ala Ala Gln Met Gly Tyr Leu
110 115 120

CCC TCT ATC TTA TGG ATT TTG ATA GGC TCG GTT TTA GGG GGT TGC GTG 496
Pro Ser Ile Leu Trp Ile Leu Ile Gly Ser Val Leu Gly Gly Cys Val
125 130 135 140

CAT GAT TTT GTG GTG CTT TTT GCT TCT ATT AGG CGC GAT GGC AAG TCT 544
His Asp Phe Val Val Leu Phe Ala Ser Ile Arg Arg Asp Gly Lys Ser
 145 150 155

TTA GGC GAA ATG ATC AAA CTT GAA ATG GGC CAA TTT GTA GGC ATG ATC 592
Leu Gly Glu Met Ile Lys Leu Glu Met Gly Gln Phe Val Gly Met Ile
 160 165 170

```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu Ala Asp |     |     |
| 50                                                              | 55  | 60  |
| Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe Leu Ile |     |     |
| 65                                                              | 70  | 75  |
| Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe Met Leu |     |     |
| 85                                                              | 90  | 95  |
| Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser Gly Thr |     |     |
| 100                                                             | 105 | 110 |
| Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys Asp Leu |     |     |
| 115                                                             | 120 | 125 |
| Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly Met Ile |     |     |
| 130                                                             | 135 | 140 |
| Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His Ala Met |     |     |
| 145                                                             | 150 | 155 |
| Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu Thr Ile |     |     |
| 165                                                             | 170 | 175 |
| Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln Lys Ser |     |     |
| 180                                                             | 185 | 190 |
| Leu Lys Leu Leu Lys Glu Gln Val Lys Gly Ser Leu Lys Glu Leu Lys |     |     |
| 195                                                             | 200 | 205 |
| Asp Asn Pro Lys Leu Lys Ile Leu Leu Val Gly His Leu Ile Thr Pro |     |     |
| 210                                                             | 215 | 220 |
| Val Phe Phe Met Ser His Phe Gln Met Trp Gln Ala Tyr Phe Leu Lys |     |     |
| 225                                                             | 230 | 235 |
| Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln |     |     |
| 245                                                             | 250 | 255 |
| Val Ile Ser Ile Leu Ile His Phe Leu Lys Ala Ser Ser Tyr Ser Gln |     |     |
| 260                                                             | 265 | 270 |
| Lys Ile Ala Leu Ser Ser Leu Val Leu Leu Gly Val Ser Pro Leu     |     |     |
| 275                                                             | 280 | 285 |
| Leu Leu Ser Asn Ile Pro Tyr Cys Phe Ile Gly Val Tyr Ala Leu Met |     |     |
| 290                                                             | 295 | 300 |
| Val Ala Phe Phe Thr Tyr Met Ser Tyr Cys Leu Asn Tyr Gln Phe Ser |     |     |
| 305                                                             | 310 | 315 |
| Lys Phe Val Ser Lys Asn Asn Ile Ser Ser Leu Ser Ser Leu Leu Ser |     |     |
| 325                                                             | 330 | 335 |
| Ser Cys Val Arg Val Val Ser Val Leu Ile Leu Ser Leu Ser Ser Leu |     |     |
| 340                                                             | 345 | 350 |
| Glu Leu Arg Tyr Phe Ser Pro Leu Thr Ile Ile Thr Met His Phe Ala |     |     |
| 355                                                             | 360 | 365 |
| Leu Thr Leu Ile Ile Leu Phe Phe Phe Leu Tyr Lys Ala Lys Pro Phe |     |     |
| 370                                                             | 375 | 380 |
| Asp Glu                                                         |     |     |
| 385                                                             |     |     |

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

[illegible]

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|          |     |     |           |     |     |     |     |           |     |     |     |     |           |     |     |
|----------|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|
| Met<br>1 | Leu | Arg | Lys<br>5  | Asn | Ile | Leu | Ala | Tyr<br>10 | Tyr | Gly | Ala | Asn | Phe<br>15 | Leu | Leu |
| Ile      | Ile | Ala | Gln<br>20 | Ser | Leu | Pro | His | Ala<br>25 | Ile | Leu | Thr | Pro | Leu<br>30 | Leu | Leu |
| Ser      | Lys | Gly | Leu       | Ser | Leu | Ser | Glu | Ile       | Leu | Leu | Val | Gln | Thr       | Phe | Phe |

- 189 -

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro
 1 5 10 15
Leu Ala Val Gly Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu
 20 25 30
Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser
 35 40 45
Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His
 50 55 60
Tyr Thr Ser Phe Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile
65 70 75 80
Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly Phe
 85 90

```

(2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...1227
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

TAGCATCAAT ACCCCTTAAA TAAAAGATAT AATGCTGTAT TATAAGCTAG TTTTAATTAC 60
AATTTTCAA ATG TTA AGG AAA AAC ATT TTA GCT TAC TAT GGG GCG AAT TTT 111
 Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe
 1 5 10

CTC TTA ATC ATC GCT CAA AGC TTA CCC CAT GCG ATT TTA ACC CCC TTG 159
Leu Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu
15 20 25 30

TTG CTT TCT AAA GGG CTT AGT TTG AGT GAA ATC TTG CTC GTG CAA ACC 207
Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr

```

370

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 103...381
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

AGTCTTTGCC CGCTATCAAA AAAGAGATTT TTTGCAATAT TTTCATAAGC ACCGAAGAAA 60
GCTTGCTTTA GCGAGTTTGT GGGTGAAACG TACGCCTTGC TC ATG ATT TTT GTC 114
 Met Ile Phe Val
 1

AAT AAA TAT CTC TAT GGG ATT AAA AGC GTT GTG CCT TTG GCG GTT GGT 162
Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro Leu Ala Val Gly
 5 10 15 20

TTT AGC AAA TAC CCT TTA AAA AAG TTT TTA TGG CTT AAT GTT TTT TCC 210
Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser
 25 30 35

AGT TTT TTG TGG GCG CTC ATC GTG GGG AGC GTT TCT TTT CAA GCG AGC 258
Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser
 40 45 50

GAT TGG GTG AAA ACG CTG TAT GAA AGG CTT TCT CAT TAC ACT TCG TTT 306
Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe
 55 60 65

TTT ATC ATA AGT TTT GTT CTT ATA GCG CTT TTA ATA TGG TTT TTA TTG 354
Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu
 70 75 80

AAA CGA TAT TCG CGC AAA ATG GGT TTT TAAGCAAGAT GTTTAATTAA ATGCGCT 408
Lys Arg Tyr Ser Arg Lys Met Gly Phe
 85 90

AGACTACGCC CACAAGCATT CGC 431

```

## (2) INFORMATION FOR SEQ ID NO:72:



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Met Leu Ile Ser Ile Ala Phe Leu Leu Val Leu Tyr Leu Leu Asn Tyr
 1 5 10 15
Ser Ser Phe Arg Met Leu Lys Ser Phe Leu Thr Leu Lys Lys Ile Ser
 20 25 30
Gln Tyr Ala Tyr Leu Trp Phe Phe Ile Leu Leu Ser Ile Gly Glu Ala
 35 40 45
Ala Phe Val Phe Tyr Arg Asn Ile Met Pro Ser His Leu Phe Val Leu
 50 55 60
Thr Ser Ala Cys Ser Phe Val Ser Phe Ile Ile Phe Ile Leu Ser Leu
 65 70 75 80
Ser Phe Tyr Gly Phe Ser Tyr Ser Ile Glu Lys Ile Asp Phe Leu His
 85 90 95
Ser Arg Arg Lys Ser Leu Lys Asn Phe Leu Lys Leu Gly Phe Tyr Leu
100 105 110
Ala Leu Leu Gly Tyr Phe Trp Arg Gly Phe Tyr Glu Gly Leu Ala Arg
115 120 125
Pro Lys Ile Lys Glu Thr Pro Ile Tyr Leu Asp Lys Leu Asp Lys Glu
130 135 140
Leu Lys Ile Ile Leu Leu Thr Asp Met His Val Gly Ser Leu Leu Gln
145 150 155 160
Lys Asp Phe Val Asp Tyr Ile Val Glu Glu Val Asn Gln Lys Glu Val
165 170 175
Asp Met Val Leu Ile Gly Gly Asp Leu Val Asp Glu Ser Ile Glu Lys
180 185 190
Val Lys Ser Phe Leu Leu Pro Leu Asn Asn Leu Lys Ser Thr His Gly
195 200 205
Thr Phe Tyr Val Pro Gly Asn His Glu Tyr Tyr His Gly Ile Glu Pro
210 215 220
Ile Leu Ser Phe Leu Asp Thr Leu Asn Leu Thr Ile Leu Gly Asn Glu
225 230 235 240
Cys Val His Leu Gly Gly Ile Asn Leu Cys Gly Val Tyr Asp Tyr Phe
245 250 255
Ala Arg Lys Arg Gln Asn Phe Ala Pro Asp Ile Asp Lys Ala Leu Lys
260 265 270
Lys Arg Asn Glu Ser Lys Pro Thr Ile Leu Leu Ala His Gln Pro Lys
275 280 285
Gln Ile Arg Ser Leu Lys Glu Ser His Ser Val Asp Leu Val Leu Ser
290 295 300
Gly His Thr His Ala Gly Gln Ile Phe Pro Phe Ser Leu Leu Val Lys
305 310 315 320
Leu Ala Gln Thr Tyr Leu His Gly Leu Tyr Lys His Ser Pro Thr Thr
325 330 335
Gln Ile Tyr Val Ser Ser Gly Ala Gly Tyr Trp Gly Ile Pro Leu Arg
340 345 350
Phe Leu Ala Pro Ser Glu Ile Ala Tyr Leu Arg Leu Leu Pro Lys Asn
355 360 365
Gln Ala

```

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTA GTG GAT GAA AGC ATT GAA AAA GTC AAA TCT TTT TTA CTG CCT TTA   | 688  |
| Leu Val Asp Glu Ser Ile Glu Lys Val Lys Ser Phe Leu Leu Pro Leu   |      |
| 185 190 195 200                                                   |      |
| AAC AAC CTT AAA AGC ACG CAT GGC ACT TTT TAT GTG CCA GGA AAT CAT   | 736  |
| Asn Asn Leu Lys Ser Thr His Gly Thr Phe Tyr Val Pro Gly Asn His   |      |
| 205 210 215                                                       |      |
| GAG TAT TAT CAT GGC ATA GAG CCG ATT TTA TCG TTT CTT GAC ACG CTT   | 784  |
| Glu Tyr Tyr His Gly Ile Glu Pro Ile Leu Ser Phe Leu Asp Thr Leu   |      |
| 220 225 230                                                       |      |
| AAT TTG ACG ATT TTA GGG AAT GAG TGC GTG CAT TTA GGG GGG ATC AAT   | 832  |
| Asn Leu Thr Ile Leu Gly Asn Glu Cys Val His Leu Gly Gly Ile Asn   |      |
| 235 240 245                                                       |      |
| TTG TGC GGC GTG TAT GAT TAT TTC GCA AGG AAG CGT CAA AAT TTT GCC   | 880  |
| Leu Cys Gly Val Tyr Asp Tyr Phe Ala Arg Lys Arg Gln Asn Phe Ala   |      |
| 250 255 260                                                       |      |
| CCT GAT ATT GAC AAA GCT TTA AAA AAG CGC AAT GAG AGT AAG CCC ACG   | 928  |
| Pro Asp Ile Asp Lys Ala Leu Lys Lys Arg Asn Glu Ser Lys Pro Thr   |      |
| 265 270 275 280                                                   |      |
| ATC CTT TTG GCC CAC CAA CCT AAA CAA ATT AGA AGC CTC AAA GAA AGC   | 976  |
| Ile Leu Leu Ala His Gln Pro Lys Gln Ile Arg Ser Leu Lys Glu Ser   |      |
| 285 290 295                                                       |      |
| CAC TCT GTA GAT TTA GTC CTT TCA GGG CAT ACC CAT GCA GGG CAA ATC   | 1024 |
| His Ser Val Asp Leu Val Leu Ser Gly His Thr His Ala Gly Gln Ile   |      |
| 300 305 310                                                       |      |
| TTT CCC TTT AGC CTT TTA GTC AAG TTG GCG CAA ACC TAT TTA CAT GGT   | 1072 |
| Phe Pro Phe Ser Leu Leu Val Lys Leu Ala Gln Thr Tyr Leu His Gly   |      |
| 315 320 325                                                       |      |
| TTA TAC AAG CAC AGC CCC ACC ACT CAA ATT TAT GTG AGC AGT GGG GCA   | 1120 |
| Leu Tyr Lys His Ser Pro Thr Thr Gln Ile Tyr Val Ser Ser Gly Ala   |      |
| 330 335 340                                                       |      |
| GGG TAT TGG GGG ATT CCT TTA AGG TTT TTA GCC CCT AGC GAG ATC GCA   | 1168 |
| Gly Tyr Trp Gly Ile Pro Leu Arg Phe Leu Ala Pro Ser Glu Ile Ala   |      |
| 345 350 355 360                                                   |      |
| TAC CTT AGG CTT TTA CCT AAA AAT CAA GCT TAGTTAAACA AAATCTTAAA ATC | 1221 |
| Tyr Leu Arg Leu Leu Pro Lys Asn Gln Ala                           |      |
| 365 370                                                           |      |
| TTAATCGTAA TCAAGCGGTT AAAAATAAGA A                                | 1252 |

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 amino acids
  - (B) TYPE: amino acid

(B) LOCATION: 89...1198

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

AAAAAGGAAA TAGCACGATG AAACCTAAAG GGGATATTAG CGTTAATATG CTAATATAGT 60
AGAACATTAT GACTACAAAA AGGGTGAT ATG CTG ATC TCC ATA GCG TTT TTA 112
 Met Leu Ile Ser Ile Ala Phe Leu
 1 5

TTG GTT TTA TAT CTT TTG AAT TAT AGT TCT TTC AGG ATG TTG AAA TCG 160
Leu Val Leu Tyr Leu Leu Asn Tyr Ser Ser Phe Arg Met Leu Lys Ser
 10 15 20

TTT TTA ACC TTA AAG AAA ATC TCT CAA TAC GCT TAT TTA TGG TTT TTT 208
Phe Leu Thr Leu Lys Lys Ile Ser Gln Tyr Ala Tyr Leu Trp Phe Phe
 25 30 35 40

ATC CTT TTG AGC ATA GGC GAG GCG GCT TTT GTT TTT TAT AGA AAT ATT 256
Ile Leu Leu Ser Ile Gly Glu Ala Ala Phe Val Phe Tyr Arg Asn Ile
 45 50 55

ATG CCT AGC CAT TTG TTT GTT TTG ACT TCA GCG TGT TCG TTT GTG TCT 304
Met Pro Ser His Leu Phe Val Leu Thr Ser Ala Cys Ser Phe Val Ser
 60 65 70

TTT ATT ATT TTT ATC CTT TCT TTA AGT TTT TAC GGG TTT TCC TAT TCC 352
Phe Ile Ile Phe Ile Leu Ser Leu Ser Phe Tyr Gly Phe Ser Tyr Ser
 75 80 85

ATA GAA AAA ATA GAT TTT TTG CAT TCA AGG CGT AAA AGT TTA AAA AAC 400
Ile Glu Lys Ile Asp Phe Leu His Ser Arg Arg Lys Ser Leu Lys Asn
 90 95 100

TTT TTA AAA TTG GGG TTT TAT CTG GCG TTA TTA GGG TAT TTT TGG CGT 448
Phe Leu Lys Leu Gly Phe Tyr Leu Ala Leu Leu Gly Tyr Phe Trp Arg
 105 110 115 120

GGG TTT TAT GAA GGG TTG GCC CGC CCT AAA ATC AAA GAA ACC CCT ATT 496
Gly Phe Tyr Glu Gly Leu Ala Arg Pro Lys Ile Lys Glu Thr Pro Ile
 125 130 135

TAT TTG GAT AAG CTG GAT AAA GAA TTA AAG ATT ATT TTA CTC ACA GAC 544
Tyr Leu Asp Lys Leu Asp Lys Glu Leu Lys Ile Ile Leu Leu Thr Asp
 140 145 150

ATG CAT GTG GGG AGT TTG TTG CAA AAA GAT TTT GTT GAT TAC ATT GTA 592
Met His Val Gly Ser Leu Leu Gln Lys Asp Phe Val Asp Tyr Ile Val
 155 160 165

GAA GAA GTC AAT CAA AAA GAA GTG GAT ATG GTG CTG ATT GGG GGG GAT 640
Glu Glu Val Asn Gln Lys Glu Val Asp Met Val Leu Ile Gly Gly Asp
 170 175 180

```

```

Ser Leu Thr Tyr Ala Cys Gly Ala Leu Cys Leu Leu Phe Ala Ser Cys
65 70 75 80
Leu Arg Ile Lys Leu Asn Gln Lys Ile Leu Phe Tyr Ser Met Ala Val
 85 90 95
Ala Asn Phe Ile Asn Gly Leu Leu Ser Leu Val Gln Lys Ile Tyr Phe
 100 105 110
Asn Met Pro Arg Ala Gln Gly Phe Ser Thr Val Lys Glu Tyr Val Val
 115 120 125
Leu Val Ser Val Ser Ile Leu Gly Cys Tyr Ile Tyr Ala Leu Tyr Ser
 130 135 140
His Asn Gln Lys Glu Lys Leu Phe Phe Thr Leu Ser Val Phe Val Gly
 145 150 155 160
Phe Leu Val Val Ile Leu Ser Ala Thr Arg Ser Ala Thr Ile Ala Phe
 165 170 175
Val Ile Thr Phe Leu Ile Leu Ser Cys Phe Ile Leu Tyr Ala Lys Lys
 180 185 190
Ser Leu Lys Pro Leu Gly Tyr Met Val Val Val Ser Leu Ile Leu Ser
 195 200 205
Ala Leu Tyr Val Gly Ser Asn Ala Leu Glu Lys Lys Gly Ala Ile Glu
 210 215 220
Gln Ser Arg Val Gln Asn Gln Ser Phe Glu Glu Asp Leu Lys Arg Tyr
 225 230 235 240
Ala Lys Lys Asp Ala Asp Ser Ser Ile Gly Trp Arg Leu Glu Arg Trp
 245 250 255
Lys Glu Ala Leu Thr Val Leu Arg Leu Arg Pro Phe Phe Gly Met Ala
 260 265 270
Ala Ser Glu Lys Cys Gln Arg Leu Glu Glu Ile Leu Ser Leu Ser Lys
 275 280 285
Ser Tyr Arg Ala Lys Asp Leu Ile Leu Cys Tyr Glu Arg Tyr Asp Asn
 290 295 300
Gln Ile Ile His Ile Leu Ala Thr Arg Gly Ile Ile Gly Phe Leu Ile
 305 310 315 320
Trp Leu Phe Phe Leu Leu Val Ile Val Lys Ile Phe Trp Ser Gly Ile
 325 330 335
Lys Gln Asn Ser Leu Ile Ser Phe Phe Ile Leu Met Thr Leu Ala Phe
 340 345 350
Tyr Leu Ile Phe Gly Ile Gly Phe Asp Pro Phe Asp Phe Phe Ile Thr
 355 360 365
Gly Ser Phe Phe Val Gly Met Ile Met Met Ala Val Phe Leu Lys Lys
 370 375 380
Asp Lys Ser Ala Phe
 385

```

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

```

TTT TTT GGT ATG GCC GCT AGC GAG AAA TGC CAG AGG TTA GAA GAG ATT 1048
Phe Phe Gly Met Ala Ala Ser Glu Lys Cys Gln Arg Leu Glu Glu Ile
 270 275 280

TTA TCC TTA TCA AAG TCT TAT AGG GCC AAA GAT TTG ATT CTC TGT TAT 1096
Leu Ser Leu Ser Lys Ser Tyr Arg Ala Lys Asp Leu Ile Leu Cys Tyr
 285 290 295

GAA AGA TAC GAC AAT CAA ATC ATT CAC ATT TTA GCC ACT AGG GGG ATC 1144
Glu Arg Tyr Asp Asn Gln Ile Ile His Ile Leu Ala Thr Arg Gly Ile
 300 305 310 315

ATA GGC TTT TTG ATC TGG CTC TTT TTT TTA TTA GTT ATT GTA AAG ATT 1192
Ile Gly Phe Leu Ile Trp Leu Phe Phe Leu Leu Val Ile Val Lys Ile
 320 325 330

TTT TGG AGC GGG ATA AAG CAA AAC TCT TTA ATA TCG TTT TTT ATA CTA 1240
Phe Trp Ser Gly Ile Lys Gln Asn Ser Leu Ile Ser Phe Phe Ile Leu
 335 340 345

ATG ACA CTC GCC TTT TAC CTC ATT TTT GGC ATT GGG TTT GAC CCC TTT 1288
Met Thr Leu Ala Phe Tyr Leu Ile Phe Gly Ile Gly Phe Asp Pro Phe
 350 355 360

GAT TTC TTC ATT ACG GGA AGT TTT TTT GTA GGA ATG ATC ATG ATG GCT 1336
Asp Phe Phe Ile Thr Gly Ser Phe Phe Val Gly Met Ile Met Met Ala
 365 370 375

GTT TTT TTA AAA AAA GAT AAA AGT GCT TTT TAGCATCAAG GGGTTTGACA TTA 1389
Val Phe Leu Lys Lys Asp Lys Ser Ala Phe
 380 385

GTCAAGCGGT AGTTTCTTGT GATTCGTTCT T 1420

```

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Val Phe Leu Phe Phe Arg Cys Tyr Phe Gln Ala Ser Leu Lys Glu
 1 5 10 15
Thr Phe Ala Ile Asn His Leu Lys Thr Met Ser Phe Lys Trp Leu Thr
 20 25 30
Leu Ala Phe Leu Gly Val Phe Leu Ser Ile Phe Pro Asn Met Phe Asn
 35 40 45
Met His Asp Ser Gln Thr Phe Arg Tyr Asn Leu Phe Ala Leu Asn Met
 50 55 60

```

|                                                                 |      |
|-----------------------------------------------------------------|------|
| CCT AAC ATG TTT AAC ATG CAT GAT AGC CAA ACT TTC CGC TAC AAT TTA | 376  |
| Pro Asn Met Phe Asn Met His Asp Ser Gln Thr Phe Arg Tyr Asn Leu |      |
| 45 50 55                                                        |      |
| TTC GCT CTA AAC ATG TCC TTA ACT TAT GCT TGC GGG GCG TTA TGC TTG | 424  |
| Phe Ala Leu Asn Met Ser Leu Thr Tyr Ala Cys Gly Ala Leu Cys Leu |      |
| 60 65 70 75                                                     |      |
| CTT TTT GCC AGT TGC TTA AGA ATC AAA TTG AAT CAA AAA ATC CTT TTT | 472  |
| Leu Phe Ala Ser Cys Leu Arg Ile Lys Leu Asn Gln Lys Ile Leu Phe |      |
| 80 85 90                                                        |      |
| TAC AGC ATG GCT GTT GCA AAT TTC ATC AAC GGC TTG CTC TCA TTG GTG | 520  |
| Tyr Ser Met Ala Val Ala Asn Phe Ile Asn Gly Leu Leu Ser Leu Val |      |
| 95 100 105                                                      |      |
| CAA AAA ATT TAT TTT AAC ATG CCC AGA GCG CAA GGG TTT AGC ACG GTT | 568  |
| Gln Lys Ile Tyr Phe Asn Met Pro Arg Ala Gln Gly Phe Ser Thr Val |      |
| 110 115 120                                                     |      |
| AAG GAG TAT GTG GTT TTA GTG AGC GTG TCC ATT TTA GGC TGT TAT ATT | 616  |
| Lys Glu Tyr Val Val Leu Val Ser Val Ser Ile Leu Gly Cys Tyr Ile |      |
| 125 130 135                                                     |      |
| TAT GCG CTT TAT TCG CAC AAT CAA AAA GAA AAA CTT TTT TTC ACG CTT | 664  |
| Tyr Ala Leu Tyr Ser His Asn Gln Lys Glu Lys Leu Phe Phe Thr Leu |      |
| 140 145 150 155                                                 |      |
| TCT GTT TTT GTG GGG TTT TTA GTC GTT ATT TTA AGC GCC ACA AGG AGC | 712  |
| Ser Val Phe Val Gly Phe Leu Val Val Ile Leu Ser Ala Thr Arg Ser |      |
| 160 165 170                                                     |      |
| GCG ACA ATC GCT TTT GTT ATT ACT TTT TTA ATC CTT TCT TGC TTT ATT | 760  |
| Ala Thr Ile Ala Phe Val Ile Thr Phe Leu Ile Leu Ser Cys Phe Ile |      |
| 175 180 185                                                     |      |
| TTA TAC GCC AAA AAA TCG CTC AAA CCA TTG GGT TAT ATG GTG GTC GTG | 808  |
| Leu Tyr Ala Lys Lys Ser Leu Lys Pro Leu Gly Tyr Met Val Val Val |      |
| 190 195 200                                                     |      |
| AGT CTT ATT TTG AGC GCT TTG TAT GTG GGG AGT AAC GCT TTA GAA AAA | 856  |
| Ser Leu Ile Leu Ser Ala Leu Tyr Val Gly Ser Asn Ala Leu Glu Lys |      |
| 205 210 215                                                     |      |
| AAG GGG GCA ATA GAG CAA TCT AGA GTT CAA AAT CAA AGC TTT GAA GAA | 904  |
| Lys Gly Ala Ile Glu Gln Ser Arg Val Gln Asn Gln Ser Phe Glu Glu |      |
| 220 225 230 235                                                 |      |
| GAT CTG AAA CGC TAC GCT AAA AAG GAC GCT GAT AGC AGT ATC GGA TGG | 952  |
| Asp Leu Lys Arg Tyr Ala Lys Lys Asp Ala Asp Ser Ser Ile Gly Trp |      |
| 240 245 250                                                     |      |
| CGT TTG GAG CGT TGG AAA GAA GCC CTA ACG GTT TTG CGT TTA AGG CCC | 1000 |
| Arg Leu Glu Arg Trp Lys Glu Ala Leu Thr Val Leu Arg Leu Arg Pro |      |
| 255 260 265                                                     |      |

```

 290 295 300
Asn Glu Ser Glu Phe Glu Glu Leu Ser Ala Phe Leu Asp Glu Phe Gln
305 310 315 320
Phe Asp Arg Leu Asn Ile Phe Ala Phe Ser Ala Glu Glu Asn Thr His
 325 330 335
Ala Tyr Ser Leu Glu Lys Val Pro Lys Lys Thr Ile Asn Ala Arg Ile
 340 345 350
Lys Ala Leu Asn Lys Ile Ala Leu Lys His Gln Asn His Ser Phe Lys
 355 360 365
Ala Leu Leu Asn Lys Pro Ile Lys Ala Leu Val Glu Asn Lys Glu Gly
 370 375 380
Glu Tyr Phe Tyr Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp
385 390 395 400
Gly Glu Ile Leu Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro
 405 410 415
Gly His Tyr Thr Ile Ala Pro Ser Glu Phe Lys Asp Asn Ile Leu Leu
 420 425 430
Ala Lys Val Leu Ser Pro Phe
 435

```

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 200...1366
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

TGC GCG TTAT RTGG TTTTGA TTG AAAAGTT AGGC ATTA AA GAC AGATAAT TTTTATCGGT 60
TTTAGGGTGT GCGGAGTTTG TGTTGAAAGA GCGTTTGAAG GCCTTTT TTA GTGCGGACTC 120
TGTTTTCAC TTAATTTT TG CCCTTTTCTT TCTCACTTCG TTTAAAAAAC CTTTAACTCA 180
AGTCTTGTTG ATTGTTT TA ATG GTT TTT TTG TTT TTT AGG TGT TAT TTC CAA 232
 Met Val Phe Leu Phe Phe Arg Cys Tyr Phe Gln
 1 5 10

GCG TCT TTG AAA GAA ACT TTC GCA ATT AAT CAT TTA AAA ACA ATG TCT 280
Ala Ser Leu Lys Glu Thr Phe Ala Ile Asn His Leu Lys Thr Met Ser
 15 20 25

TTT AAA TGG CTC ACT CTG GCT TTT TTG GGC GTG TTT TTA AGC ATC TTC 328
Phe Lys Trp Leu Thr Leu Ala Phe Leu Gly Val Phe Leu Ser Ile Phe
 30 35 40

```

TTA AGC CCT TTT TAAAAGTTAG CCATAAGGCT AAAAGCACGG CTAAAGCGT  
 Leu Ser Pro Phe

1405

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Val | Lys | Glu | Asn | Lys | Gln | Leu | Cys | Leu | Ile | Ser | Leu | Gly | Cys | 1   | 5   | 10  | 15  |
| Ser | Lys | Asn | Leu | Val | Asp | Ser | Glu | Val | Met | Leu | Gly | Lys | Leu | Tyr | Asn | 20  | 25  | 30  |     |
| Tyr | Thr | Leu | Thr | Asn | Asp | Ala | Lys | Ser | Ala | Asp | Val | Ile | Leu | Ile | Asn | 35  | 40  | 45  |     |
| Thr | Cys | Gly | Phe | Ile | Glu | Ser | Ala | Lys | Gln | Glu | Ser | Ile | Gln | Thr | Ile | 50  | 55  | 60  |     |
| Leu | Asn | Ala | Ala | Lys | Asp | Lys | Lys | Glu | Gly | Ala | Ile | Leu | Ile | Ala | Ser | 65  | 70  | 75  | 80  |
| Gly | Cys | Leu | Ser | Glu | Arg | Tyr | Lys | Asp | Glu | Ile | Lys | Glu | Leu | Ile | Pro | 85  | 90  | 95  |     |
| Glu | Val | Asp | Ile | Phe | Thr | Gly | Val | Gly | Asp | Tyr | Asp | Lys | Ile | Asp | Ile | 100 | 105 | 110 |     |
| Met | Ile | Ala | Lys | Lys | Gln | Asn | Gln | Phe | Ser | Glu | Gln | Val | Phe | Leu | Ser | 115 | 120 | 125 |     |
| Glu | His | Tyr | Asn | Ala | Arg | Ile | Ile | Thr | Gly | Ser | Ser | Val | His | Ala | Tyr | 130 | 135 | 140 |     |
| Val | Lys | Ile | Ser | Glu | Gly | Cys | Asn | Gln | Lys | Cys | Ser | Phe | Cys | Ala | Ile | 145 | 150 | 155 | 160 |
| Pro | Ser | Phe | Lys | Gly | Lys | Leu | Gln | Ser | Arg | Glu | Leu | Asp | Ser | Ile | Leu | 165 | 170 | 175 |     |
| Lys | Glu | Val | Glu | Asn | Leu | Ala | Leu | Lys | Gly | Tyr | Thr | Asp | Met | Thr | Phe | 180 | 185 | 190 |     |
| Ile | Ala | Gln | Asp | Ser | Ser | Ser | Phe | Leu | Tyr | Asp | Lys | Gly | Gln | Lys | Asp | 195 | 200 | 205 |     |
| Gly | Leu | Ile | Gln | Leu | Ile | Arg | Ala | Ile | Asp | Lys | Gln | Gln | Ala | Leu | Lys | 210 | 215 | 220 |     |
| Ser | Ala | Arg | Ile | Leu | Tyr | Leu | Tyr | Pro | Ser | Ser | Thr | Thr | Leu | Glu | Leu | 225 | 230 | 235 | 240 |
| Ile | Gly | Ala | Ile | Glu | Ser | Ser | Pro | Ile | Phe | Gln | Asn | Tyr | Phe | Asp | Met | 245 | 250 | 255 |     |
| Pro | Ile | Gln | His | Ile | Ser | Asp | Ser | Met | Leu | Lys | Lys | Met | Arg | Arg | Asn | 260 | 265 | 270 |     |
| Ser | Ser | Gln | Ala | His | His | Leu | Lys | Leu | Leu | Asp | Ala | Met | Lys | Gln | Val | 275 | 280 | 285 |     |
| Lys | Glu | Ser | Phe | Ile | Arg | Ser | Thr | Ile | Ile | Val | Gly | His | Pro | Glu | Glu |     |     |     |     |



|                                                                 |      |
|-----------------------------------------------------------------|------|
| CAG CTC ATT AGA GCG ATT GAT AAA CAG CAA GCC TTA AAG AGC GCG CGT | 730  |
| Gln Leu Ile Arg Ala Ile Asp Lys Gln Gln Ala Leu Lys Ser Ala Arg |      |
| 215 220 225                                                     |      |
| ATT TTA TAT CTC TAC CCC TCT AGC ACC ACG CTA GAG CTT ATT GGC GCG | 778  |
| Ile Leu Tyr Leu Tyr Pro Ser Ser Thr Thr Leu Glu Leu Ile Gly Ala |      |
| 230 235 240                                                     |      |
| ATT GAA AGT TCG CCC ATT TTT CAA AAT TAT TTT GAC ATG CCC ATC CAG | 826  |
| Ile Glu Ser Ser Pro Ile Phe Gln Asn Tyr Phe Asp Met Pro Ile Gln |      |
| 245 250 255                                                     |      |
| CAC ATC AGC GAC TCC ATG CTC AAA AAG ATG CGG CGC AAC TCT AGC CAA | 874  |
| His Ile Ser Asp Ser Met Leu Lys Lys Met Arg Arg Asn Ser Ser Gln |      |
| 260 265 270 275                                                 |      |
| GCG CAC CAT TTA AAG CTT TTA GAT GCC ATG AAG CAG GTT AAA GAA AGC | 922  |
| Ala His His Leu Lys Leu Leu Asp Ala Met Lys Gln Val Lys Glu Ser |      |
| 280 285 290                                                     |      |
| TTT ATC AGA AGC ACG ATC ATT GTA GGG CAT CCG GAA GAA AAT GAG AGC | 970  |
| Phe Ile Arg Ser Thr Ile Ile Val Gly His Pro Glu Glu Asn Glu Ser |      |
| 295 300 305                                                     |      |
| GAA TTT GAA GAA TTG AGC GCG TTT TTA GAC GAG TTC CAG TTT GAT AGA | 1018 |
| Glu Phe Glu Glu Leu Ser Ala Phe Leu Asp Glu Phe Gln Phe Asp Arg |      |
| 310 315 320                                                     |      |
| TTG AAT ATT TTT GCT TTC AGC GCT GAA GAA AAC ACG CAT GCC TAT TCT | 1066 |
| Leu Asn Ile Phe Ala Phe Ser Ala Glu Glu Asn Thr His Ala Tyr Ser |      |
| 325 330 335                                                     |      |
| TTA GAA AAA GTG CCT AAA AAA ACC ATC AAC GCT CGC ATC AAA GCC TTG | 1114 |
| Leu Glu Lys Val Pro Lys Lys Thr Ile Asn Ala Arg Ile Lys Ala Leu |      |
| 340 345 350 355                                                 |      |
| AAT AAA ATC GCT TTA AAG CAC CAA AAC CAT TCC TTT AAG GCT TTG TTG | 1162 |
| Asn Lys Ile Ala Leu Lys His Gln Asn His Ser Phe Lys Ala Leu Leu |      |
| 360 365 370                                                     |      |
| AAT AAG CCC ATT AAG GCG TTA GTG GAA AAT AAA GAG GGC GAG TAT TTT | 1210 |
| Asn Lys Pro Ile Lys Ala Leu Val Glu Asn Lys Glu Gly Glu Tyr Phe |      |
| 375 380 385                                                     |      |
| TAC AAA GCA AGG GAT CTC AGA TGG GCG CCT GAA GTG GAT GGG GAA ATC | 1258 |
| Tyr Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp Gly Glu Ile |      |
| 390 395 400                                                     |      |
| TTG ATC AAT GAT AGC GAA CTA ACC ACC CCC TTA AAA CCC GGC CAT TAT | 1306 |
| Leu Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro Gly His Tyr |      |
| 405 410 415                                                     |      |
| ACG ATT GCA CCT AGC GAA TTT AAA GAT AAT ATC CTA CTC GCT AAG GTT | 1354 |
| Thr Ile Ala Pro Ser Glu Phe Lys Asp Asn Ile Leu Leu Ala Lys Val |      |
| 420 425 430 435                                                 |      |

ATTGATTTCT TTTGGGAAGT GGATTGAAA AACTTAAAAA GCCATTAAC ATG CAA GTT 58  
Met Gln Val  
1

AAA GAA AAC AAA CAA CTC TGC TTA ATT TCA TTA GGT TGC TCT AAA AAT 106  
Lys Glu Asn Lys Lys Gln Leu Cys Leu Ile Ser Leu Gly Cys Ser Lys Asn  
5 10 15

TTG GTG GAT TCA GAG GTG ATG TTA GGC AAG CTT TAT AAT TAC ACG CTC 154  
Leu Val Asp Ser Glu Val Met Leu Gly Lys Leu Tyr Asn Tyr Thr Leu  
20 25 30 35

ACT AAT GAC GCT AAG AGC GCT GAT GTG ATT TTG ATC AAC ACT TGC GGG 202  
Thr Asn Asp Ala Lys Ser Ala Asp Val Ile Leu Ile Asn Thr Cys Gly  
40 45 50

TTT ATT GAA AGC GCT AAA CAA GAG AGT ATC CAA ACC ATT CTC AAC GCC 250  
Phe Ile Glu Ser Ala Lys Lys Glu Ser Ile Gln Thr Ile Leu Asn Ala  
55 60 65

GCC AAA GAC AAA AAA GAG GGA GCG ATT TTG ATT GCG AGC GGG TGC TTG 298  
Ala Lys Asp Lys Lys Glu Gly Ala Ile Leu Ile Ala Ser Gly Cys Leu  
70 75 80

AGC GAA CGC TAT AAA GAT GAA ATC AAA GAA TTG ATC CCT GAA GTG GAT 346  
Ser Glu Arg Tyr Lys Asp Glu Ile Lys Glu Leu Ile Pro Glu Val Asp  
85 90 95

ATT TTT ACC GGC GTG GGG GAT TAT GAC AAG ATC GAT ATA ATG ATT GCT 394  
Ile Phe Thr Gly Val Gly Asp Tyr Asp Lys Ile Asp Ile Met Ile Ala  
100 105 110 115

AAA AAA CAA AAC CAG TTC AGC GAG CAA GTG TTT TTA AGC GAG CAT TAC 442  
Lys Lys Lys Asn Gln Phe Ser Glu Gln Val Phe Leu Ser Glu His Tyr  
120 125 130

AAC GCA CGC ATC ATC ACG GGA TCG AGC GTG CAT GCG TAT GTG AAA ATT 490  
Asn Ala Arg Ile Ile Thr Gly Ser Ser Val His Ala Tyr Val Lys Ile  
135 140 145

TCT GAG GGT TGC AAT CAA AAA TGT TCT TTT TGC GCT ATC CCT AGC TTT 538  
Ser Glu Gly Cys Asn Gln Lys Cys Ser Phe Cys Ala Ile Pro Ser Phe  
150 155 160

AAG GGG AAA TTG CAA AGC AGG GAA TTG GAC TCC ATT TTA AAA GAA GTG 586  
Lys Gly Lys Leu Gln Ser Arg Glu Leu Asp Ser Ile Leu Lys Glu Val  
165 170 175

GAA AAT CTC GCG CTT AAA GGC TAT ACG GAT ATG ACT TTT ATC GCT CAA 634  
Glu Asn Leu Ala Leu Lys Gly Tyr Thr Asp Met Thr Phe Ile Ala Gln  
180 185 190 195

GAC TCT AGC TCC TTT TTA TAC GAT AAG GGG CAA AAA GAC GGC TTG ATC 682  
Asp Ser Ser Ser Phe Leu Tyr Asp Lys Gly Gln Lys Asp Gly Leu Ile  
200 205 210

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr Leu Ala Leu Ile Ala
 1 5 10 15
Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile Val Leu
 20 25 30
Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys Ala Leu
 35 40 45
Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys Phe Cys
 50 55 60
Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser Ile Leu
 65 70 75 80
Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys Asn Val
 85 90 95
Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe Ile Lys
 100 105 110
Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala Phe Gln
 115 120 125
Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe Ile Ile
 130 135 140
Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu Leu Thr
 145 150 155 160
Pro Lys Glu Arg Met Arg
 165

```

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...1366
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 70...567  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTAGCGCGAT CTTTGGTCTC ACACAAGCTA TAACAAGCTT GAGAATCGCA TAATATATTC | 60  |
| TTGTTCTAC ATG CTA TCA CCA GCA ACT TTC AAA CAA ATA ACT CTA GCA TTA | 111 |
| Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr Leu Ala Leu           |     |
| 1 5 10                                                            |     |
| ATC GCT TCA AGA CTA ATC GTT GTA ATC CTA TAT GCT TTT ATC TTT ATT   | 159 |
| Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile   |     |
| 15 20 25 30                                                       |     |
| GTT CTC TCT TTT TAT ATG CTC AAT ATC ATC ACT ATT CTT AAT TTT AAA   | 207 |
| Val Leu Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys   |     |
| 35 40 45                                                          |     |
| GCG CTT ATT TTG GGG TTT GTT AGT GTT TTT TCA AGC GCA TTG TTT TGT   | 255 |
| Ala Leu Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys   |     |
| 50 55 60                                                          |     |
| TTT TGC TTG GCA ATT TTT GTA GCT AGA ATT TTT CAA AAC GAA CAA AGC   | 303 |
| Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser   |     |
| 65 70 75                                                          |     |
| ATC TTA GGA TTT TGT AAT ATC ATC AAT CTC TAT GCG CTA ATG TCT TGT   | 351 |
| Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys   |     |
| 80 85 90                                                          |     |
| AAT GTT TTT GTT CCT TTA GAA TAC CTA CCT AGT ATT GGT CAA TTA TTT   | 399 |
| Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe   |     |
| 95 100 105 110                                                    |     |
| ATC AAA ACA TCT ATT TTT TAC TAC CTT AAT CAA CTT CTA ATC AAA GCT   | 447 |
| Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala   |     |
| 115 120 125                                                       |     |
| TTT CAA GGG ATT GAT ACT ATA CTG GTT TTA GCA ACT TCA ACA TTT TTC   | 495 |
| Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe   |     |
| 130 135 140                                                       |     |
| ATT ATT GGT GGC ATT ATT TTA TTT TTA CTA AGC GCT AAT CGC ATG TTA   | 543 |
| Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu   |     |
| 145 150 155                                                       |     |
| CTA ACA CCA AAA GAA CGC ATG CGT TAAAGGCTTA GTCCCACCAT TGATTTATTT  | 597 |
| Leu Thr Pro Lys Glu Arg Met Arg                                   |     |
| 160 165                                                           |     |
| AATGGCTCAA AAAAGGGGTA AGC                                         | 620 |

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Met Arg Leu Leu Phe Leu Leu Leu Ser Ala Ala Phe Met Leu Leu Ala
 1 5 10 15
Glu Glu Lys Ile Ser Leu Asn Asp Asp Ala Pro Ile Lys Leu Val His
 20 25 30
Trp Gln Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala
 35 40 45
Thr Pro Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro
 50 55 60
Phe Asn Lys Thr Pro Lys Ile Met Glu Val Glu Gly Gln Lys Val Ile
65 70 75 80
Val Leu Lys Asn Ala Lys Leu Asp Ser Lys Lys Thr Met Asp Phe Lys
 85 90 95
Glu Ala Ser Leu Asn Ala Leu Glu Met Phe Ser Tyr Gln Asn Asp Ile
 100 105 110
Tyr Leu Leu Ser Lys Lys Ala Lys Val Glu Leu Glu Ile Gln Ala Ser
 115 120 125
Asn Ser Lys Asp Lys Lys Arg Leu Arg Phe Leu Phe Leu Pro Lys Gly
 130 135 140
Phe His Leu Ala Pro Pro Pro Asn Leu Lys Glu Lys Ser Gln Gln Thr
145 150 155 160
Asn Leu Ala Gln Lys Asp Thr Asn Glu Gln Pro Gln Ser Pro Leu Asn
 165 170 175
Thr Leu Glu Leu Lys Pro Pro Leu Asn Leu Ser His Ala Tyr Lys Ala
 180 185 190
Leu Ala Val Ile Ala Ala Leu Leu Ile Leu Tyr Val Ile Lys Lys
 195 200 205
Lys Ile Val Pro Thr Gln Gly Ser Phe Ser Ala Lys Asp Phe Lys Leu
 210 215 220
Glu Ile Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser
225 230 235 240
Ile Glu Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr
 245 250 255
Gly Leu Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu
 260 265 270
Ile Lys Glu Ala Glu Asn Asn Ile Lys Asn Ser Lys Leu Gly Asn Leu
 275 280 285
Tyr Ala Gly Lys Phe
 290

```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTG TCT AAA AAA GCT AAA GTG GAA TTA GAA ATC CAA GCT TCA AAC AGC   | 442 |
| Leu Ser Lys Lys Ala Lys Val Glu Leu Glu Ile Gln Ala Ser Asn Ser   |     |
| 115 120 125 130                                                   |     |
| AAG GAT AAA AAA CGG CTC CGC TTT CTC TTT TTA CCC AAA GGT TTT CAT   | 490 |
| Lys Asp Lys Lys Arg Leu Arg Phe Leu Phe Leu Pro Lys Gly Phe His   |     |
| 135 140 145                                                       |     |
| TTA GCC CCA CCG CCT AAC CTG AAA GAA AAA TCT CAG CAA ACT AAC CTT   | 538 |
| Leu Ala Pro Pro Pro Asn Leu Lys Glu Lys Ser Gln Gln Thr Asn Leu   |     |
| 150 155 160                                                       |     |
| GCA CAA AAA GAC ACC AAC GAG CAA CCC CAA AGC CCT TTA AAC ACT CTA   | 586 |
| Ala Gln Lys Asp Thr Asn Glu Gln Pro Gln Ser Pro Leu Asn Thr Leu   |     |
| 165 170 175                                                       |     |
| GAG TTA AAA CCC CCA CTA AAT TTA AGC CAT GCT TAT AAG GCG CTA GCG   | 634 |
| Glu Leu Lys Pro Pro Leu Asn Leu Ser His Ala Tyr Lys Ala Leu Ala   |     |
| 180 185 190                                                       |     |
| GTT ATT GCT GCC TTA CTC TTA ATA TTG TAT GTC ATC AAA AAA AAA ATT   | 682 |
| Val Ile Ala Ala Leu Leu Leu Ile Leu Tyr Val Ile Lys Lys Lys Ile   |     |
| 195 200 205 210                                                   |     |
| GTT CCC ACA CAA GGG TCT TTT TCT GCA AAA GAT TTT AAG TTA GAA ATT   | 730 |
| Val Pro Thr Gln Gly Ser Phe Ser Ala Lys Asp Phe Lys Leu Glu Ile   |     |
| 215 220 225                                                       |     |
| AGC GTT TTG GGT CGT GTT GAT GCG AAC CAT AAA ATC ATT TCA ATA GAA   | 778 |
| Ser Val Leu Gly Arg Val Asp Ala Asn His Lys Ile Ile Ser Ile Glu   |     |
| 230 235 240                                                       |     |
| ACC AAT AAG GAG CGT TAC TTG GTC TTA CTA AGC GAT AAA TAC GGC CTG   | 826 |
| Thr Asn Lys Glu Arg Tyr Leu Val Leu Leu Ser Asp Lys Tyr Gly Leu   |     |
| 245 250 255                                                       |     |
| CTT TTA GAC AAA ATA AGC CCA AAA ACA TCT AAA GAA GAA CTG ATT AAA   | 874 |
| Leu Leu Asp Lys Ile Ser Pro Lys Thr Ser Lys Glu Glu Leu Ile Lys   |     |
| 260 265 270                                                       |     |
| GAA GCT GAA AAT AAT ATA AAG AAT TCA AAA TTA GGA AAT TTA TAT GCC   | 922 |
| Glu Ala Glu Asn Asn Ile Lys Asn Ser Lys Leu Gly Asn Leu Tyr Ala   |     |
| 275 280 285 290                                                   |     |
| GGA AAA TTC TAAACTACAA CCTGCTAAGT TAGGGAAAAA TTTTGACCCT GTGGATCAT | 980 |
| Gly Lys Phe                                                       |     |

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Gln Asp Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr  
 195 200 205  
 Ile Lys Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn  
 210 215 220

(2) INFORMATION FOR SEO ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 980 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 53...931  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:61:

|            |            |            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGAATGAAAT | CCTAGATTCT | AACGCCATTG | TATATTATCT | CGCTAAAAAT | TC  | ATG | AGA |     |     |     |     |     |     |     |     | 58  |
|            |            |            |            |            |     |     | Met | Arg |     |     |     |     |     |     |     |     |
|            |            |            |            |            |     |     | 1   |     |     |     |     |     |     |     |     |     |
| TTG        | TTA        | TTC        | TTG        | TTA        | TTG | AGT | GCT | GCT | TTT | ATG | TTA | CTG | GCT | GAA | GAA | 106 |
| Leu        | Leu        | Phe        | Leu        | Leu        | Leu | Ser | Ala | Ala | Phe | Met | Leu | Leu | Ala | Glu | Glu |     |
|            |            | 5          |            |            |     |     | 10  |     |     |     |     | 15  |     |     |     |     |
| AAA        | ATA        | TCT        | TTA        | AAC        | GAT | GAC | GCC | CCC | ATT | AAA | CTA | GTG | CAT | TGG | CAA | 154 |
| Lys        | Ile        | Ser        | Leu        | Asn        | Asp | Asp | Ala | Pro | Ile | Lys | Leu | Val | His | Trp | Gln |     |
|            | 20         |            |            |            |     | 25  |     |     |     |     | 30  |     |     |     |     |     |
| AAT        | GCA        | TTA        | AAA        | GAA        | GTC | CAA | CCT | GAT | TCA | AAC | GCT | CCA | GCA | ACA | CCA | 202 |
| Asn        | Ala        | Leu        | Lys        | Glu        | Val | Gln | Pro | Asp | Ser | Asn | Ala | Pro | Ala | Thr | Pro |     |
| 35         |            |            |            |            | 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |
| CCT        | ATA        | AAA        | GCC        | GTG        | CAA | ACC | ACG | CTC | ACT | TTT | GAA | ACG | CCT | TTT | AAC | 250 |
| Pro        | Ile        | Lys        | Ala        | Val        | Gln | Thr | Thr | Leu | Thr | Phe | Glu | Thr | Pro | Phe | Asn |     |
|            |            |            |            | 55         |     |     |     |     | 60  |     |     |     |     | 65  |     |     |
| AAA        | ACG        | CCT        | AAA        | ATC        | ATG | GAA | GTT | GAA | GGG | CAA | AAG | GTG | ATC | GTC | TTA | 298 |
| Lys        | Thr        | Pro        | Lys        | Ile        | Met | Glu | Val | Glu | Gly | Gln | Lys | Val | Ile | Val | Leu |     |
|            |            |            | 70         |            |     |     |     | 75  |     |     |     |     | 80  |     |     |     |
| AAA        | AAC        | GCT        | AAA        | CTG        | GAT | TCT | AAA | AAA | ACC | ATG | GAT | TTT | AAA | GAA | GCC | 346 |
| Lys        | Asn        | Ala        | Lys        | Leu        | Asp | Ser | Lys | Lys | Thr | Met | Asp | Phe | Lys | Glu | Ala |     |
|            |            | 85         |            |            |     |     | 90  |     |     |     |     | 95  |     |     |     |     |
| TCT        | TTG        | AAT        | GCT        | TTA        | GAA | ATG | TTT | TCC | TAC | CAA | AAT | GAC | ATC | TAC | CTC | 394 |
| Ser        | Leu        | Asn        | Ala        | Leu        | Glu | Met | Phe | Ser | Tyr | Gln | Asn | Asp | Ile | Tyr | Leu |     |
|            | 100        |            |            |            |     | 105 |     |     |     |     | 110 |     |     |     |     |     |

```

AAA ACC GGC AAA ACC ATC TAT GAA TTG CCC GGC TAT ATG CCC TCT ACG 584
Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro Ser Thr
 165 170 175

CAA TTT TTA GCC GTG TTA GAA TTT ATC GGC GAT GGG AAG TAT CAA GAC 632
Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr Gln Asp
 180 185 190

ACA AAA GAC GAT GAG GAT CTC ACT AAA AAA TTA AAG GCT TAC ATC AAG 680
Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr Ile Lys
 195 200 205 210

TAT AAA ACC AAC CTT TCT AAA AGC AAG TCT AAC TAGGAAAAGCC TAATGAAGAA 733
Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn
 215 220

TCTCAAAAGC CTGCTTTCTT TTTTGCTGGC TTC 766

```

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

Met Phe Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu
 1 5 10 15
Leu Ile Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys
 20 25 30
Leu Asp Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu
 35 40 45
Asn Asp Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu
 50 55 60
Asp Val Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met
 65 70 75 80
Leu Leu Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys
 85 90 95
Lys Asp Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His
 100 105 110
Phe Ser Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe
 115 120 125
Lys Val Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu
 130 135 140
Glu Leu Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu
 145 150 155 160
Ser Asp Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro
 165 170 175
Ser Thr Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr
 180 185 190

```



(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 51...713  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TGTAGTAAGA TACCTAGTTT TCAAATCTAT TAAAAGATAA AGGTTATTAC ATG TTT  | 56  |
| Met Phe                                                         |     |
| 1                                                               |     |
| TCA CTT TCT TAT GTT TCC AAG AAA TTT TTA AGC GTT TTA TTA TTG ATT | 104 |
| Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu Leu Ile |     |
| 5 10 15                                                         |     |
| TCG CTG TTT TTA AGC GCT TGC AAA TCC AAC AAT AAA GAC AAG TTA GAC | 152 |
| Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys Leu Asp |     |
| 20 25 30                                                        |     |
| GAA AAT CTT TTA AGC TCT GGC TCT CAA AGC TCC AAA GAA TTA AAC GAT | 200 |
| Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu Asn Asp |     |
| 35 40 45 50                                                     |     |
| GAG CGA GAC AAT ATA GAC AAA AAG AGT TAC GCT GGT TTA GAA GAT GTT | 248 |
| Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu Asp Val |     |
| 55 60 65                                                        |     |
| TTT TCA GAC AAT AAG TCC ATT AGT CCT AAC GAT AAA TAC ATG CTT TTA | 296 |
| Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met Leu Leu |     |
| 70 75 80                                                        |     |
| GTT TTT GGC CGT AAT GGT TGC TCC TAT TGC GAA AGG TTT AAA AAA GAT | 344 |
| Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys Lys Asp |     |
| 85 90 95                                                        |     |
| CTC AAA AAT GTC AAA GAA TTG CGC GAC TAC ATT AAA GAG CAT TTT AGC | 392 |
| Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His Phe Ser |     |
| 100 105 110                                                     |     |
| GCT TAC TAT GTC AAT ATC AGC TAC TCC AAA GAG CAT GAT TTT AAA GTC | 440 |
| Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe Lys Val |     |
| 115 120 125 130                                                 |     |
| GGC GAT AAA AAT AAT GAA AAA GAA ATC AAA ATG TCC ACA GAA GAA TTA | 488 |
| Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu Glu Leu |     |
| 135 140 145                                                     |     |
| GCG CAA ATT TAT GCC GTC CAA TCC ACC CCT ACG ATT GTT TTA TCC GAT | 536 |
| Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu Ser Asp |     |
| 150 155 160                                                     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Phe | Phe | Val | Gly | Ala | Leu | Leu | Phe | Tyr | Trp | Cys | Ala | Leu | Ser | Phe | 65  | 70  | 75  | 80  |
| Arg | Tyr | Ser | Asp | Phe | Thr | Tyr | Leu | Leu | Pro | Leu | Ile | Ile | Val | Leu | Ile | 85  | 90  | 95  |     |
| Ala | Leu | Val | Tyr | Gly | Val | Leu | Phe | Tyr | Leu | Leu | Leu | Tyr | Phe | Glu | Asn | 100 | 105 | 110 |     |
| Pro | Tyr | Phe | Arg | Leu | Leu | Ser | Phe | Leu | Gly | Ser | Ser | Phe | Ile | His | Pro | 115 | 120 | 125 |     |
| Phe | Gly | Phe | Asp | Trp | Leu | Val | Pro | Asp | Ser | Phe | Phe | Ser | Tyr | Ser | Val | 130 | 135 | 140 |     |
| Phe | Arg | Val | Asp | Lys | Leu | Ser | Leu | Gly | Leu | Val | Phe | Leu | Ala | Cys | Ile | 145 | 150 | 155 | 160 |
| Phe | Leu | Ser | Thr | Lys | Pro | Leu | Lys | Lys | Tyr | Arg | Ile | Ile | Gly | Val | Leu | 165 | 170 | 175 |     |
| Leu | Leu | Leu | Gly | Ala | Leu | Asp | Phe | Asn | Gly | Phe | Lys | Thr | Ser | Asp | Leu | 180 | 185 | 190 |     |
| Lys | Lys | Val | Gly | Asn | Ile | Glu | Leu | Val | Ser | Thr | Lys | Thr | Pro | Gln | Asp | 195 | 200 | 205 |     |
| Leu | Lys | Phe | Asp | Ser | Ser | Tyr | Leu | Asn | Asp | Ile | Glu | Asn | Asn | Ile | Leu | 210 | 215 | 220 |     |
| Lys | Glu | Ile | Lys | Leu | Ala | Gln | Ser | Lys | Gln | Lys | Thr | Leu | Ile | Val | Phe | 225 | 230 | 235 | 240 |
| Pro | Glu | Thr | Ala | Tyr | Pro | Ile | Ala | Leu | Glu | Asn | Ser | Pro | Phe | Lys | Ala | 245 | 250 | 255 |     |
| Lys | Leu | Glu | Asp | Leu | Ser | Asp | Asn | Ile | Ala | Ile | Leu | Ile | Gly | Thr | Leu | 260 | 265 | 270 |     |
| Arg | Thr | Gln | Gly | Tyr | Asn | Leu | Tyr | Asn | Ser | Ser | Phe | Leu | Phe | Ser | Lys | 275 | 280 | 285 |     |
| Glu | Ser | Val | Gln | Ile | Ala | Asp | Lys | Val | Ile | Leu | Ala | Pro | Phe | Gly | Glu | 290 | 295 | 300 |     |
| Thr | Met | Pro | Leu | Pro | Glu | Phe | Leu | Gln | Lys | Pro | Leu | Glu | Lys | Leu | Phe | 305 | 310 | 315 | 320 |
| Phe | Gly | Glu | Ser | Thr | Tyr | Leu | Tyr | Arg | Asn | Ala | Pro | His | Phe | Ser | Asp | 325 | 330 | 335 |     |
| Phe | Thr | Leu | Asp | Asp | Phe | Thr | Phe | Arg | Pro | Leu | Ile | Cys | Tyr | Glu | Gly | 340 | 345 | 350 |     |
| Thr | Ser | Lys | Pro | Ala | Tyr | Ser | Asn | Ser | Pro | Ser | Lys | Ile | Phe | Ile | Val | 355 | 360 | 365 |     |
| Met | Ser | Asn | Asn | Ala | Trp | Phe | Ser | Pro | Ser | Ile | Glu | Pro | Thr | Leu | Gln | 370 | 375 | 380 |     |
| Arg | Thr | Leu | Leu | Lys | Tyr | Tyr | Ala | Arg | Arg | Tyr | Asp | Lys | Ile | Ile | Leu | 385 | 390 | 395 | 400 |
| His | Ser | Ala | Asn | Phe | Ser | Thr | Ser | Tyr | Ile | Leu | Ser | Pro | Ser | Leu | Leu | 405 | 410 | 415 |     |
| Gly | Asp | Ile | Leu | Phe | Arg | Lys | Arg | Ser |     |     |     |     |     |     |     | 420 | 425 |     |     |

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TTT CTT CAA AAA CCC CTT GAA AAG CTC TTT TTT GGC GAG AGC ACT TAT    | 1074 |
| Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe Gly Glu Ser Thr Tyr    |      |
| 315 320 325                                                        |      |
| TTA TAC CGC AAT GCT CCT CAT TTC AGC GAT TTT ACA TTA GAC GAT TTT    | 1122 |
| Leu Tyr Arg Asn Ala Pro His Phe Ser Asp Phe Thr Leu Asp Asp Phe    |      |
| 330 335 340                                                        |      |
| ACT TTT CGC CCC CTG ATT TGC TAT GAA GGC ACT TCC AAA CCC GCT TAT    | 1170 |
| Thr Phe Arg Pro Leu Ile Cys Tyr Glu Gly Thr Ser Lys Pro Ala Tyr    |      |
| 345 350 355                                                        |      |
| TCA AAC AGC CCT TCA AAA ATT TTT ATC GTG ATG AGC AAT AAC GCA TGG    | 1218 |
| Ser Asn Ser Pro Ser Lys Ile Phe Ile Val Met Ser Asn Asn Ala Trp    |      |
| 360 365 370                                                        |      |
| TTT AGC CCA AGC ATT GAA CCC ACC TTA CAA AGA ACG CTT TTA AAA TAC    | 1266 |
| Phe Ser Pro Ser Ile Glu Pro Thr Leu Gln Arg Thr Leu Leu Lys Tyr    |      |
| 375 380 385 390                                                    |      |
| TAC GCA AGG CGT TAT GAT AAG ATC ATC TTG CAC AGC GCG AAC TTT TCA    | 1314 |
| Tyr Ala Arg Arg Tyr Asp Lys Ile Ile Leu His Ser Ala Asn Phe Ser    |      |
| 395 400 405                                                        |      |
| ACT TCT TAC ATC TTA AGC CCT AGT TTA TTA GGC GAT ATT CTT TTT AGG    | 1362 |
| Thr Ser Tyr Ile Leu Ser Pro Ser Leu Leu Gly Asp Ile Leu Phe Arg    |      |
| 410 415 420                                                        |      |
| AAA CGA TCA TGATTAAAGC GATTAAATATT TCTCATGCTT TTGAAAAGCC TCTTTATAA | 1420 |
| Lys Arg Ser                                                        |      |
| 425                                                                |      |
| TGGCG                                                              | 1425 |

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|                                                                 |
|-----------------------------------------------------------------|
| Met Arg Leu Leu Leu Phe Asn Gln Asn Ala Phe Leu Leu Ala Cys Met |
| 1 5 10 15                                                       |
| Phe Val Ser Ser Val Tyr Val Asn Ala Val Leu Asp Ala Tyr Ala Ile |
| 20 25 30                                                        |
| Glu Asn Pro Tyr Ile Ser Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu |
| 35 40 45                                                        |
| Ser Met Leu Ala Phe Leu Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu |
| 50 55 60                                                        |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Tyr | Leu | Leu | Pro | Leu | Ile | Ile | Val | Leu | Ile | Ala | Leu | Val | Tyr | Gly | Val |      |  |
|     |     |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |     |      |  |
| TTA | TTT | TAT | TTG | TTG | CTC | TAT | TTT | GAA | AAC | CCC | TAT | TTC | AGG | CTT | TTG | 450  |  |
| Leu | Phe | Tyr | Leu | Leu | Leu | Tyr | Phe | Glu | Asn | Pro | Tyr | Phe | Arg | Leu | Leu |      |  |
|     |     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |      |  |
| AGT | TTT | TTA | GGC | TCT | AGT | TTT | ATC | CAC | CCC | TTT | GGA | TTT | GAT | TGG | TTA | 498  |  |
| Ser | Phe | Leu | Gly | Ser | Ser | Phe | Ile | His | Pro | Phe | Gly | Phe | Asp | Trp | Leu |      |  |
|     |     | 120 |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     |      |  |
| GTC | CCA | GAT | AGC | TTT | TTT | TCT | TAT | AGC | GTG | TTT | AGA | GTG | GAT | AAA | TTA | 546  |  |
| Val | Pro | Asp | Ser | Phe | Phe | Ser | Tyr | Ser | Val | Phe | Arg | Val | Asp | Lys | Leu |      |  |
| 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |      |  |
| TCG | CTA | GGG | CTT | GTT | TTT | TTG | GCT | TGC | ATT | TTT | TTG | AGC | ACT | AAA | CCA | 594  |  |
| Ser | Leu | Gly | Leu | Val | Phe | Leu | Ala | Cys | Ile | Phe | Leu | Ser | Thr | Lys | Pro |      |  |
|     |     |     | 155 |     |     |     |     | 160 |     |     |     |     |     | 165 |     |      |  |
| TTG | AAA | AAA | TAT | AGG | ATC | ATA | GGG | GTT | TTA | TTG | TTA | CTT | GGC | GCG | TTG | 642  |  |
| Leu | Lys | Lys | Tyr | Arg | Ile | Ile | Gly | Val | Leu | Leu | Leu | Leu | Gly | Ala | Leu |      |  |
|     |     |     | 170 |     |     |     | 175 |     |     |     |     |     | 180 |     |     |      |  |
| GAT | TTT | AAT | GGT | TTC | AAA | ACA | AGC | GAT | TTA | AAA | AAG | GTT | GGA | AAT | ATT | 690  |  |
| Asp | Phe | Asn | Gly | Phe | Lys | Thr | Ser | Asp | Leu | Lys | Lys | Val | Gly | Asn | Ile |      |  |
|     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |     |      |  |
| GAA | TTA | GTC | TCT | ACA | AAA | ACG | CCC | CAA | GAT | TTG | AAA | TTT | GAC | TCA | AGT | 738  |  |
| Glu | Leu | Val | Ser | Thr | Lys | Thr | Pro | Gln | Asp | Leu | Lys | Phe | Asp | Ser | Ser |      |  |
|     |     | 200 |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     |      |  |
| TAC | CTT | AAT | GAT | ATT | GAA | AAC | AAC | ATT | CTT | AAA | GAA | ATC | AAG | CTC | GCT | 786  |  |
| Tyr | Leu | Asn | Asp | Ile | Glu | Asn | Asn | Ile | Leu | Lys | Glu | Ile | Lys | Leu | Ala |      |  |
| 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |      |  |
| CAA | AGC | AAG | CAA | AAA | ACC | TTG | ATT | GTT | TTT | CCA | GAA | ACC | GCC | TAC | CCC | 834  |  |
| Gln | Ser | Lys | Gln | Lys | Thr | Leu | Ile | Val | Phe | Pro | Glu | Thr | Ala | Tyr | Pro |      |  |
|     |     |     | 235 |     |     |     |     |     | 240 |     |     |     |     | 245 |     |      |  |
| ATC | GCT | TTA | GAA | AAC | TCC | CCC | TTT | AAA | GCG | AAG | CTA | GAA | GAT | TTA | AGC | 882  |  |
| Ile | Ala | Leu | Glu | Asn | Ser | Pro | Phe | Lys | Ala | Lys | Leu | Glu | Asp | Leu | Ser |      |  |
|     |     |     | 250 |     |     |     | 255 |     |     |     |     |     |     | 260 |     |      |  |
| GAT | AAT | ATT | GCT | ATT | TTA | ATA | GGG | ACA | TTA | CGG | ACT | CAA | GGC | TAT | AAT | 930  |  |
| Asp | Asn | Ile | Ala | Ile | Leu | Ile | Gly | Thr | Leu | Arg | Thr | Gln | Gly | Tyr | Asn |      |  |
|     |     | 265 |     |     |     |     | 270 |     |     |     |     | 275 |     |     |     |      |  |
| CTT | TAT | AAC | AGC | TCG | TTT | TTA | TTT | TCT | AAA | GAA | AGC | GTT | CAG | ATC | GCT | 978  |  |
| Leu | Tyr | Asn | Ser | Ser | Phe | Leu | Phe | Ser | Lys | Glu | Ser | Val | Gln | Ile | Ala |      |  |
|     |     | 280 |     |     |     | 285 |     |     |     |     | 290 |     |     |     |     |      |  |
| GAT | AAA | GTA | ATT | TTA | GCC | CCC | TTT | GGC | GAG | ACC | ATG | CCT | TTA | CCG | GAA | 1026 |  |
| Asp | Lys | Val | Ile | Leu | Ala | Pro | Phe | Gly | Glu | Thr | Met | Pro | Leu | Pro | Glu |      |  |
| 295 |     |     |     |     | 300 |     |     |     |     | 305 |     |     |     |     | 310 |      |  |

```

Arg Gln Ala Leu Lys Ile Leu Ala Ile Asn Tyr Leu Lys Asn Asn Thr
 180 185 190
Leu Asn Val Glu Ser Lys Ala Lys Gly Gly Phe Val Val Val Asp Thr
 195 200 205
Lys Asn Leu Lys Thr Pro Gly Val Val Val Val Lys Val Phe Leu Glu
 210 215 220
Asp Glu Ile His Thr Phe Lys Ile Asp Ile Ser Lys Met
 225 230 235

```

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 97...1371
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

TAAAAAAAC TACCCTTAAA AAAATCAATC TAAATTCTT AAATTAAAAT ATAGCTATAA 60
TACACTAAAA CAATCTCAAG GTTTCAAAAT TTAGCC ATG CGT CTT CTT CTG TTC 114
 Met Arg Leu Leu Leu Phe
 1 5

AAT CAA AAC GCT TTT TTA TTA GCG TGC ATG TTT GTT TCA AGC GTC TAT 162
Asn Gln Asn Ala Phe Leu Leu Ala Cys Met Phe Val Ser Ser Val Tyr
 10 15 20

GTG AAC GCT GTC TTA GAC GCT TAT GCA ATT GAA AAC CCC TAT ATT TCT 210
Val Asn Ala Val Leu Asp Ala Tyr Ala Ile Glu Asn Pro Tyr Ile Ser
 25 30 35

ATC ACA CTC ACA AGC CTA TTA GCC CCT TTA AGC ATG CTA GCG TTT TTA 258
Ile Thr Leu Thr Ser Leu Leu Ala Pro Leu Ser Met Leu Ala Phe Leu
 40 45 50

AAA ACC CCT AGA AAT AGT GCT TTT GCT TTG GGG TTT TTT GTG GGG GCG 306
Lys Thr Pro Arg Asn Ser Ala Phe Ala Leu Gly Phe Phe Val Gly Ala
 55 60 65 70

TTA TTG TTT TAT TGG TGC GCT TTA AGC TTT CGC TAC TCG GAT TTC ACT 354
Leu Leu Phe Tyr Trp Cys Ala Leu Ser Phe Arg Tyr Ser Asp Phe Thr
 75 80 85

TAT TTA TTG CCC TTA ATC ATT GTT TTA ATA GCG TTA GTT TAT GGG GTT 402

```

| 165                                                                | 170 | 175 |     |
|--------------------------------------------------------------------|-----|-----|-----|
| GCT TTA AAA ATC CTA GCG ATC AAT TAC CTT AAA AAC AAC ACC CTT AAT    |     |     | 632 |
| Ala Leu Lys Ile Leu Ala Ile Asn Tyr Leu Lys Asn Asn Thr Leu Asn    |     |     |     |
| 180                                                                | 185 | 190 |     |
| GTT GAG AGT AAG GCT AAG GGA GGG TTT GTG GTG GTG GAT ACC AAA AAC    |     |     | 680 |
| Val Glu Ser Lys Ala Lys Gly Gly Phe Val Val Val Asp Thr Lys Asn    |     |     |     |
| 195                                                                | 200 | 205 | 210 |
| CTT AAA ACC CCG GGT GTG GTG GTG GTT AAA GTC TTT TTA GAA GAT GAA    |     |     | 728 |
| Leu Lys Thr Pro Gly Val Val Val Val Lys Val Phe Leu Glu Asp Glu    |     |     |     |
| 215                                                                | 220 | 225 |     |
| ATC CAC ACC TTT AAA ATT GAT ATT TCT AAG ATG TAATCGCCCC CTTTAATAAAA |     |     | 781 |
| Ile His Thr Phe Lys Ile Asp Ile Ser Lys Met                        |     |     |     |
| 230                                                                | 235 |     |     |
| AGCCTTTGGG CCATCCACCT AAAGGTTTTT                                   |     |     | 811 |

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Ile | Val | Leu | Val | Ala | Ile | Ala | Leu | Leu | Met | Ser | Ala | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Tyr | Lys | Ile | Thr | Pro | Glu | His | Val | Thr | Ser | Tyr | Asn | Asn | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gln | Val | Met | Thr | Ser | Thr | Gln | Ala | Lys | Ser | Lys | Val | Gln | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Gln | Ser | Lys | Leu | Lys | Gly | Leu | Asn | Glu | Ser | Pro | Leu | Val | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Tyr | Val | Ala | Ala | Gln | Val | Ile | Glu | Gly | Ser | Pro | Val | Val | Phe | Ser | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Ala | Ile | Ser | Val | Ser | Ile | Asn | Gln | Thr | Asn | Leu | Pro | Val | Leu | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Arg | Gln | Val | Met | Lys | Ser | Ser | Phe | Asp | Phe | Glu | Gly | Ile | Leu | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Phe | Asn | Ile | Ala | Val | Pro | Thr | Thr | Pro | Ile | Asp | Asn | Val | Asn | Met |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Thr | Pro | Pro | Met | Phe | Tyr | Gly | Gln | Gly | Gly | Phe | Leu | Ala | Tyr |     |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Asn | Gly | Met | Met | Tyr | Gly | Gly | Met | Gly | Met | Tyr | Gly | Pro | Gly | Phe | Gly |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Met | Met | Met | Met | Asp | Asp | Val | Glu | Glu | Gln | Glu | Val | Met | Gln | Glu | Ser |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...761

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TATAATAAGG AAATTCTAAA CGAAAATTAA ACTGAATGAA AGGAGTTTGA ATG AAA  | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| AAA ATC GTT TTA GTA GCG ATA GCC TTA TTG ATG AGC GCT TGC GCG AGC | 104 |
| Lys Ile Val Leu Val Ala Ile Ala Leu Leu Met Ser Ala Cys Ala Ser |     |
| 5 10 15                                                         |     |
| TAT AAG ATC ACG CCT GAA CAT GTT ACT TCC TAT AAT AAT GGG ATT CAA | 152 |
| Tyr Lys Ile Thr Pro Glu His Val Thr Ser Tyr Asn Asn Gly Ile Gln |     |
| 20 25 30                                                        |     |
| GTG ATG ACT TCC ACG CAA GCC AAA TCT AAA GTC CAG CTA GAA ATC GCT | 200 |
| Val Met Thr Ser Thr Gln Ala Lys Ser Lys Val Gln Leu Glu Ile Ala |     |
| 35 40 45 50                                                     |     |
| CAA AGC AAG TTG AAA GGC TTG AAC GAG TCC CCC TTA GTG CTG TAT GTA | 248 |
| Gln Ser Lys Leu Lys Gly Leu Asn Glu Ser Pro Leu Val Leu Tyr Val |     |
| 55 60 65                                                        |     |
| GCG GCG CAA GTT ATA GAG GGA AGT CCT GTG GTG TTT AGC CGT AAA GCC | 296 |
| Ala Ala Gln Val Ile Glu Gly Ser Pro Val Val Phe Ser Arg Lys Ala |     |
| 70 75 80                                                        |     |
| ATT TCA GTG TCT ATC AAC CAA ACG AAT TTA CCG GTC TTA AGC CTG AGA | 344 |
| Ile Ser Val Ser Ile Asn Gln Thr Asn Leu Pro Val Leu Ser Leu Arg |     |
| 85 90 95                                                        |     |
| CAG GTG ATG AAA TCC AGT TTT GAT TTT GAG GGT ATT TTA CAA AGT TTT | 392 |
| Gln Val Met Lys Ser Ser Phe Asp Phe Glu Gly Ile Leu Gln Ser Phe |     |
| 100 105 110                                                     |     |
| AAT ATC GCC GTG CCG ACC ACC CCT ATT GAT AAT GTC AAT ATG ATC ACC | 440 |
| Asn Ile Ala Val Pro Thr Thr Pro Ile Asp Asn Val Asn Met Ile Thr |     |
| 115 120 125 130                                                 |     |
| CCG CCT ATG TTT TAT TAC GGG CAA GGG GGA TTT TTA GCT TAT AAC GGC | 488 |
| Pro Pro Met Phe Tyr Tyr Gly Gln Gly Gly Phe Leu Ala Tyr Asn Gly |     |
| 135 140 145                                                     |     |
| ATG ATG TAT GGG GGA ATG GGC ATG TAT GGG CCA GGC TTT GGC ATG ATG | 536 |
| Met Met Tyr Gly Gly Met Gly Met Tyr Gly Pro Gly Phe Gly Met Met |     |
| 150 155 160                                                     |     |
| ATG ATG GAT GAT GTA GAA GAG CAA GAA GTC ATG CAA GAA AGC CGC CAA | 584 |
| Met Met Asp Asp Val Glu Glu Gln Glu Val Met Gln Glu Ser Arg Gln |     |

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu
 1 5 10 15
Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr
 20 25 30
Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro
 35 40 45
Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe
 50 55 60
Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu
 65 70 75 80
Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg
 85 90 95
Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu
 100 105 110
Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His
 115 120 125
Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr
 130 135 140
Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn
 145 150 155 160
Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro
 165 170 175
Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Ala Arg Asp
 180 185 190
Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu
 195 200 205
Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala
 210 215 220
Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu
 225 230 235 240
Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg
 245 250 255
Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn
 260 265 270
Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val
 275 280 285
Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys
 290 295 300
Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu
 305 310 315

```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:



|                                                                   |      |
|-------------------------------------------------------------------|------|
| GCC GCG CAC AAA ACT TTA CCC ATG AAC ACC GTG GTG AAA GTC ATC AAT   | 600  |
| Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn   |      |
| 145 150 155 160                                                   |      |
| GTT GAT AAT AAC TTA AGC ACC ATT GTG CGC ATC AAC GAT AGA GGG CCT   | 648  |
| Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro   |      |
| 165 170 175                                                       |      |
| TTT GTG AGC GAT CGC ATC ATT GAT TTG TCT AAT GCG GCC GCT AGG GAT   | 696  |
| Phe Val Ser Asp Arg Ile Ile Asp Leu Ser Asn Ala Ala Arg Asp       |      |
| 180 185 190                                                       |      |
| ATT GAC ATG GTT AAA AAA GGC ACA GCC AGC GTG CGT CTC ATT GTT TTG   | 744  |
| Ile Asp Met Val Lys Lys Gly Thr Ala Ser Val Arg Leu Ile Val Leu   |      |
| 195 200 205                                                       |      |
| GGC TTT GGT GGG GTT ATC TCC ACG CAA TAC GAA CAA TCC TTT AAC GCC   | 792  |
| Gly Phe Gly Gly Val Ile Ser Thr Gln Tyr Glu Gln Ser Phe Asn Ala   |      |
| 210 215 220                                                       |      |
| AGC TCT TCA AAG ATC TTG CAC AAG GAA TTT AAA GTC GGC GAG AGC GAA   | 840  |
| Ser Ser Ser Lys Ile Leu His Lys Glu Phe Lys Val Gly Glu Ser Glu   |      |
| 225 230 235 240                                                   |      |
| AAA AGC GTG AGC GGA GGG AAA TTT TCT TTG CAA ATG GGG GCT TTT AGA   | 888  |
| Lys Ser Val Ser Gly Gly Lys Phe Ser Leu Gln Met Gly Ala Phe Arg   |      |
| 245 250 255                                                       |      |
| AAC CAA ATA GGT GCT CAA ACT TTA GCG GAT AAA TTG CAA GCA GAA AAT   | 936  |
| Asn Gln Ile Gly Ala Gln Thr Leu Ala Asp Lys Leu Gln Ala Glu Asn   |      |
| 260 265 270                                                       |      |
| CCA AAT TAC AGC GTC AAG GTT GCT TTT AAA GAC GAT TTG TAT AAA GTT   | 984  |
| Pro Asn Tyr Ser Val Lys Val Ala Phe Lys Asp Asp Leu Tyr Lys Val   |      |
| 275 280 285                                                       |      |
| TTA GTT CAA GGG TTT CAA AGC GAA GAA GAG GCT AGG GAT TTT ATG AAA   | 1032 |
| Leu Val Gln Gly Phe Gln Ser Glu Glu Glu Ala Arg Asp Phe Met Lys   |      |
| 290 295 300                                                       |      |
| AAA TAC AAC CAG AAT GCG GTT TTA ACG AGA GAA TGATTAAGTT ATTGCTTTTA | 1085 |
| Lys Tyr Asn Gln Asn Ala Val Leu Thr Arg Glu                       |      |
| 305 310 315                                                       |      |
| GATGTGGATG GCACGCTCAC AGACGGATCG TTGTAT                           | 1121 |

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 121...1065
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

CTATCAAGTC AGTATTTCCA ATATCCAATT AGCCAATGAT CTCAAAGATT CTAATATTTT 60
TATCCACCAG CGTTTAATCA TCCCCACCAA CAAAAAATTA CTCGCTACAA GGGAATTTTA 120
 ATG GGT TTG GCG TTG GAA AAA GTT TGT TTT TTA GGC GTT ATT TTT TTG 168
 Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu
 1 5 10 15

ATT AGC GCT TGC ACG GTT AAA AAA GAG GGG GTA AAG AAT TTG TCT TAC 216
Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr
 20 25 30

AAG CAT GAA AGC TTG CGC GCT TAT GAA AAC GCT AAA GAT TAT GAT CCG 264
Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro
 35 40 45

ACA ACC AAA AAA GCC GCC TAT AAA CGC AAT TTT TTT GAA CGC CAT TTC 312
Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe
 50 55 60

AAA CGC TAC TCC GAT TCG CAA GAT AGC AAC ACA AAA GAT CAG CCA CTA 360
Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu
 65 70 75 80

GAT AAC GGC ATG CGC GAT TCT AGC TCG ATC CAA AGA GCC ACC ATG CGC 408
Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg
 85 90 95

CCT TAT CAA GTG GGG GGC AAG TGG TAT TAC CCC ACT AAA GTG GAT TTA 456
Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu
 100 105 110

GGC GAA AAA TTT GAT GGC GTT GCG AGT TGG TAT GGC CCT AAC TTC CAT 504
Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His
 115 120 125

GCC AAA AAA ACC AGT AAT GGG GAA ATT TAT AAC ATG TAT GCC CAC ACC 552
Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr
 130 135 140

```

```

Asn Thr Lys Ile Thr Lys Asn Asn Pro Ile Asn Gln Ala Asn Asn Asp
35 40 45 50

ATA AGA AAA ATT GAG CAT GAA GAA GAA GAT GAA AAA GCC ACC AAA GAA 248
Ile Arg Lys Ile Glu His Glu Glu Glu Asp Glu Lys Ala Thr Lys Glu
 55 60 65

GTG AAC GAT TTG ATC AAT AAC GAA AAT AAA ATT GAT GAA ATC AAT AAT 296
Val Asn Asp Leu Ile Asn Asn Glu Asn Lys Ile Asp Glu Ile Asn Asn
 70 75 80

GAA GAA AAC GCT GAT CCT TCG CAA AAA AGA ACG AAC AAC GTT TTG CAA 344
Glu Glu Asn Ala Asp Pro Ser Gln Lys Arg Thr Asn Asn Val Leu Gln
 85 90 95

CGA GCC ACT AAC CAC CAA GAC AAT CTC AAT TCC CCA CTC AAC AGG AAG 392
Arg Ala Thr Asn His Gln Asp Asn Leu Asn Ser Pro Leu Asn Arg Lys
 100 105 110

TAT TAAAGTGTGA AACTTTTTTC AAAGGATTTA TTTAAAAAAG TAACCCCTTT ATT 448
Tyr
115

```

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Met Lys Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser
1 5 10 15
Leu Phe Ser Ala Cys Lys Asp Glu Pro Lys Lys Ser Ser Gln Ser His
 20 25 30
Gln Asn Asn Thr Lys Ile Thr Lys Asn Asn Pro Ile Asn Gln Ala Asn
 35 40 45
Asn Asp Ile Arg Lys Ile Glu His Glu Glu Glu Asp Glu Lys Ala Thr
 50 55 60
Lys Glu Val Asn Asp Leu Ile Asn Asn Glu Asn Lys Ile Asp Glu Ile
65 70 75 80
Asn Asn Glu Glu Asn Ala Asp Pro Ser Gln Lys Arg Thr Asn Asn Val
 85 90 95
Leu Gln Arg Ala Thr Asn His Gln Asp Asn Leu Asn Ser Pro Leu Asn
 100 105 110
Arg Lys Tyr
115

```

## (2) INFORMATION FOR SEQ ID NO:53:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Ile | Thr | His | Gly | Lys | His | Gln | Lys | Trp | Ile | Asp | Leu | Pro | Arg | Asn | Met |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Lys | Thr | Met | Phe | Met | Gln | Glu | Ala | Gln | Lys | Ala | Cys | Leu | Gly | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Pro | Pro | Tyr | Gly | Ala | Gly | Ala | Pro | Thr | Tyr | Ala | Val | Arg | Phe |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Thr | Ile | Leu | Ser | Phe | Ser | Leu | Glu | Lys | Glu | Asn | Ser | Thr | Tyr | Arg |     |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ala | Glu | Phe | Ala | Leu | Gly | Tyr | Asp | Ile | Ser | Val | Lys | Gly | Asp | Ser | His |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Gly | Val | Ile | Ile | Lys | His | Glu | Asn | Ile | Ser | Ser | Leu | Glu | Asn | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Thr | Thr | Lys | Thr | Ser | Lys | Asn | Gly | Asn | Gln | Asp | Phe | Gln | Glu | Ser | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Gln | Ser | Leu | Gln | His | Val | Ser | Val | Gln | Ala | Ile | Gln | Glu | Ala | Val |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ser | Leu | Ile | Lys | Lys | Ala | Ile | Glu | Ala | Gln | Ser | Val | Ser | Pro | Leu | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...395
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTTTATGATA AGATAGTCAA ATTATACATT GACTTAAGGA AATTTAATTG ATG AAA  | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| TCT AAA ATC ACT CAT TTT ATC GCT ATC TCT TTT GTT TTA AGC CTG TTT | 104 |
| Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser Leu Phe |     |
| 5 10 15                                                         |     |
| AGC GCA TGC AAA GAC GAG CCT AAA AAA TCG TCT CAA TCG CAC CAA AAC | 152 |
| Ser Ala Cys Lys Asp Glu Pro Lys Lys Ser Ser Gln Ser His Gln Asn |     |
| 20 25 30                                                        |     |
| AAC ACT AAA ATC ACT AAA AAC AAT CCA ATC AAT CAA GCG AAT AAT GAT | 200 |

|            |     |     |     |     |            |            |             |            |     |     |     |     |     |     |     |     |  |
|------------|-----|-----|-----|-----|------------|------------|-------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Cys        | Leu | Gly | Val | Ala | Leu        | Pro        | Pro         | Tyr        | Gly | Ala | Gly | Ala | Pro | Thr | Tyr |     |  |
| 110        |     |     |     |     |            | 115        |             |            |     |     | 120 |     |     |     |     |     |  |
| GCG        | GTT | CGT | TTT | ACG | ATT        | TTA        | TCG         | TTT        | TCT | CTT | TTA | GAA | AAA | GAA | AAT | 494 |  |
| Ala        | Val | Arg | Phe | Thr | Ile        | Leu        | Ser         | Phe        | Ser | Leu | Leu | Glu | Lys | Glu | Asn |     |  |
| 125        |     |     |     |     | 130        |            |             |            |     | 135 |     |     |     |     | 140 |     |  |
| TCT        | ACC | TAT | AGG | GCG | GAA        | TTT        | GCA         | CTA        | GGC | TAT | GAC | ATT | AGC | GTG | AAA | 542 |  |
| Ser        | Thr | Tyr | Arg | Ala | Glu        | Phe        | Ala         | Leu        | Gly | Tyr | Asp | Ile | Ser | Val | Lys |     |  |
|            |     |     |     | 145 |            |            |             |            | 150 |     |     |     |     | 155 |     |     |  |
| GGC        | GAT | TCG | CAT | TCT | GGG        | GTG        | ATC         | ATT        | AAG | CAT | GAA | AAT | ATT | TCT | AGC | 590 |  |
| Gly        | Asp | Ser | His | Ser | Gly        | Val        | Ile         | Ile        | Lys | His | Glu | Asn | Ile | Ser | Ser |     |  |
|            |     |     | 160 |     |            |            |             | 165        |     |     |     |     | 170 |     |     |     |  |
| TTG        | GAA | AAT | AAA | ACG | ACC        | AAA        | ACG         | AGT        | AAA | AAT | GGC | AAT | CAA | GAT | TTT | 638 |  |
| Leu        | Glu | Asn | Lys | Thr | Thr        | Lys        | Thr         | Ser        | Lys | Asn | Gly | Asn | Gln | Asp | Phe |     |  |
|            | 175 |     |     |     |            |            | 180         |            |     |     |     |     | 185 |     |     |     |  |
| CAA        | GAA | AGC | GCG | ATA | CAA        | TCT        | CTC         | CAA        | CAT | GTA | AGC | GTG | CAA | GCG | ATT | 686 |  |
| Gln        | Glu | Ser | Ala | Ile | Gln        | Ser        | Leu         | Gln        | His | Val | Ser | Val | Gln | Ala | Ile |     |  |
|            | 190 |     |     |     |            | 195        |             |            |     |     | 200 |     |     |     |     |     |  |
| CAA        | GAA | GCG | GTT | TCT | TTG        | ATT        | AAA         | AAA        | GCC | ATT | GAA | GCG | CAA | AGC | GTA | 734 |  |
| Gln        | Glu | Ala | Val | Ser | Leu        | Ile        | Lys         | Lys        | Ala | Ile | Glu | Ala | Gln | Ser | Val |     |  |
| 205        |     |     |     |     | 210        |            |             |            | 215 |     |     |     |     | 220 |     |     |  |
| AGC        | CCG | TTA | AAA | AAA | TAAAAAATAA | GGAGGAATTG | TTTGATTTTTA | CGATTGGCTG | G   |     |     |     |     |     |     | 790 |  |
| Ser        | Pro | Leu | Lys | Lys |            |            |             |            |     |     |     |     |     |     |     |     |  |
|            |     |     |     | 225 |            |            |             |            |     |     |     |     |     |     |     |     |  |
| AGCAAGCGTT | T   |     |     |     |            |            |             |            |     |     |     |     |     |     |     | 801 |  |

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Arg | Ala | Thr | Ala | Ile | Lys | Ile | Phe | Ser | Leu | Ser | Ser | Ala | Leu | Ala |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Leu | Leu | Leu | His | Gly | Cys | Leu | Ser | Ile | Asn | Leu | Lys | Gln | Met | Leu | Pro |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |
| Glu | Ile | Arg | Thr | Tyr | Asp | Leu | Asn | Ala | Ser | Ser | Phe | Glu | Ile | Thr | Gln |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Cys | Ala | Lys | Pro | Leu | Thr | Glu | Val | Arg | Leu | Ile | Ser | Ile | Leu | Ser | Ala |  |  |
| 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |  |
| Asp | Leu | Phe | Asn | Thr | Lys | Glu | Ile | Val | Phe | Lys | Ala | Lys | Asp | Gly | Gln |  |  |

Leu Glu Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro  
           195                                  200                                  205  
 Ser His Met Pro Trp Tyr Val Leu Ile Phe Asp Trp  
           210                                  215                                  220

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 75...749
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|                                                                                                                |     |
|----------------------------------------------------------------------------------------------------------------|-----|
| GAAAAAGGCT CTGCTTTGAT AGATAAATTT GACGCTAACC CCTATAAAAC GATTTTGGGA                                              | 60  |
| GAAAGGAAAT AATC ATG AGA GCT ACG GCG ATA AAA ATC TTT TCA CTC TCA                                                | 110 |
| Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser                                                                |     |
| 1                                  5                                  10                                       |     |
| TCA GCA TTA GCC CTA TTG CTT CAT GGT TGC TTG AGC ATC AAT TTA AAA                                                | 158 |
| Ser Ala Leu Ala Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys                                                |     |
| 15                                  20                                  25                                     |     |
| CAA ATG CTA CCA GAG ATC AGA ACT TAC GAT TTG AAT GCG AGT TCT TTT                                                | 206 |
| Gln Met Leu Pro Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe                                                |     |
| 30                                  35                                  40                                     |     |
| GAA ATC ACG CAA TGC GCT AAA CCT TTG ACT GAA GTG AGG CTC ATT AGT                                                | 254 |
| Glu Ile Thr Gln Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser                                                |     |
| 45                                  50                                  55                                  60 |     |
| ATT TTG AGC GCG GAT TTA TTC AAC ACT AAA GAG ATC GTT TTT AAA GCC                                                | 302 |
| Ile Leu Ser Ala Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala                                                |     |
| 65                                  70                                  75                                     |     |
| AAA GAC GGG CAG ATC ACG CAT GGG AAG CAC CAA AAA TGG ATA GAC TTG                                                | 350 |
| Lys Asp Gly Gln Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu                                                |     |
| 80                                  85                                  90                                     |     |
| CCT CGC AAC ATG CTA AAA ACC ATG TTC ATG CAA GAA GCG CAA AAA GCA                                                | 398 |
| Pro Arg Asn Met Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala                                                |     |
| 95                                  100                                  105                                   |     |
| TGC TTA GGC GTG GCT TTG CCT CCT TAT GGC GCG GGT GCA CCC ACT TAT                                                | 446 |

```

ATC AAA TTC ATT TTA GGG CAA AAT GAG CTC AAT CGC GCG ATC GCG AAT 584
Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn
 165 170 175

GTC TAT AAA AAA CGC CAC AAG CCT GAG GGC GTG AAA CGC TAT TTA GAA 632
Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr Leu Glu
 180 185 190

AGG ATA GAT GAG ACT TTA GAA AAA GAG ACT AAA CCC AAA CCA TCG CAC 680
Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro Ser His
 195 200 205 210

ATG CCT TGG TAT GTG TTA ATT TTT GAT TGG TAGGATATTT CAAAACCATA CAC 733
Met Pro Trp Tyr Val Leu Ile Phe Asp Trp
 215 220

ATTATAACAG AGAGATGAAA AATGACTGAA 763

```

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

Met Arg Leu Lys His Phe Lys Thr Phe Leu Phe Ile Thr Met Ala Ile
 1 5 10 15
Ile Val Ile Gly Thr Gly Cys Ala Asn Lys Lys Lys Lys Lys Asp Glu
 20 25 30
Tyr Asn Lys Pro Ala Ile Phe Trp Tyr Gln Gly Ile Leu Arg Glu Ile
 35 40 45
Leu Phe Ala Asn Leu Glu Thr Ala Asp Asn Tyr Tyr Ser Ser Leu Gln
 50 55 60
Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala Met Leu Ala Leu
 65 70 75 80
Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu Ala Ser Phe Tyr
 85 90 95
Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp Asn Val Asp Tyr
 100 105 110
Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His
 115 120 125
Ser Lys Asp Gln Glu Phe Ile Ser Asn Ser Ile Val Ser Leu Gly Glu
 130 135 140
Phe Ile Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro Tyr Val Glu Tyr
 145 150 155 160
Met Gln Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile
 165 170 175
Ala Asn Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr
 180 185 190

```

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...710  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAAAATAAC CATGAGTTAT TCAAAAATTT AACTTTATAA GACAGGTGGC ATG CGT  | 56  |
| Met Arg                                                         |     |
| 1                                                               |     |
| TTA AAA CAT TTT AAA ACT TTC CTT TTT ATC ACA ATG GCA ATC ATT GTA | 104 |
| Leu Lys His Phe Lys Thr Phe Leu Phe Ile Thr Met Ala Ile Ile Val |     |
| 5 10 15                                                         |     |
| ATA GGT ACC GGT TGC GCG AAC AAA AAG AAA AAA AAA GAC GAA TAC AAC | 152 |
| Ile Gly Thr Gly Cys Ala Asn Lys Lys Lys Lys Lys Asp Glu Tyr Asn |     |
| 20 25 30                                                        |     |
| AAA CCG GCG ATC TTT TGG TAT CAA GGG ATT TTG AGA GAA ATC CTT TTT | 200 |
| Lys Pro Ala Ile Phe Trp Tyr Gln Gly Ile Leu Arg Glu Ile Leu Phe |     |
| 35 40 45 50                                                     |     |
| GCT AAT TTA GAA ACA GCG GAC AAT TAC TAT TCT TCT TTA CAA AGC GAA | 248 |
| Ala Asn Leu Glu Thr Ala Asp Asn Tyr Tyr Ser Ser Leu Gln Ser Glu |     |
| 55 60 65                                                        |     |
| CAC ATC AAT TCC CCC CTT GTC CCA GAA GCG ATG CTA GCT TTA GGG CAA | 296 |
| His Ile Asn Ser Pro Leu Val Pro Glu Ala Met Leu Ala Leu Gly Gln |     |
| 70 75 80                                                        |     |
| GCG CAC ATG AAA AAG AAA GAG TAT GTT TTA GCG TCT TTT TAC TTT GAT | 344 |
| Ala His Met Lys Lys Lys Glu Tyr Val Leu Ala Ser Phe Tyr Phe Asp |     |
| 85 90 95                                                        |     |
| GAA TAC ATC AAG CGC TTT GGG ACT AAG GAC AAT GTG GAT TAT TTG ACT | 392 |
| Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp Asn Val Asp Tyr Leu Thr |     |
| 100 105 110                                                     |     |
| TTT TTA AAA TTG CAA TCG CAT TAT TAC GCT TTC AAA AAC CAT TCT AAA | 440 |
| Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His Ser Lys |     |
| 115 120 125 130                                                 |     |
| GAC CAG GAA TTT ATC TCT AAT TCT ATT GTG AGT TTA GGC GAA TTT ATA | 488 |
| Asp Gln Glu Phe Ile Ser Asn Ser Ile Val Ser Leu Gly Glu Phe Ile |     |
| 135 140 145                                                     |     |
| GAA AAA TAC CCT AAC AGC CGT TAC CGC CCC TAT GTA GAA TAC ATG CAA | 536 |
| Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro Tyr Val Glu Tyr Met Gln |     |
| 150 155 160                                                     |     |



AAT GCA GAG TGG CTT TAAGGCATGA AAAAGATTGC ATTTTATT TTTGTCATTT T 745  
 Asn Ala Glu Trp Leu  
 205

GTTTTCGGTA GGGATTTATT TAATTTGGCA TGTTTATTG GAAAAAGCCC TAGAATTGAA 805  
 ATTAGCAACC TCAGCTAATG ATTTGCTTTT 835

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Arg | Val | Leu | Ser | Val | Gly | Val | Ala | Phe | Ile | Leu | Leu | Gly | Cys | 1   | 5   | 10  | 15  |
| Gln | Phe | Phe | Asn | Lys | Thr | Thr | Leu | His | Leu | Lys | Tyr | Lys | Asp | Tyr | Pro | 20  | 25  | 30  |     |
| Lys | Asn | Ser | Ala | Leu | Lys | Thr | Ala | Phe | Thr | Leu | Thr | Pro | Pro | Lys | Ile | 35  | 40  | 45  |     |
| Phe | Phe | Asn | Ala | Arg | Phe | Val | Pro | Pro | Phe | Tyr | Gln | Lys | Glu | Phe | Lys | 50  | 55  | 60  |     |
| Lys | Ala | Ile | Thr | Gln | Gln | Ile | Ala | Tyr | Phe | Leu | Lys | Asp | Lys | Ser | Ala | 65  | 70  | 75  | 80  |
| Phe | Ile | Leu | Asn | Val | Ser | Gly | Asn | Val | Phe | Phe | Ser | Phe | Glu | Glu | Asn | 85  | 90  | 95  |     |
| Pro | Lys | Asp | Leu | Lys | Ala | Ile | Lys | Glu | Arg | Leu | Lys | Lys | Thr | Ile | Glu | 100 | 105 | 110 |     |
| Pro | Asn | Ala | Asp | Pro | Lys | Ala | Val | Met | Arg | Phe | Leu | Asn | Leu | Gln | Ala | 115 | 120 | 125 |     |
| Ser | Leu | Ile | Leu | Glu | Cys | Val | Pro | Gln | Thr | Thr | Cys | Pro | Phe | Asp | Thr | 130 | 135 | 140 |     |
| Leu | Leu | Ile | Pro | Thr | Ala | Phe | Ser | Val | Pro | Val | Tyr | Tyr | Ala | Asn | Arg | 145 | 150 | 155 | 160 |
| Leu | Gly | Asp | Asn | Pro | Ser | Leu | Phe | Ser | Gln | Glu | Asp | Lys | Thr | Tyr | His | 165 | 170 | 175 |     |
| Asn | Ala | Leu | Ile | Lys | Ala | Leu | Asn | Lys | Ala | Tyr | Tyr | Ser | Leu | Met | Glu | 180 | 185 | 190 |     |
| Gly | Leu | Glu | Lys | Arg | Leu | Asn | Ala | Ile | Lys | Asn | Ala | Glu | Trp | Leu |     | 195 | 200 | 205 |     |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

TTGATCATTC TTATTTTCGCA CAACCCCAAGC ACGCTAAAAT TAGCCACTAA GCATGTGAAA 60
TTAGAGCATG GGC GTTTGAC AGA ATG CTA AGG GTT TTA AGC GTT GGT GTT GCT 113
 Met Leu Arg Val Leu Ser Val Gly Val Ala
 1 5 10

TTT ATT TTA CTA GGG TGT CAG TTT TTC AAC AAA ACG ACG CTG CAT TTA 161
Phe Ile Leu Leu Gly Cys Gln Phe Phe Asn Lys Thr Thr Leu His Leu
 15 20 25

AAA TAT AAA GAT TAC CCC AAA AAT AGC GCT TTA AAA ACC GCT TTC ACT 209
Lys Tyr Lys Asp Tyr Pro Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr
 30 35 40

TTA ACC CCC CCT AAA ATC TTT TTT AAC GCC CGT TTT GTG CCG CCC TTT 257
Leu Thr Pro Pro Lys Ile Phe Phe Asn Ala Arg Phe Val Pro Pro Phe
 45 50 55

TAC CAA AAA GAA TTT AAA AAA GCG ATC ACC CAA CAA ATC GCT TAT TTT 305
Tyr Gln Lys Glu Phe Lys Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe
 60 65 70

TTA AAA GAT AAA AGT GCT TTT ATT CTC AAT GTT TCA GGC AAT GTT TTT 353
Leu Lys Asp Lys Ser Ala Phe Ile Leu Asn Val Ser Gly Asn Val Phe
 75 80 85 90

TTT TCT TTT GAA GAG AAT CCT AAA GAT TTA AAA GCC ATT AAA GAA AGG 401
Phe Ser Phe Glu Glu Asn Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg
 95 100 105

CTT AAA AAG ACG ATT GAG CCT AAC GCT GAC CCA AAA GCC GTC ATG CGT 449
Leu Lys Lys Thr Ile Glu Pro Asn Ala Asp Pro Lys Ala Val Met Arg
 110 115 120

TTT TTA AAC CTT CAA GCG AGC TTG ATT TTA GAA TGC GTC CCG CAA ACC 497
Phe Leu Asn Leu Gln Ala Ser Leu Ile Leu Glu Cys Val Pro Gln Thr
 125 130 135

ACT TGC CCG TTT GAC ACC CTT TTA ATC CCC ACC GCT TTC AGC GTG CCT 545
Thr Cys Pro Phe Asp Thr Leu Leu Ile Pro Thr Ala Phe Ser Val Pro
 140 145 150

GTT TAT TAC GCT AAT CGT TTG GGC GAT AAC CCC TCT CTT TTT TCC CAA 593
Val Tyr Tyr Ala Asn Arg Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln
 155 160 165 170

GAG GAT AAA ACC TAT CAT AAC GCT TTG ATC AAA GCC CTT AAT AAG GCT 641
Glu Asp Lys Thr Tyr His Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala
 175 180 185

TAC TAT TCT CTT ATG GAG GGT TTA GAA AAG CGT TTG AAC GCT ATA AAA 689
Tyr Tyr Ser Leu Met Glu Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys
 190 195 200

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |  |  |  |  |
| Ile | Ile | Gln | Lys | Gln | Glu | Arg | Arg | Phe | Ser | Cys | Ser | Asp | Phe | His | Asn |  |  |  |  |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |  |  |  |  |
| Pro | Glu | Leu | Lys | Glu | Gln | Cys | Met | Asp | Lys | Thr | Asn | Ala | Tyr | Glu | Lys |  |  |  |  |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |  |  |  |
| Gln | Lys | Asp | Arg | Gln | Lys | Arg | Leu | Ile | Asn | Leu | Val | Gln | Leu | Glu | Ala |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Phe | Glu | Lys | Glu | Tyr | Ala | Gln | Tyr | Lys | Pro | Tyr | Ile | Ile | Pro | Tyr | Phe |  |  |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |
| Thr | Lys | Glu | Cys | Val | Lys | Asn | Ala | Pro | His | Leu | Ala | Asn | Lys | Glu | Arg |  |  |  |  |
|     |     | 180 |     |     |     |     |     |     | 185 |     |     |     | 190 |     |     |  |  |  |  |
| Leu | Cys | Gln | Lys | Glu | Val | His | Glu | Lys | Phe | Asp | Asp | Pro | Tyr | Ser | Ser |  |  |  |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| Ser | Lys | Glu | Leu | Ser | Val | Gln | Ser | Ala | Ile | Ser | Phe | Cys | Ile | Lys | Lys |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |
| Val | Asp | Ala | Lys | Leu | Glu | Lys | Ala | Ala | Leu | Met | Asn | Gly | Val | Tyr | Ile |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |
| Ser | Pro | Tyr | Lys | Lys | Ser | Thr | His | Cys | Gln | Arg | Thr | His | Leu | Glu | Asn |  |  |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |  |  |  |
| Lys | Ser | Leu | Lys | Glu | Ile | Ala | Leu | Asn | Met | Asn | Pro | Lys | Leu | Glu | Lys |  |  |  |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |
| Gln | Ser | Pro | Phe | Ile | Asp | Ala | Asp | Lys | Met | Ala | Met | Gln | Ser | Ala | Gly |  |  |  |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |
| Leu | Leu | Arg | Lys | Asn | Lys | Gly | Val | Leu | Ile | Ala | Phe | Ala | Thr | Asp | Ile |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |
| Cys | Met | Glu | Arg | Asn | Glu | His | Lys | Lys | Glu | Glu | Phe | Ile | Ser | Leu | Lys |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |
| Asp | Ser | Cys | Thr | Gln | Ser | Gln | Ala | Lys | Ile | Tyr | Asn | Asn | Lys | Glu | Arg |  |  |  |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |  |  |
| Phe | Asp | Lys | Phe | Ile | Gln | Asp | Tyr | Gln | Lys | Asp | Leu | Lys | Thr | Cys | Leu |  |  |  |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |  |  |
| Leu | Asp | Thr | Ser | Asn | Thr | Lys | Glu | Glu | Val | Glu | Gln | Asn | Phe | Ser | Gln |  |  |  |  |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |
| Cys | Gln | Lys | Glu | Gln | Leu | Arg | Asp | Asp | Asn | Lys | Gly | Leu | Gly | Phe | Thr |  |  |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |
| Leu | Glu | Glu | Leu | Val | Lys | Lys | Tyr | Ala | Lys |     |     |     |     |     |     |  |  |  |  |
| 385 |     |     |     |     |     | 390 |     |     |     |     |     |     |     |     |     |  |  |  |  |

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic RNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 84...704
- (D) OTHER INFORMATION:

|            |            |     |     |     |     |     |     |            |            |             |      |     |     |     |     |      |  |
|------------|------------|-----|-----|-----|-----|-----|-----|------------|------------|-------------|------|-----|-----|-----|-----|------|--|
| Arg        | Lys        | Asn | Lys | Gly | Val | Leu | Ile | Ala        | Phe        | Ala         | Thr  | Asp | Ile | Cys | Met |      |  |
|            |            |     |     | 295 |     |     |     |            | 300        |             |      |     |     | 305 |     |      |  |
| GAG        | CGT        | AAC | GAA | CAT | AAA | AAA | GAA | GAG        | TTT        | ATC         | AGC  | CTT | AAA | GAT | AGT | 1016 |  |
| Glu        | Arg        | Asn | Glu | His | Lys | Lys | Glu | Glu        | Phe        | Ile         | Ser  | Leu | Lys | Asp | Ser |      |  |
|            |            |     | 310 |     |     |     |     | 315        |            |             |      |     | 320 |     |     |      |  |
| TGC        | ACC        | CAA | TCG | CAA | GCC | AAA | ATC | TAT        | AAC        | AAC         | AAG  | GAG | CGC | TTT | GAC | 1064 |  |
| Cys        | Thr        | Gln | Ser | Gln | Ala | Lys | Ile | Tyr        | Asn        | Asn         | Lys  | Glu | Arg | Phe | Asp |      |  |
|            |            |     | 325 |     |     |     | 330 |            |            |             |      | 335 |     |     |     |      |  |
| AAA        | TTC        | ATA | CAA | GAT | TAC | CAA | AAA | GAC        | TTA        | AAA         | ACT  | TGT | CTT | TTA | GAC | 1112 |  |
| Lys        | Phe        | Ile | Gln | Asp | Tyr | Gln | Lys | Asp        | Leu        | Lys         | Thr  | Cys | Leu | Leu | Asp |      |  |
|            | 340        |     |     |     |     | 345 |     |            |            |             | 350  |     |     |     |     |      |  |
| ACT        | TCT        | AAC | ACT | AAA | GAA | GAA | GTG | GAG        | CAA        | AAT         | TTT  | TCA | CAA | TGC | CAA | 1160 |  |
| Thr        | Ser        | Asn | Thr | Lys | Glu | Glu | Val | Glu        | Gln        | Asn         | Phe  | Ser | Gln | Cys | Gln |      |  |
| 355        |            |     |     |     | 360 |     |     |            | 365        |             |      |     |     | 370 |     |      |  |
| AAA        | GAG        | CAA | TTG | AGA | GAT | GAT | AAC | AAA        | GGC        | TTG         | GGT  | TTC | ACT | TTA | GAA | 1208 |  |
| Lys        | Glu        | Gln | Leu | Arg | Asp | Asp | Asn | Lys        | Gly        | Leu         | Gly  | Phe | Thr | Leu | Glu |      |  |
|            |            |     |     | 375 |     |     |     |            | 380        |             |      |     |     | 385 |     |      |  |
| GAA        | TTG        | GTT | AAA | AAA | TAC | GCT | AAG | TAAAGTTATT | TAATTTTATG | GATGGTTTTTA | 1262 |     |     |     |     |      |  |
| Glu        | Leu        | Val | Lys | Lys | Tyr | Ala | Lys |            |            |             |      |     |     |     |     |      |  |
|            |            |     |     | 390 |     |     |     |            |            |             |      |     |     |     |     |      |  |
| AAAATCCATT | CCATAGTTAT | TGT |     |     |     |     |     |            |            |             |      |     |     |     |     | 1285 |  |

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Lys | Glu | Thr | Arg | Leu | Leu | Lys | Leu | Arg | Ala | Leu | Ser | Leu | Ala | Cys |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Leu | Met | Gly | Leu | Gly | Val | Ser | Gly | Cys | Ala | Phe | Leu | Asp | Lys | Gln | Ile |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Leu | Asn | Asp | His | Leu | Thr | Lys | Ala | Lys | Asn | Asn | Pro | Lys | Tyr | Asp | Cys |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Gln | Lys | Glu | Met | Trp | Ser | Phe | Pro | Lys | Lys | Tyr | Asp | Gly | Ile | Asn | Gln |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Cys | Leu | Lys | Ala | Gln | Glu | Glu | Leu | Ile | Glu | Pro | Ile | Ile | Thr | Lys | Lys |  |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |  |
| Ile | Asp | Gln | Tyr | Gln | Cys | Asp | Asp | Phe | Thr | Asn | Glu | Gly | Leu | Lys | Asp |  |  |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |  |  |
| Lys | Cys | Phe | Lys | Arg | Asn | Asp | Ala | Tyr | Leu | Asn | Thr | Leu | Leu | Thr | Pro |  |  |

| 70  |     |     |     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| CAG | TAT | CAA | TGC | GAT | GAT | TTC | ACT | AAT | GAA | GGC | TTA | AAA | GAT | AAG | TGT | 344 |  |
| Gln | Tyr | Gln | Cys | Asp | Asp | Phe | Thr | Asn | Glu | Gly | Leu | Lys | Asp | Lys | Cys |     |  |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |  |
| TTC | AAA | AGA | AAC | GAT | GCC | TAC | TTA | AAC | ACC | CTT | TTA | ACG | CCC | ATC | ATT | 392 |  |
| Phe | Lys | Arg | Asn | Asp | Ala | Tyr | Leu | Asn | Thr | Leu | Leu | Thr | Pro | Ile | Ile |     |  |
|     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |     |  |
| CAA | AAA | CAA | GAG | CGT | CGT | TTT | AGC | TGC | TCT | GAT | TTC | CAT | AAC | CCA | GAG | 440 |  |
| Gln | Lys | Gln | Glu | Arg | Arg | Phe | Ser | Cys | Ser | Asp | Phe | His | Asn | Pro | Glu |     |  |
|     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |  |
| CTA | AAA | GAA | CAA | TGC | ATG | GAT | AAA | ACT | AAC | GCT | TAT | GAA | AAG | CAA | AAA | 488 |  |
| Leu | Lys | Glu | Gln | Cys | Met | Asp | Lys | Thr | Asn | Ala | Tyr | Glu | Lys | Gln | Lys |     |  |
|     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     | 145 |     |     |  |
| GAC | CGA | CAA | AAA | AGA | CTA | ATT | AAT | CTC | GTG | CAA | TTA | GAA | GCG | TTT | GAA | 536 |  |
| Asp | Arg | Gln | Lys | Arg | Leu | Ile | Asn | Leu | Val | Gln | Leu | Glu | Ala | Phe | Glu |     |  |
|     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |  |
| AAA | GAA | TAC | GCG | CAA | TAT | AAA | CCA | TAC | ATT | ATC | CCT | TAC | TTC | ACC | AAA | 584 |  |
| Lys | Glu | Tyr | Ala | Gln | Tyr | Lys | Pro | Tyr | Ile | Ile | Pro | Tyr | Phe | Thr | Lys |     |  |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     |  |
| GAA | TGC | GTT | AAA | AAT | GCG | CCC | CAT | TTA | GCC | AAC | AAG | GAA | AGA | CTA | TGC | 632 |  |
| Glu | Cys | Val | Lys | Asn | Ala | Pro | His | Leu | Ala | Asn | Lys | Glu | Arg | Leu | Cys |     |  |
|     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |     |  |
| CAA | AAA | GAA | GTG | CAT | GAA | AAA | TTT | GAC | GAC | CCT | TAT | TCT | AGC | TCT | AAA | 680 |  |
| Gln | Lys | Glu | Val | His | Glu | Lys | Phe | Asp | Asp | Pro | Tyr | Ser | Ser | Ser | Lys |     |  |
|     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |     | 210 |     |  |
| GAA | TTG | AGC | GTT | CAA | TCG | GCT | ATT | TCT | TTT | TGC | ATT | AAA | AAA | GTT | GAT | 728 |  |
| Glu | Leu | Ser | Val | Gln | Ser | Ala | Ile | Ser | Phe | Cys | Ile | Lys | Lys | Val | Asp |     |  |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |  |
| GCT | AAA | TTA | GAA | AAA | GCC | GCT | CTT | ATG | AAT | GGC | GTT | TAT | ATA | AGC | CCT | 776 |  |
| Ala | Lys | Leu | Glu | Lys | Ala | Ala | Leu | Met | Asn | Gly | Val | Tyr | Ile | Ser | Pro |     |  |
|     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |     |  |
| TAT | AAA | AAA | TCC | ACC | CAT | TGC | CAA | AGA | ACG | CAT | TTG | GAA | AAT | AAG | AGC | 824 |  |
| Tyr | Lys | Lys | Ser | Thr | His | Cys | Gln | Arg | Thr | His | Leu | Glu | Asn | Lys | Ser |     |  |
|     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     |  |
| TTG | AAA | GAA | ATC | GCT | TTA | AAT | ATG | AAC | CCT | AAA | TTA | GAA | AAG | CAA | AGC | 872 |  |
| Leu | Lys | Glu | Ile | Ala | Leu | Asn | Met | Asn | Pro | Lys | Leu | Glu | Lys | Gln | Ser |     |  |
|     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |     |  |
| CCT | TTT | ATT | GAT | GCG | GAT | AAA | ATG | GCT | ATG | CAA | TCT | GCG | GGG | TTA | TTG | 920 |  |
| Pro | Phe | Ile | Asp | Ala | Asp | Lys | Met | Ala | Met | Gln | Ser | Ala | Gly | Leu | Leu |     |  |
|     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |     | 290 |     |  |
| AGA | AAG | AAT | AAA | GGT | GTC | TTG | ATT | GCT | TTT | GCT | ACA | GAT | ATT | TGC | ATG | 968 |  |

```

Thr Asn Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro
 35 40 45
Ile Tyr Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu
 50 55 60
Pro Ser Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn
 65 70 75 80
Pro Thr Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val
 85 90 95
Ile Glu Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe
 100 105 110
His Pro Leu Lys Pro Trp Leu
 115

```

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1232
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

GTTGTGATTT TATTGTGTTT TCATATCAAT TTTCATATCA AGGAGTTTAA ATG AAA 56
 Met Lys
 1

GAA ACA AGA CTT TTA AAA TTG AGA GCG TTG AGC TTA GCA TGT TTA ATG 104
Glu Thr Arg Leu Leu Lys Leu Arg Ala Leu Ser Leu Ala Cys Leu Met
 5 10 15

GGA TTA GGC GTG AGT GGG TGC GCG TTT TTA GAT AAG CAA ATC TTA AAC 152
Gly Leu Gly Val Ser Gly Cys Ala Phe Leu Asp Lys Gln Ile Leu Asn
 20 25 30

GAC CAT TTG ACT AAA GCT AAA AAT AAC CCA AAA TAC GAT TGC CAA AAA 200
Asp His Leu Thr Lys Ala Lys Asn Asn Pro Lys Tyr Asp Cys Gln Lys
 35 40 45 50

GAA ATG TGG TCT TTC CCT AAA AAA TAC GAT GGG ATA AAT CAG TGT TTA 248
Glu Met Trp Ser Phe Pro Lys Lys Tyr Asp Gly Ile Asn Gln Cys Leu
 55 60 65

AAG GCT CAA GAA GAG CTT ATT GAA CCA ATC ATC ACT AAA AAG ATC GAT 296
Lys Ala Gln Glu Glu Leu Ile Glu Pro Ile Ile Thr Lys Lys Ile Asp

```

|                                                        |     |     |     |     |                                             |     |     |     |     |     |     |     |     |         |     |     |
|--------------------------------------------------------|-----|-----|-----|-----|---------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|---------|-----|-----|
| AATCCCTTCA AAAATGATAT AATAGACTTG ATGAACTCAT TTTAAGGAAA |     |     |     |     |                                             |     |     |     |     |     |     |     |     | ATG CCC | 56  |     |
|                                                        |     |     |     |     |                                             |     |     |     |     |     |     |     |     | Met Pro |     |     |
|                                                        |     |     |     |     |                                             |     |     |     |     |     |     |     |     | 1       |     |     |
| ATG                                                    | CGT | TTG | CAC | ACT | GCC                                         | TTT | TTT | GGT | ATT | AAT | TCA | TTG | CTT | GTT     | GCC | 104 |
| Met                                                    | Arg | Leu | His | Thr | Ala                                         | Phe | Phe | Gly | Ile | Asn | Ser | Leu | Leu | Val     | Ala |     |
|                                                        |     | 5   |     |     |                                             | 10  |     |     |     |     |     | 15  |     |         |     |     |
| TCT                                                    | CTT | TTG | ATA | AGC | GGT                                         | TGC | AGT | CTC | TTT | AAA | AAG | CGT | AAC | ACT     | AAC | 152 |
| Ser                                                    | Leu | Leu | Ile | Ser | Gly                                         | Cys | Ser | Leu | Phe | Lys | Lys | Arg | Asn | Thr     | Asn |     |
|                                                        |     | 20  |     |     |                                             | 25  |     |     |     | 30  |     |     |     |         |     |     |
| GCC                                                    | CAG | CTA | ATC | CCC | CCT                                         | TCA | GCT | AAT | GGC | TTG | CAA | GCC | CCC | ATT     | TAT | 200 |
| Ala                                                    | Gln | Leu | Ile | Pro | Pro                                         | Ser | Ala | Asn | Gly | Leu | Gln | Ala | Pro | Ile     | Tyr |     |
| 35                                                     |     |     |     | 40  |                                             |     |     | 45  |     |     |     |     |     | 50      |     |     |
| CCC                                                    | CCA | ACC | AAT | TTC | ACC                                         | CCT | AGA | AAG | AGC | ATT | CAG | CCT | CTC | CCA     | AGC | 248 |
| Pro                                                    | Pro | Thr | Asn | Phe | Thr                                         | Pro | Arg | Lys | Ser | Ile | Gln | Pro | Leu | Pro     | Ser |     |
|                                                        |     |     |     | 55  |                                             |     |     | 60  |     |     |     |     |     | 65      |     |     |
| CCT                                                    | CGC | CTT | GAG | AAT | AAC                                         | GAT | CAG | CCC | GTC | ATT | AGT | TCT | AAC | CCC     | ACT | 296 |
| Pro                                                    | Arg | Leu | Glu | Asn | Asn                                         | Asp | Gln | Pro | Val | Ile | Ser | Ser | Asn | Pro     | Thr |     |
|                                                        |     | 70  |     |     |                                             | 75  |     |     |     |     |     | 80  |     |         |     |     |
| AAC                                                    | GCT | ATC | CCT | AAC | ACC                                         | CCC | ATT | CTC | ACG | CCT | AAT | AAT | GTC | ATT     | GAA | 344 |
| Asn                                                    | Ala | Ile | Pro | Asn | Thr                                         | Pro | Ile | Leu | Thr | Pro | Asn | Asn | Val | Ile     | Glu |     |
|                                                        |     | 85  |     |     |                                             | 90  |     |     |     |     |     | 95  |     |         |     |     |
| TTG                                                    | AAC | GCA | TGG | GCA | TGG                                         | GCG | TGG | CTC | CAG | AAT | CCA | CCA | TTT | CAC     | CCT | 392 |
| Leu                                                    | Asn | Ala | Trp | Ala | Trp                                         | Ala | Trp | Leu | Gln | Asn | Pro | Pro | Phe | His     | Pro |     |
|                                                        |     | 100 |     |     |                                             | 105 |     |     |     | 110 |     |     |     |         |     |     |
| CTC                                                    | AAG | CCC | TGG | CTC | TAGCCAAGCG GCGGGCTATC GTTGATGGCT ACCGCCAGTT |     |     |     |     |     |     |     |     |         | G   | 448 |
| Leu                                                    | Lys | Pro | Trp | Leu |                                             |     |     |     |     |     |     |     |     |         |     |     |
| 115                                                    |     |     |     |     |                                             |     |     |     |     |     |     |     |     |         |     |     |
| GGTGAAAAAA TG                                          |     |     |     |     |                                             |     |     |     |     |     |     |     |     |         | 460 |     |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Met | Arg | Leu | His | Thr | Ala | Phe | Phe | Gly | Ile | Asn | Ser | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ala | Ser | Leu | Leu | Ile | Ser | Gly | Cys | Ser | Leu | Phe | Lys | Lys | Arg | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Met Arg Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile
 1 5 10 15
Val Leu Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp
 20 25 30
Ser Gln Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala
 35 40 45
Met Asp Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser
 50 55 60
Leu Asn Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser
 65 70 75 80
Ala Leu Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu
 85 90 95
Lys Lys Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Leu Asn Lys
 100 105 110
Pro Tyr Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala
 115 120 125
Asp Leu Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu
 130 135 140
Lys Tyr Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys
 145 150 155 160
His Gln Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu
 165 170 175
Gln Phe Asp Ile Ser Asn Leu Lys Asp
 180 185

```

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...407
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:



1

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATT AAG GCT TAT TTT TTG CGT TTT ATC GCG CTG GTT TTG ATT GTT TTG | 104 |
| Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile Val Leu |     |
| 5 10 15                                                         |     |
| TTA GGT TTT AGT GCT TGT AAA AAT TCT CAA AAA TCT CAA GAT TCT CAA | 152 |
| Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp Ser Gln |     |
| 20 25 30                                                        |     |
| AAC AAT ACC CCC CAA CAA GAT AGC CCT AAA ACC TAC ACC GCT ATG GAT | 200 |
| Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala Met Asp |     |
| 35 40 45 50                                                     |     |
| TTG AAT AAC CAA GAA TAC ACC ATC ACA GGC GAT TTA GAT TCT CTC AAT | 248 |
| Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser Leu Asn |     |
| 55 60 65                                                        |     |
| ATC AGC CCG GAT TCC AAC ACC CCT ACC CTA TTA GTT TTA AGC GCT TTA | 296 |
| Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser Ala Leu |     |
| 70 75 80                                                        |     |
| GAT AAT TCT TTA AAA GAT TAC GCC CCC AGC TTT AAC ATC TTA AAA AAA | 344 |
| Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu Lys Lys |     |
| 85 90 95                                                        |     |
| ACT TTT AAA GAT CGT TTG AGG GTG CTT ATT TTA CTC AAT AAA CCC TAT | 392 |
| Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Asn Lys Pro Tyr     |     |
| 100 105 110                                                     |     |
| TCA AGC GAT GCA ATC AAA GAC TTT AGC GCG CAT TTT CAA GCT GAT TTG | 440 |
| Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala Asp Leu |     |
| 115 120 125 130                                                 |     |
| ATG ATT TTA AAC CCT AAA GAT ACC GCT CTT TTT GAT CAT TTA AAG TAT | 488 |
| Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu Lys Tyr |     |
| 135 140 145                                                     |     |
| GAC GCT TTA AAC CAT TCT TTT AAC ATG CTC TTA TAC CAC AAA CAC CAA | 536 |
| Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys His Gln |     |
| 150 155 160                                                     |     |
| TTG ATC AAA ATG TAT CAA GGG ATC GTG CCA ATA GAA ATG CTC CAA TTT | 584 |
| Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu Gln Phe |     |
| 165 170 175                                                     |     |
| GAT ATT TCC AAT TTA AAG GAT TAAAAAAAC CATGTTTAAT TTTTCAAAA AAAT | 639 |
| Asp Ile Ser Asn Leu Lys Asp                                     |     |
| 180 185                                                         |     |
| TGTCAATAAA ATTAAGGGT                                            | 658 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

```

Phe Gly Arg Tyr Tyr Thr Ser Gly Lys Ala Leu Met Val Ala Asp Leu
225 230 235 240
Lys Tyr Glu Lys Asp Asn Leu Lys Ile Asn Pro Tyr Phe Tyr Ala Ile
 245 250 255
Phe Gln Arg Met Tyr Ala Pro Gly Ile Asn Ile Thr Tyr Asp Thr Asn
 260 265 270
Pro Asn Phe Asn Asn Lys Gly Phe Arg Phe Val Gly Thr Phe Val Gly
 275 280 285
Phe Phe Pro Ile Phe Ala Thr Pro Ala Asn Gln Asn Asp Ile Ile Leu
 290 295 300
Phe Gln Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg
305 310 315 320
Thr Arg Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys
 325 330 335
Asn Ile Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu
 340 345 350
Gly Tyr Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn
 355 360 365
Ile Val Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln
 370 375 380
Tyr Arg Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro
385 390 395 400
Arg Ala Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn
 405 410 415
Lys Tyr Asn Ile Arg Met Asp Leu Lys Leu Glu Tyr Tyr Gly Asn Ile
 420 425 430
Thr Lys Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val
 435 440 445
Asp Pro Asn Gly Pro Gly Thr Gln Pro Leu Thr His Asn Val Tyr Ser
 450 455 460
Asp Arg Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr
465 470 475 480

```

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...605
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

AATTTTAGGT TATTAGTTAC CATTTTATTA TTCTTAAGGA TGTGTTTATA ATG AGA
 Met Arg

```

56

```

AAA GGC TAT TGT ATT GGG TAT TGT GGC ATG TAT GTT CCA GTC GAT CCT 1401
Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val Asp Pro
435 440 445 450

AAC GGG CCT GGG ACA CAG CCT TTA ACG CAC AAT GTG TAT TCT GAC AGG 1449
Asn Gly Pro Gly Thr Gln Pro Leu Thr His Asn Val Tyr Ser Asp Arg
 455 460 465

AGC CAT ATA ATG TTT AAC ATT GCT TAC GGT TTT AGG ATT TAC TAGCATT TTT 1500
Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr
 470 475 480

ATCCTTAATG GATATTTTGT ATTAGCCTTT TTAAATATT GAAA 1544

```

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Met Pro Phe Cys Ile Phe Ile Leu Ile Ser Leu Gly Val Arg Val Leu
 1 5 10 15
Glu Ile Lys Lys Tyr Phe Ser Tyr Ser Leu Phe Phe Leu Leu Phe Ser
20 25 30
Ser Leu Phe Leu Ser Lys Leu Gln Ala Tyr Lys Phe Asn Met Ser Ile
35 40 45
Val Gly Lys Val Ser Ser Tyr Thr Lys Phe Gly Phe Asn Asn Gln Arg
50 55 60
Tyr Gln Pro Ser Lys Asp Ile Tyr Pro Thr Gly Ser Tyr Thr Ser Leu
65 70 75 80
Leu Gly Glu Leu Asn Leu Ser Met Gly Leu Tyr Lys Gly Leu Arg Ala
85 90 95
Glu Val Gly Ala Met Met Ala Ala Leu Pro Tyr Asp Ser Thr Ala Tyr
100 105 110
Gln Gly Asn Asn Ile Pro Asn Gly Gln Pro Gly Ser Arg Thr Asp Pro
115 120 125
Phe Gly Ala Gly Ile Phe Trp Gln Tyr Ile Gly Trp Tyr Ala Gly His
130 135 140
Ser Gly Leu Gln Val Gln Lys Pro Arg Leu Ala Met Val His Asn Ala
145 150 155 160
Phe Leu Ser Tyr Asn Tyr Lys Lys Asp Lys Phe Ser Phe Gly Val Lys
165 170 175
Gly Gly Arg Tyr Asp Ala Glu Glu Tyr Asp Trp Phe Thr Ser Tyr Thr
180 185 190
Gln Gly Val Glu Gly Phe Val Lys Tyr Lys Asp Thr Arg Phe Arg Val
195 200 205
Met Tyr Ser Asp Ala Arg Ala Ser Ala Ser Ser Asp Trp Phe Trp Tyr
210 215 220

```

|                                                                 |      |
|-----------------------------------------------------------------|------|
| TCA GAC GCT AGG GCT TCA GCG TCA AGC GAC TGG TTT TGG TAT TTT GGG | 729  |
| Ser Asp Ala Arg Ala Ser Ala Ser Ser Asp Trp Phe Trp Tyr Phe Gly |      |
| 215 220 225                                                     |      |
| CGT TAC TAT ACA AGC GGT AAG GCT CTA ATG GTA GCT GAT TTG AAA TAT | 777  |
| Arg Tyr Tyr Thr Ser Gly Lys Ala Leu Met Val Ala Asp Leu Lys Tyr |      |
| 230 235 240                                                     |      |
| GAA AAA GAC AAC CTA AAA ATC AAC CCT TAT TTT TAT GCG ATC TTT CAA | 825  |
| Glu Lys Asp Asn Leu Lys Ile Asn Pro Tyr Phe Tyr Ala Ile Phe Gln |      |
| 245 250 255                                                     |      |
| AGA ATG TAT GCG CCA GGC ATT AAT ATC ACT TAT GAC ACC AAC CCT AAT | 873  |
| Arg Met Tyr Ala Pro Gly Ile Asn Ile Thr Tyr Asp Thr Asn Pro Asn |      |
| 260 265 270                                                     |      |
| TTC AAC AAT AAG GGT TTT CGT TTT GTA GGC ACT TTC GTA GGG TTT TTC | 921  |
| Phe Asn Asn Lys Gly Phe Arg Phe Val Gly Thr Phe Val Gly Phe Phe |      |
| 275 280 285 290                                                 |      |
| CCC ATT TTT GCC ACT CCG GCT AAT CAA AAT GAT ATT ATC CTC TTC CAA | 969  |
| Pro Ile Phe Ala Thr Pro Ala Asn Gln Asn Asp Ile Ile Leu Phe Gln |      |
| 295 300 305                                                     |      |
| CAA GTG CCA TTA GGC AAG AGT GGG CAA ACT TAT TTC TTC CGC ACT CGT | 1017 |
| Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg Thr Arg |      |
| 310 315 320                                                     |      |
| TTT TAC TAT AAT AAG TGG CAA TTT GGG GGC AGC GTC TAT AAA AAC ATC | 1065 |
| Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys Asn Ile |      |
| 325 330 335                                                     |      |
| GGT AAC GCT AAT GGT GAT ATA GGT ATT TAT GGC GAC CCT TTG GGG TAT | 1113 |
| Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu Gly Tyr |      |
| 340 345 350                                                     |      |
| AAC ATT TGG ACG AAT AGT ATT TAT GAC GCA GAA ATT AAC AAT ATT GTT | 1161 |
| Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn Ile Val |      |
| 355 360 365 370                                                 |      |
| GGC GCT GAT GTT ATT AAC GGG TTT TTG TAT GTA GGC TCA CAA TAT AGA | 1209 |
| Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln Tyr Arg |      |
| 375 380 385                                                     |      |
| GGG TTT AGT TGG AAA ATT TTA GGC CGT TGG ACG GAT AGC CCA AGG GCT | 1257 |
| Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro Arg Ala |      |
| 390 395 400                                                     |      |
| GAT GAA AGG AGT CTC GCG CTC TTT TTG AGT TAT TTT TCT AAT AAG TAT | 1305 |
| Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn Lys Tyr |      |
| 405 410 415                                                     |      |
| AAT ATT AGA ATG GAT TTA AAA CTA GAA TAT TAT GGC AAT ATC ACC AAA | 1353 |
| Asn Ile Arg Met Asp Leu Lys Leu Glu Tyr Tyr Gly Asn Ile Thr Lys |      |
| 420 425 430                                                     |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |         |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---------|--|
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | Met Pro |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1       |  |
| TTT | TGT | ATT | TTT | ATT | TTA | ATA | TCT | TTG | GGA | GTT | AGG | GTT | TTG | GAA | ATT | 105     |  |
| Phe | Cys | Ile | Phe | Ile | Leu | Ile | Ser | Leu | Gly | Val | Arg | Val | Leu | Glu | Ile |         |  |
| 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |     |     |     |         |  |
| AAG | AAA | TAT | TTT | TCT | TAC | TCT | CTA | TTT | TTT | TTG | CTT | TTT | TCT | AGT | CTC | 153     |  |
| Lys | Lys | Tyr | Phe | Ser | Tyr | Ser | Leu | Phe | Phe | Leu | Leu | Phe | Ser | Ser | Leu |         |  |
| 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |     |     |     |         |  |
| TTT | TTA | TCC | AAA | CTT | CAA | GCT | TAT | AAA | TTC | AAC | ATG | AGC | ATT | GTT | GGA | 201     |  |
| Phe | Leu | Ser | Lys | Leu | Gln | Ala | Tyr | Lys | Phe | Asn | Met | Ser | Ile | Val | Gly |         |  |
| 35  |     |     |     | 40  |     |     |     | 45  |     |     |     | 50  |     |     |     |         |  |
| AAG | GTG | AGC | AGC | TAT | ACC | AAG | TTT | GGC | TTT | AAC | AAC | CAA | AGA | TAC | CAG | 249     |  |
| Lys | Val | Ser | Ser | Tyr | Thr | Lys | Phe | Gly | Phe | Asn | Asn | Gln | Arg | Tyr | Gln |         |  |
|     |     |     |     | 55  |     |     |     | 60  |     |     |     | 65  |     |     |     |         |  |
| CCT | TCT | AAA | GAC | ATT | TAT | CCT | ACA | GGT | AGC | TAC | ACT | TCT | TTA | CTC | GGC | 297     |  |
| Pro | Ser | Lys | Asp | Ile | Tyr | Pro | Thr | Gly | Ser | Tyr | Thr | Ser | Leu | Leu | Gly |         |  |
|     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |         |  |
| GAA | TTG | AAT | TTG | AGC | ATG | GGT | TTA | TAC | AAG | GGT | TTG | AGA | GCG | GAA | GTG | 345     |  |
| Glu | Leu | Asn | Leu | Ser | Met | Gly | Leu | Tyr | Lys | Gly | Leu | Arg | Ala | Glu | Val |         |  |
| 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |     |     |     |         |  |
| GGG | GCT | ATG | ATG | GCA | GCG | CTC | CCC | TAT | GAC | TCT | ACC | GCC | TAT | CAA | GGC | 393     |  |
| Gly | Ala | Met | Met | Ala | Ala | Leu | Pro | Tyr | Asp | Ser | Thr | Ala | Tyr | Gln | Gly |         |  |
| 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |     |     |     |     |         |  |
| AAC | AAT | ATC | CCT | AAC | GGC | CAG | CCC | GGC | TCT | AGG | ACC | GAT | CCT | TTT | GGG | 441     |  |
| Asn | Asn | Ile | Pro | Asn | Gly | Gln | Pro | Gly | Ser | Arg | Thr | Asp | Pro | Phe | Gly |         |  |
| 115 |     |     |     | 120 |     |     |     | 125 |     |     |     | 130 |     |     |     |         |  |
| GCG | GGT | ATC | TTT | TGG | CAA | TAT | ATT | GGT | TGG | TAT | GCG | GGG | CAT | AGT | GGT | 489     |  |
| Ala | Gly | Ile | Phe | Trp | Gln | Tyr | Ile | Gly | Trp | Tyr | Ala | Gly | His | Ser | Gly |         |  |
|     |     |     |     | 135 |     |     |     | 140 |     |     |     | 145 |     |     |     |         |  |
| TTG | CAA | GTG | CAA | AAA | CCT | CGT | TTA | GCC | ATG | GTG | CAT | AAC | GCT | TTT | TTG | 537     |  |
| Leu | Gln | Val | Gln | Lys | Pro | Arg | Leu | Ala | Met | Val | His | Asn | Ala | Phe | Leu |         |  |
|     |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |     |         |  |
| AGC | TAC | AAC | TAC | AAA | AAA | GAC | AAA | TTC | AGT | TTT | GGC | GTG | AAA | GGG | GGG | 585     |  |
| Ser | Tyr | Asn | Tyr | Lys | Lys | Asp | Lys | Phe | Ser | Phe | Gly | Val | Lys | Gly | Gly |         |  |
| 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |     |     |     |     |         |  |
| CGC | TAT | GAC | GCT | GAA | GAG | TAT | GAT | TGG | TTC | ACT | TCT | TAC | ACT | CAA | GGG | 633     |  |
| Arg | Tyr | Asp | Ala | Glu | Glu | Tyr | Asp | Trp | Phe | Thr | Ser | Tyr | Thr | Gln | Gly |         |  |
| 180 |     |     |     | 185 |     |     |     | 190 |     |     |     |     |     |     |     |         |  |
| GTT | GAA | GGC | TTT | GTC | AAA | TAT | AAA | GAC | ACC | AGA | TTC | AGG | GTG | ATG | TAT | 681     |  |
| Val | Glu | Gly | Phe | Val | Lys | Tyr | Lys | Asp | Thr | Arg | Phe | Arg | Val | Met | Tyr |         |  |
| 195 |     |     |     | 200 |     |     |     | 205 |     |     |     | 210 |     |     |     |         |  |

|                                                                   |    |    |     |
|-------------------------------------------------------------------|----|----|-----|
| 20                                                                | 25 | 30 |     |
| GAT GAT GAA GTT GAG AGT GAT GGG TTT TTT AGT AGA ATA TGG GAT AAA   |    |    | 200 |
| Asp Asp Glu Val Glu Ser Asp Gly Phe Phe Ser Arg Ile Trp Asp Lys   |    |    |     |
| 35                                                                | 40 | 45 | 50  |
|                                                                   |    |    |     |
| TTC GTT GAA TAT TTC GGC TAT ACT CTA GTT ACT ATA TAATGTTTTT TCCTTA |    |    | 252 |
| Phe Val Glu Tyr Phe Gly Tyr Thr Leu Val Thr Ile                   |    |    |     |
|                                                                   | 55 | 60 |     |
|                                                                   |    |    |     |
| TATAATTGGA CCAGTTATCG CTTTAATTTT TATATTT                          |    |    | 289 |

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Arg | Asp | Ile | Val | Asp | Ile | Leu | Ile | Ser | Val | Val | Ile | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Val | Leu | Thr | Ala | Ile | Arg | Ala | Thr | Ile | Met | Ala | Phe | Lys | Gly | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Asp | Asp | Asp | Glu | Val | Glu | Ser | Asp | Gly | Phe | Phe | Ser | Arg | Ile | Trp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Lys | Phe | Val | Glu | Tyr | Phe | Gly | Tyr | Thr | Leu | Val | Thr | Ile |     |     |
| 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1491
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|                                                                  |    |
|------------------------------------------------------------------|----|
| GACACACATT AGTTATAGTT TCTAAGAGAG TTCTCCCCCT ATCTCTTAGA T ATG CCT | 57 |
|------------------------------------------------------------------|----|

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Gly | Tyr | Lys | Gly | Leu | Ser | Asn | Gln | Gln | Tyr | Ala | Ile | Asn | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gly | Phe | Val | Val | Gly | Tyr | Lys | His | Phe | Phe | Lys | Lys | Ser | Pro | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Gly | Met | Arg | Tyr | Tyr | Gly | Phe | Phe | Asp | Phe | Ala | Ser | Ser | Tyr | Tyr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Tyr | Tyr | Thr | Tyr | Asn | Asp | Tyr | Gly | Met | Arg | Asp | Ala | Arg | Lys | Gly |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gln | Ser | Phe | Met | Phe | Gly | Tyr | Gly | Ala | Gly | Thr | Asp | Val | Leu | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asn | Pro | Ala | Ile | Phe | Asn | Arg | Glu | Asn | Leu | His | Phe | Gly | Phe | Phe | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Val | Ala | Ile | Gly | Gly | Thr | Ser | Trp | Gly | Pro | Thr | Asn | Tyr | Tyr | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Asp | Leu | Ala | Asp | Glu | Tyr | Arg | Gly | Ser | Phe | His | Pro | Ser | Asn | Phe |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Val | Leu | Val | Asn | Gly | Gly | Ile | Arg | Leu | Gly | Thr | Lys | His | Gln | Gly |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Phe | Glu | Ile | Gly | Leu | Lys | Ile | Gln | Thr | Ile | Arg | Asn | Asn | Tyr | Tyr | Thr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ala | Ser | Ala | Asp | Asn | Val | Pro | Glu | Gly | Thr | Thr | Tyr | Arg | Phe | Thr | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Arg | Pro | Tyr | Ala | Phe | Tyr | Trp | Arg | Tyr | Ile | Val | Ser | Phe |     |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...236
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGGATTTTAT TTCTTATAGC AGAAATTATT TTAAAGTAA AAGACAAATC ATG TTT   | 56  |
| Met Phe                                                         |     |
| 1                                                               |     |
| AGA GAT ATA GTA GAT ATT TTA ATA TCT GTT GTT ATT ATT GGA TTA GTA | 104 |
| Arg Asp Ile Val Asp Ile Leu Ile Ser Val Val Ile Ile Gly Leu Val |     |
| 5 10 15                                                         |     |
| TTA ACA GCT ATT AGA GCT ACT ATA ATG GCG TTT AAA GGC GAT ACT GAT | 152 |
| Leu Thr Ala Ile Arg Ala Thr Ile Met Ala Phe Lys Gly Asp Thr Asp |     |

```

GCT ATT TTC AAT CGT GAG AAC TTG CAT TTT GGG TTT TTC TTG GGC GTT 632
Ala Ile Phe Asn Arg Glu Asn Leu His Phe Gly Phe Phe Leu Gly Val
 180 185 190

GCG ATC GGT GGC ACC TCT TGG GGT CCA ACA AAC TAT TAT TTT AAG GAC 680
Ala Ile Gly Gly Thr Ser Trp Gly Pro Thr Asn Tyr Tyr Phe Lys Asp
 195 200 205 210

TTG GCT GAT GAG TAT AGA GGG AGT TTC CAC CCA TCA AAT TTC CAG GTC 728
Leu Ala Asp Glu Tyr Arg Gly Ser Phe His Pro Ser Asn Phe Gln Val
 215 220 225

TTA GTT AAT GGT GGG ATT CGC TTA GGC ACT AAA CAC CAA GGT TTT GAA 776
Leu Val Asn Gly Gly Ile Arg Leu Gly Thr Lys His Gln Gly Phe Glu
 230 235 240

ATT GGC TTG AAA ATC CAA ACC ATC CGC AAC AAT TAC TAC ACC GCT AGT 824
Ile Gly Leu Lys Ile Gln Thr Ile Arg Asn Asn Tyr Tyr Thr Ala Ser
 245 250 255

GCG GAT AAT GTG CCT GAA GGG ACT ACT TAT AGA TTC ACT TTC CAC CGC 872
Ala Asp Asn Val Pro Glu Gly Thr Thr Tyr Arg Phe Thr Phe His Arg
 260 265 270

CCC TAT GCC TTT TAT TGG CGT TAC ATT GTA AGC TTT TAAGGTGTTT TAGGGC 924
Pro Tyr Ala Phe Tyr Trp Arg Tyr Ile Val Ser Phe
 275 280 285

TAATCTTATG GGGGCATAGA AAAGGGCTTT TGCTCTT 961

```

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Met Lys Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser
 1 5 10 15
Leu Leu Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser
 20 25 30
Pro Thr Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr
 35 40 45
Gln Leu Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn
 50 55 60
Cys Asn Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met
 65 70 75 80
Pro Thr Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly
 85 90 95

```



## (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GAATGTAGCA TTTAGAACTC AAGTAGAGAA AATGTAGAAG GAAGGAATAC ATG AAG  | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| AAA TCT GTT ATA GTA GGT GCT ATC TCT CTA GCA ATG ACA AGC TTA TTG | 104 |
| Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser Leu Leu |     |
| 5 10 15                                                         |     |
| TCA GCA GAG ACC CCT AAG CAA GAA AAA GCT ATT AAG ACT AGC CCT ACC | 152 |
| Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser Pro Thr |     |
| 20 25 30                                                        |     |
| AAA AAA GGT GAA AGA AAT GCT GCT TTT ATA GGG ATT GAT TAC CAG TTG | 200 |
| Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr Gln Leu |     |
| 35 40 45 50                                                     |     |
| GGT ATG CTC AGC ACT ACC GCT CAA AAT TGT TCC CAT GGG AAT TGC AAT | 248 |
| Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn Cys Asn |     |
| 55 60 65                                                        |     |
| GGT AAT CAA AGT GGG GCT TAC GGC TCT AAT ACG CCT AAC ATG CCT ACA | 296 |
| Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met Pro Thr |     |
| 70 75 80                                                        |     |
| GCG TCA AAC CCA ACA GGA GGG TTT ACT CAT GGC GCT CTA GGG ACT CGT | 344 |
| Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly Thr Arg |     |
| 85 90 95                                                        |     |
| GGG TAT AAA GGC TTA AGC AAC CAA CAA TAC GCT ATC AAT GGT TTT GGT | 392 |
| Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly Phe Gly |     |
| 100 105 110                                                     |     |
| TTT GTT GTA GGG TAT AAG CAT TTT TTC AAG AAA TCC CCG CAA TTT GGA | 440 |
| Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln Phe Gly |     |
| 115 120 125 130                                                 |     |
| ATG CGT TAT TAC GGA TTC TTT GAT TTT GCA AGC TCT TAT TAT AAG TAT | 488 |
| Met Arg Tyr Tyr Gly Phe Phe Asp Phe Ala Ser Ser Tyr Tyr Lys Tyr |     |
| 135 140 145                                                     |     |
| TAC ACT TAT AAT GAT TAT GGC ATG AGA GAC GCT CGC AAG GGT TCT CAA | 536 |
| Tyr Thr Tyr Asn Asp Tyr Gly Met Arg Asp Ala Arg Lys Gly Ser Gln |     |
| 150 155 160                                                     |     |
| AGT TTC ATG TTT GGC TAT GGG GCT GGC ACA GAT GTG TTG TTT AAC CCG | 584 |
| Ser Phe Met Phe Gly Tyr Gly Ala Gly Thr Asp Val Leu Phe Asn Pro |     |
| 165 170 175                                                     |     |

|                                                                   |     |    |    |     |
|-------------------------------------------------------------------|-----|----|----|-----|
| 35                                                                | 40  | 45 | 50 |     |
| GAC ACT TCA ATG TTT GGC AGC AAC AAA ACA GCT CCA GCC CAA GAA ACG   | 248 |    |    |     |
| Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln Glu Thr   |     |    |    |     |
| 55 60 65                                                          |     |    |    |     |
| CAA AGC GCT TCC AAA CCG GAC ACT AAA GTC AAT CCA AGC GCA AGT TGG   | 296 |    |    |     |
| Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala Ser Trp   |     |    |    |     |
| 70 75 80                                                          |     |    |    |     |
| ATG AAA AAA TAAGAAGGAA GTTATGAAAA AGTCATTCAA AAAATTAGGC TTTGTCTCT | 354 |    |    |     |
| Met Lys Lys                                                       |     |    |    |     |
| 85                                                                |     |    |    |     |
| TTA                                                               |     |    |    | 357 |

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Val | Phe | Leu | Gly | Met | Ala | Leu | Ala | Phe | Ser | Val | Ser | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Glu | Lys | Ser | Gly | Ala | Phe | Leu | Gly | Gly | Phe | Gln | Tyr | Ser | Asn |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Glu | Asn | Gln | Asn | Thr | Thr | Arg | Thr | Pro | Gly | Ala | Asn | Asn | Asn | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Ile | Asp | Thr | Ser | Met | Phe | Gly | Ser | Asn | Lys | Thr | Ala | Pro | Ala | Gln |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Glu | Thr | Gln | Ser | Ala | Ser | Lys | Pro | Asp | Thr | Lys | Val | Asn | Pro | Ser | Ala |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ser | Trp | Met | Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...908

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Met Arg Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser
 1 5 10 15
Ala Leu Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro
 20 25 30
Ala His Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser
 35 40 45
Phe Phe Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp
 50 55 60
Tyr Phe Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly
 65 70 75 80
Xaa Leu Ile Val Phe Phe Lys Thr His
 85

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 51...305  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

ATGCAATAAA AAAAGAAATT CTTAGGATTT CTCACATTAA GGAGTTTAA ATG AAA 56
 Met Lys
 1

AAG GTT TTT TTA GGT ATG GCA TTA GCC TTT AGT GTG TCC ATG GCA GAA 104
Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met Ala Glu
 5 10 15

AAA AGT GGC GCG TTT TTA GGA GGG GGG TTT CAA TAT TCT AAT TTA GAA 152
Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn Leu Glu
 20 25 30

AAC CAA AAC ACC ACC CGC ACC CCA GGC GCT AAC AAT AAC ACC CCG ATA 200
Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Asn Thr Pro Ile

```

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...317
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTTAAAATCA CCCGTTACAG CATCACTGAA ATCACTAATA GGGGTGATTG ATG CGT    | 56  |
| Met Arg                                                           |     |
| 1                                                                 |     |
| AAG GTT TTA TAC GCT CTT GTG GGC TTT TTG TTG GCT TTT AGC GCT TTA   | 104 |
| Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser Ala Leu   |     |
| 5 10 15                                                           |     |
| AAA GCC GAT GAT TTT TTA GAA GAA GCG AAC GAA ACA GCC CCG GCG CAT   | 152 |
| Lys Ala Asp Asp Phe Leu Glu Ala Asn Glu Thr Ala Pro Ala His       |     |
| 20 25 30                                                          |     |
| TTA AAC CAC CCT ATG CAG GAT TTA AAC GCC ATT CAA GGG AGC TTT TTT   | 200 |
| Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser Phe Phe   |     |
| 35 40 45 50                                                       |     |
| GAC AAA AAC CGC TCA AAA ATG TCC AAC ACT TTG AAC ATT GAT TAC TTT   | 248 |
| Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp Tyr Phe   |     |
| 55 60 65                                                          |     |
| CAA GGG CAA ACT TAT AAA ATC CCG CTT GCG TTA TGC GAT GGC GMC CTT   | 296 |
| Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly Xaa Leu   |     |
| 70 75 80                                                          |     |
| ATT GTT TTT TTC AAA ACC CAT TAGCGATTTT GTTTTAGGGG ATAAGGTGGG TTTT | 351 |
| Ile Val Phe Phe Lys Thr His                                       |     |
| 85                                                                |     |
| GATGCGAAAA TTTTAGAAA                                              | 370 |

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 435                                                             | 440 | 445 |
| Gly Asn Ala Asp Ala Glu Gly Thr Leu Ala Arg Arg Ile Phe Leu Ile |     |     |
| 450                                                             | 455 | 460 |
| Asn Ser Gly Val Asn Phe Lys Val Thr His Pro Ile Ser Glu Asp Tyr |     |     |
| 465                                                             | 470 | 475 |
| Gly Asn Val Phe Glu Tyr Gly Met Ile Tyr Gln Asn Leu Ser Val Phe |     | 480 |
|                                                                 | 485 | 490 |
| Ser Gly Leu Asp Lys Gly Lys Asn Gly Tyr Tyr Lys Asn Asn Ile Asp |     | 495 |
|                                                                 | 500 | 505 |
| Pro Asn Asp Pro Asn Gly Pro Gly Leu Pro Tyr Arg His Tyr Tyr Thr |     | 510 |
|                                                                 | 515 | 520 |
| Asp Gln Ser Ser Gln Tyr Pro Gln Asn Leu Asn Thr Pro Asn Pro Leu |     | 525 |
|                                                                 | 530 | 535 |
| Tyr Arg Asn Met Pro Gln Asn Ser His Ala Ile Gly Asn Ile Ile Gly |     | 540 |
| 545                                                             | 550 | 555 |
| Gly Phe Met Gln Ala Asn Tyr Asn Ile Leu Ser Asn Val Ile Val Gly |     | 560 |
|                                                                 | 565 | 570 |
| Ala Gly Thr Arg Tyr Asp Ile Tyr Thr Leu Leu Asp Lys Asn Gly Arg |     | 575 |
|                                                                 | 580 | 585 |
| Thr His Val Thr Ser Gly Phe Ser Pro Ser Ala Thr Val Leu Tyr Asn |     | 590 |
|                                                                 | 595 | 600 |
| Pro Ile Glu Ser Ile Gly Leu Lys Val Ser Tyr Ala Tyr Val Thr Lys |     | 605 |
|                                                                 | 610 | 615 |
| Gly Ala Leu Pro Gly Asp Gly Val Leu Met Arg Asp Pro Thr Val Ile |     | 620 |
| 625                                                             | 630 | 635 |
| Tyr Gln Arg Asn Leu Arg Pro Ala Ile Gly Gln Asn Val Glu Phe Asn |     | 640 |
|                                                                 | 645 | 650 |
| Val Asp Phe Asn Ser Lys Tyr Phe Asn Val Arg Gly Ala Ala Phe Tyr |     | 655 |
|                                                                 | 660 | 665 |
| Gln Val Ile Asn Asn Phe Ile Asn Ser Tyr Gly Gln Asp Thr Ser Lys |     | 670 |
|                                                                 | 675 | 680 |
| Asn Gly Gly Gly Asn Ala Thr Ala Lys Asn Met Ser Gly Asn Leu Pro |     | 685 |
|                                                                 | 690 | 695 |
| Glu Thr Ile Asn Ile Tyr Gly Tyr Glu Val Ser Gly Asn Val Arg Tyr |     | 700 |
| 705                                                             | 710 | 715 |
| Lys Asn Phe Leu Gly Thr Phe Ser Val Ala Arg Ser Trp Pro Thr Ala |     | 720 |
|                                                                 | 725 | 730 |
| Arg Gly His Leu Leu Ala Asp Thr Tyr Ala Leu Ala Ala Thr Thr Gly |     | 735 |
|                                                                 | 740 | 745 |
| Asn Val Phe Ile Leu Lys Ala Asp Tyr Asp Val Arg Arg Trp Gly Leu |     | 750 |
|                                                                 | 755 | 760 |
| Thr Leu Thr Trp Leu Ser Arg Phe Val Thr Asn Met Tyr Tyr Glu Gly |     | 765 |
|                                                                 | 770 | 775 |
| Tyr Ser Ile Tyr Tyr Pro Gln Tyr Gly Leu Ile Lys Ile His Lys Pro |     | 780 |
| 785                                                             | 790 | 795 |
| Gly Tyr Gly Val His Asn Val Phe Ile Asn Trp Thr Pro Pro Ser Lys |     | 800 |
|                                                                 | 805 | 810 |
| Lys Trp Gln Gly Leu Arg Ile Ser Ala Val Phe Asn Asn Ile Leu Asn |     | 815 |
|                                                                 | 820 | 825 |
| Lys Gln Tyr Val Asp Gln Thr Ser Val Phe Gln Ala Ser Ala Asp Ala |     | 830 |
|                                                                 | 835 | 840 |
| Pro Ala Ser Asp Met Ile Pro Lys Gly Lys Arg Met Ala Leu Pro Ala |     | 845 |
|                                                                 | 850 | 855 |
| Pro Gly Phe Asn Ala Arg Phe Glu Val Ser Tyr Gln Phe             |     | 860 |
| 865                                                             | 870 | 875 |

```

Met Leu Arg Asn Gln Phe Arg Ile Val Phe Val Ser Cys Ile Val Ala
 1 5 10 15
Ser Asn Leu Gln Ala Gln Glu Thr Thr His Thr Leu Gly Lys Val Thr
 20 25 30
Thr Lys Gly Glu Arg Thr Phe Glu Tyr Asn Asn Lys Met Tyr Ile Asp
 35 40 45
Arg Lys Glu Leu Gln Gln Arg Gln Ser Asn Gln Ile Arg Asp Ile Phe
 50 55 60
Arg Thr Arg Ala Asp Val Asn Val Ala Ser Gly Gly Leu Met Ala Gln
 65 70 75 80
Lys Ile Tyr Val Arg Gly Ile Glu Ser Arg Leu Leu Arg Val Thr Ile
 85 90 95
Asp Gly Val Ala Gln Asn Gly Asn Ile Phe His His Asp Ala Asn Thr
 100 105 110
Val Ile Asp Pro Asn Met Ile Lys Glu Val Glu Val Ile Lys Gly Ala
 115 120 125
Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu Ser Phe
 130 135 140
Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr Tyr Gly
 145 150 155 160
Ala Lys Ala Glu Ala Ala Phe Tyr Thr Asn Phe Gly Tyr Arg Met Asn
 165 170 175
Ala Thr Ala Ala Tyr Arg Gly Lys Asn Trp Asp Ile Leu Ala Tyr Tyr
 180 185 190
Asn His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly Asn Asn Ala Phe Arg
 195 200 205
Asn Val Phe His Pro Asn Tyr Asp Leu Gln Asp Pro Ser Asn Ser Asp
 210 215 220
Met Ser Val Gly Thr Pro Ser Glu Val Asn Ser Val Leu Ala Lys Ile
 225 230 235 240
Asn Gly Tyr Ile Asn Glu Thr Asp Ser Ile Ser Val Ser Tyr Asn Leu
 245 250 255
Thr Arg Asp Asn Ser Thr Arg Leu Leu Arg Pro Asn Thr Thr Ser Ala
 260 265 270
Leu Ser Lys Ala Asn Asp Pro Gly Ser Gln Pro Ala Pro Phe Val Ile
 275 280 285
Asp Phe Gly Lys Glu Leu Ala His Thr Ile Asn Phe Asn His Asn Leu
 290 295 300
Ser Leu Lys Tyr Lys His Glu Gly Gly Pro Asn Phe Asn Gln Pro Arg
 305 310 315 320
Val Glu Ser Thr Ala Phe Leu Gly Val Arg Gly Gly Asn Tyr Asn Pro
 325 330 335
Val Val Asn Pro Phe Ala Tyr Asn Ser Asn Glu Pro Ala Asn Pro Asp
 340 345 350
Tyr Ile Pro Glu Val Lys Glu Trp Cys Asn Asn Pro Asp Asn Ile Ser
 355 360 365
Gln Cys Thr Gln Gly Ala Ile Arg Pro Ser Asn Gly Gly Tyr Gln Ile
 370 375 380
Gly Tyr Gly Thr Pro Asn Ser Ile Asn Trp Gln Gly Thr Ser Asp Ser
 385 390 395 400
Ser Gly Gly Ala Gln Ala Gly Tyr Gly Gln Leu Asn Ala Ile Ser Thr
 405 410 415
Ser Ala Asn Val Tyr His Gly Leu Val Pro Lys Asn Pro Asp Tyr Asp
 420 425 430
Met Thr Pro Pro Asn Ala Gln Asn Pro Ser Ala Asn Asp Trp Thr Leu

```

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AGG TAT AAG AAT TTC TTA GGG ACT TTC TCA GTG GCT CGC TCT TGG CCA   | 2270 |
| Arg Tyr Lys Asn Phe Leu Gly Thr Phe Ser Val Ala Arg Ser Trp Pro   |      |
| 720 725 730                                                       |      |
| ACG GCT AGG GGG CAT TTA TTA GCG GAC ACT TAC GCT CTA GCT GCA ACG   | 2318 |
| Thr Ala Arg Gly His Leu Leu Ala Asp Thr Tyr Ala Leu Ala Ala Thr   |      |
| 735 740 745 750                                                   |      |
| ACT GGG AAT GTG TTT ATT TTA AAA GCC GAT TAT GAT GTT CGC AGG TGG   | 2366 |
| Thr Gly Asn Val Phe Ile Leu Lys Ala Asp Tyr Asp Val Arg Arg Trp   |      |
| 755 760 765                                                       |      |
| GGG CTT ACT TTA ACC TGG CTC TCG CGC TTT GTA ACT AAC ATG TAT TAT   | 2414 |
| Gly Leu Thr Leu Thr Trp Leu Ser Arg Phe Val Thr Asn Met Tyr Tyr   |      |
| 770 775 780                                                       |      |
| GAG GGC TAT TCT ATC TAT TAC CCG CAA TAC GGC TTG ATC AAA ATC CAT   | 2462 |
| Glu Gly Tyr Ser Ile Tyr Tyr Pro Gln Tyr Gly Leu Ile Lys Ile His   |      |
| 785 790 795                                                       |      |
| AAA CCC GGG TAT GGC GTG CAT AAT GTC TTT ATC AAC TGG ACT CCG CCT   | 2510 |
| Lys Pro Gly Tyr Gly Val His Asn Val Phe Ile Asn Trp Thr Pro Pro   |      |
| 800 805 810                                                       |      |
| TCT AAA AAA TGG CAG GGT TTA AGG ATT TCA GCC GTG TTT AAT AAT ATC   | 2558 |
| Ser Lys Lys Trp Gln Gly Leu Arg Ile Ser Ala Val Phe Asn Asn Ile   |      |
| 815 820 825 830                                                   |      |
| TTA AAC AAG CAA TAT GTG GAT CAA ACT TCT GTG TTT CAA GCG AGC GCG   | 2606 |
| Leu Asn Lys Gln Tyr Val Asp Gln Thr Ser Val Phe Gln Ala Ser Ala   |      |
| 835 840 845                                                       |      |
| GAC GCT CCA GCG AGC GAT ATG ATC CCT AAA GGT AAG CGC ATG GCG CTC   | 2654 |
| Asp Ala Pro Ala Ser Asp Met Ile Pro Lys Gly Lys Arg Met Ala Leu   |      |
| 850 855 860                                                       |      |
| CCG GCT CCT GGA TTT AAC GCG CGT TTT GAG GTA TCC TAT CAG TTC TAAAA | 2704 |
| Pro Ala Pro Gly Phe Asn Ala Arg Phe Glu Val Ser Tyr Gln Phe       |      |
| 865 870 875                                                       |      |
| TGAAAGGAAT CTTAGGATTT CTTTTTGAAT TTTGAACATG GAAACA                | 2750 |

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GTT TTC TCT GGA TTG GAT AAA GGC AAA AAC GGC TAT TAT AAA AAC AAC | 1598 |
| Val Phe Ser Gly Leu Asp Lys Gly Lys Asn Gly Tyr Tyr Lys Asn Asn |      |
| 495 500 505 510                                                 |      |
| ATT GAT CCT AAC GAC CCT AAC GGG CCG GGC TTG CCT TAC CGC CAT TAC | 1646 |
| Ile Asp Pro Asn Asp Pro Asn Gly Pro Gly Leu Pro Tyr Arg His Tyr |      |
| 515 520 525                                                     |      |
| TAC ACC GAT CAA AGC TCC CAA TAC CCC CAA AAT CTC AAC ACC CCT AAC | 1694 |
| Tyr Thr Asp Gln Ser Ser Gln Tyr Pro Gln Asn Leu Asn Thr Pro Asn |      |
| 530 535 540                                                     |      |
| CCG CTC TAT CGT AAC ATG CCC CAA AAT TCG CAT GCG ATC GGC AAT ATC | 1742 |
| Pro Leu Tyr Arg Asn Met Pro Gln Asn Ser His Ala Ile Gly Asn Ile |      |
| 545 550 555                                                     |      |
| ATC GGA GGG TTT ATG CAA GCA AAC TAC AAC ATT TTA AGC AAT GTG ATC | 1790 |
| Ile Gly Gly Phe Met Gln Ala Asn Tyr Asn Ile Leu Ser Asn Val Ile |      |
| 560 565 570                                                     |      |
| GTG GGT GCG GGA ACT CGT TAT GAT ATT TAC ACC TTG CTA GAC AAA AAC | 1838 |
| Val Gly Ala Gly Thr Arg Tyr Asp Ile Tyr Thr Leu Leu Asp Lys Asn |      |
| 575 580 585 590                                                 |      |
| GGC CGC ACG CAT GTA ACT TCT GGT TTC TCG CCT TCT GCA ACC GTG CTT | 1886 |
| Gly Arg Thr His Val Thr Ser Gly Phe Ser Pro Ser Ala Thr Val Leu |      |
| 595 600 605                                                     |      |
| TAT AAC CCC ATT GAA AGC ATT GGC TTG AAA GTG AGT TAT GCG TAT GTA | 1934 |
| Tyr Asn Pro Ile Glu Ser Ile Gly Leu Lys Val Ser Tyr Ala Tyr Val |      |
| 610 615 620                                                     |      |
| ACT AAG GGG GCT TTG CCT GGC GAT GGC GTT TTG ATG CGC GAT CCT ACG | 1982 |
| Thr Lys Gly Ala Leu Pro Gly Asp Gly Val Leu Met Arg Asp Pro Thr |      |
| 625 630 635                                                     |      |
| GTG ATT TAT CAA AGG AAT TTG CGC CCT GCG ATC GGT CAA AAT GTG GAA | 2030 |
| Val Ile Tyr Gln Arg Asn Leu Arg Pro Ala Ile Gly Gln Asn Val Glu |      |
| 640 645 650                                                     |      |
| TTT AAT GTG GAT TTC AAC AGC AAG TAT TTC AAT GTG CGC GGG GCA GCG | 2078 |
| Phe Asn Val Asp Phe Asn Ser Lys Tyr Phe Asn Val Arg Gly Ala Ala |      |
| 655 660 665 670                                                 |      |
| TTC TAT CAA GTC ATC AAT AAT TTC ATC AAC AGC TAC GGG CAA GAC ACT | 2126 |
| Phe Tyr Gln Val Ile Asn Asn Phe Ile Asn Ser Tyr Gly Gln Asp Thr |      |
| 675 680 685                                                     |      |
| TCT AAA AAT GGA GGG GGT AAC GCA ACC GCA AAA AAC ATG TCA GGG AAT | 2174 |
| Ser Lys Asn Gly Gly Gly Asn Ala Thr Ala Lys Asn Met Ser Gly Asn |      |
| 690 695 700                                                     |      |
| TTA CCC GAA ACC ATT AAC ATT TAT GGT TAT GAA GTT TCA GGG AAT GTG | 2222 |
| Leu Pro Glu Thr Ile Asn Ile Tyr Gly Tyr Glu Val Ser Gly Asn Val |      |
| 705 710 715                                                     |      |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TCA | GCC | CTC | TCT | AAA | GCC | AAT | GAC | CCA | GGA | AGC | CAG | CCA | GCC | CCC | TTT | 926  |
| Ser | Ala | Leu | Ser | Lys | Ala | Asn | Asp | Pro | Gly | Ser | Gln | Pro | Ala | Pro | Phe |      |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |      |
| GTG | ATT | GAC | TTT | GGG | AAA | GAA | TTA | GCC | CAT | ACG | ATC | AAC | TTC | AAC | CAC | 974  |
| Val | Ile | Asp | Phe | Gly | Lys | Glu | Leu | Ala | His | Thr | Ile | Asn | Phe | Asn | His |      |
|     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |      |
| AAT | TTG | AGC | TTG | AAA | TAC | AAG | CAT | GAA | GGC | GGC | CCT | AAT | TTT | AAC | CAG | 1022 |
| Asn | Leu | Ser | Leu | Lys | Tyr | Lys | His | Glu | Gly | Gly | Pro | Asn | Phe | Asn | Gln |      |
|     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |      |
| CCG | CGC | GTT | GAA | TCC | ACC | GCC | TTT | TTA | GGG | GTA | AGG | GGG | GGC | AAT | TAT | 1070 |
| Pro | Arg | Val | Glu | Ser | Thr | Ala | Phe | Leu | Gly | Val | Arg | Gly | Gly | Asn | Tyr |      |
|     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |      |
| AAC | CCT | GTG | GTG | AAT | CCT | TTC | GCT | TAC | AAT | TCT | AAC | GAG | CCG | GCT | AAC | 1118 |
| Asn | Pro | Val | Val | Asn | Pro | Phe | Ala | Tyr | Asn | Ser | Asn | Glu | Pro | Ala | Asn |      |
| 335 |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |      |
| CCA | GAT | TAT | ATC | CCT | GAA | GTG | AAA | GAG | TGG | TGT | AAT | AAC | CCA | GAT | AAT | 1166 |
| Pro | Asp | Tyr | Ile | Pro | Glu | Val | Lys | Glu | Trp | Cys | Asn | Asn | Pro | Asp | Asn |      |
|     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |      |
| ATC | AGC | CAG | TGC | ACG | CAA | GGG | GCT | ATC | AGG | CCT | TCT | AAT | GGA | GGC | TAT | 1214 |
| Ile | Ser | Gln | Cys | Thr | Gln | Gly | Ala | Ile | Arg | Pro | Ser | Asn | Gly | Gly | Tyr |      |
|     |     | 370 |     |     |     | 375 |     |     |     |     |     |     | 380 |     |     |      |
| CAA | ATA | GGC | TAT | GGC | ACG | CCT | AAT | TCT | ATT | AAT | TGG | CAA | GGG | ACT | AGC | 1262 |
| Gln | Ile | Gly | Tyr | Gly | Thr | Pro | Asn | Ser | Ile | Asn | Trp | Gln | Gly | Thr | Ser |      |
|     | 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     |      |
| GAT | TCT | AGT | GGA | GGG | GCG | CAA | GCA | GGG | TAT | GGG | CAG | CTT | AAC | GCT | ATT | 1310 |
| Asp | Ser | Ser | Gly | Gly | Ala | Gln | Ala | Gly | Tyr | Gly | Gln | Leu | Asn | Ala | Ile |      |
|     | 400 |     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     |      |
| TCT | ACA | AGC | GCG | AAC | GTT | TAT | CAT | GGG | CTT | GTC | CCT | AAA | AAT | CCT | GAT | 1358 |
| Ser | Thr | Ser | Ala | Asn | Val | Tyr | His | Gly | Leu | Val | Pro | Lys | Asn | Pro | Asp |      |
| 415 |     |     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |      |
| TAT | GAC | ATG | ACC | CCC | CCT | AAC | GCT | CAA | AAC | CCT | AGC | GCA | AAC | GAT | TGG | 1406 |
| Tyr | Asp | Met | Thr | Pro | Pro | Asn | Ala | Gln | Asn | Pro | Ser | Ala | Asn | Asp | Trp |      |
|     |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |      |
| ACT | TTA | GGG | AAT | GCG | GAC | GCT | GAG | GGG | ACT | TTA | GCC | AGA | AGG | ATT | TTT | 1454 |
| Thr | Leu | Gly | Asn | Ala | Asp | Ala | Glu | Gly | Thr | Leu | Ala | Arg | Arg | Ile | Phe |      |
|     |     | 450 |     |     |     | 455 |     |     |     |     |     | 460 |     |     |     |      |
| TTA | ATC | AAC | TCG | GGC | GTT | AAT | TTT | AAA | GTA | ACC | CAC | CCC | ATT | AGC | GAA | 1502 |
| Leu | Ile | Asn | Ser | Gly | Val | Asn | Phe | Lys | Val | Thr | His | Pro | Ile | Ser | Glu |      |
|     | 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     |      |
| GAT | TAT | GGG | AAT | GTG | TTT | GAA | TAC | GGC | ATG | ATT | TAT | CAA | AAC | CTG | AGC | 1550 |
| Asp | Tyr | Gly | Asn | Val | Phe | Glu | Tyr | Gly | Met | Ile | Tyr | Gln | Asn | Leu | Ser |      |
|     | 480 |     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     |      |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATT GAC AGA AAA GAG CTC CAA CAA CGC CAA AGT AAC CAA ATC CGT GAT | 254 |
| Ile Asp Arg Lys Glu Leu Gln Gln Arg Gln Ser Asn Gln Ile Arg Asp |     |
| 50 55 60                                                        |     |
| ATT TTT AGG ACT AGA GCG GAT GTG AAT GTG GCC AGT GGG GGC TTG ATG | 302 |
| Ile Phe Arg Thr Arg Ala Asp Val Asn Val Ala Ser Gly Gly Leu Met |     |
| 65 70 75                                                        |     |
| GCG CAA AAG ATC TAT GTT AGG GGG ATT GAG AGC CGT CTC TTA AGG GTA | 350 |
| Ala Gln Lys Ile Tyr Val Arg Gly Ile Glu Ser Arg Leu Leu Arg Val |     |
| 80 85 90                                                        |     |
| ACA ATA GAT GGC GTC GCC CAA AAT GGT AAC ATT TTC CAC CAT GAC GCT | 398 |
| Thr Ile Asp Gly Val Ala Gln Asn Gly Asn Ile Phe His His Asp Ala |     |
| 95 100 105 110                                                  |     |
| AAC ACC GTG ATC GAT CCT AAC ATG ATT AAA GAA GTG GAA GTG ATC AAG | 446 |
| Asn Thr Val Ile Asp Pro Asn Met Ile Lys Glu Val Glu Val Ile Lys |     |
| 115 120 125                                                     |     |
| GGG GCG GCG AAC GCT TCA GCA GGC CCA GGT GCG GTG GCG GGT AAA TTG | 494 |
| Gly Ala Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu |     |
| 130 135 140                                                     |     |
| TCT TTC ACC ACG ATT GAC GCT AAC GAC TTC TTA AGA AAG AAT CAA ACT | 542 |
| Ser Phe Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr |     |
| 145 150 155                                                     |     |
| TAT GGC GCT AAA GCG GAA GCG GCC TTT TAT ACC AAC TTC GGG TAT CGC | 590 |
| Tyr Gly Ala Lys Ala Glu Ala Ala Phe Tyr Thr Asn Phe Gly Tyr Arg |     |
| 160 165 170                                                     |     |
| ATG AAC GCC ACT GCG GCT TAC CGG GGG AAA AAC TGG GAC ATC CTA GCC | 638 |
| Met Asn Ala Thr Ala Ala Tyr Arg Gly Lys Asn Trp Asp Ile Leu Ala |     |
| 175 180 185 190                                                 |     |
| TAT TAC AAC CAT CAA AAT ATT TTT TAC TAC AGA GAC GGG AAC AAC GCT | 686 |
| Tyr Tyr Asn His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly Asn Asn Ala |     |
| 195 200 205                                                     |     |
| TTT AGG AAT GTC TTC CAC CCT AAC TAC GAT TTA CAA GAT CCA AGC AAT | 734 |
| Phe Arg Asn Val Phe His Pro Asn Tyr Asp Leu Gln Asp Pro Ser Asn |     |
| 210 215 220                                                     |     |
| AGC GAT ATG AGC GTA GGG ACT CCC AGT GAA GTC AAT AGC GTT TTA GCT | 782 |
| Ser Asp Met Ser Val Gly Thr Pro Ser Glu Val Asn Ser Val Leu Ala |     |
| 225 230 235                                                     |     |
| AAA ATT AAT GGC TAT ATC AAC GAA ACA GAC AGC ATT AGC GTG AGC TAC | 830 |
| Lys Ile Asn Gly Tyr Ile Asn Glu Thr Asp Ser Ile Ser Val Ser Tyr |     |
| 240 245 250                                                     |     |
| AAC CTC ACA CGA GAC AAT TCT ACA AGG CTT TTA CGC CCT AAC ACC ACT | 878 |
| Asn Leu Thr Arg Asp Asn Ser Thr Arg Leu Leu Arg Pro Asn Thr Thr |     |
| 255 260 265 270                                                 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |
| Pro | Val | Gly | Asp | Ser | Gly | Phe | Ile | Tyr | Asn | Ser | Phe | Ser | Phe | Gly | Gly |  |  |  |  |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |  |  |  |  |
| Asn | Thr | Leu | Thr | Glu | Arg | Asp | Ser | Tyr | Gln | Gly | Gln | Tyr | Tyr | Val | Asn |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Leu | Phe | Thr | Tyr | Gly | Val | Gly | Leu | Asp | Thr | Leu | Trp | Asn | Phe | Val | Asn |  |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |
| Lys | Glu | Asn | Met | Val | Phe | Gly | Phe | Val | Val | Gly | Ile | Gln | Leu | Ala | Gly |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Asp | Ser | Trp | Ala | Thr | Ser | Ile | Ser | Lys | Glu | Ile | Ala | His | Tyr | Ala | Lys |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |  |  |  |  |
| His | His | Ser | Asn | Ser | Ser | Tyr | Ser | Pro | Ala | Asn | Phe | Gln | Phe | Leu | Trp |  |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |
| Lys | Phe | Gly | Val | Arg | Thr | His | Ile | Ala | Lys | His | Asn | Ser | Leu | Glu | Leu |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| Gly | Ile | Lys | Val | Pro | Thr | Ile | Thr | His | Gln | Leu | Phe | Ser | Leu | Thr | Asn |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |
| Glu | Lys | Gly | Tyr | Thr | Leu | Gln | Ala | Asp | Val | Arg | Arg | Val | Tyr | Ala | Phe |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |  |  |  |  |
| Gln | Ile | Ser | Tyr | Leu | Arg | Asp | Phe |     |     |     |     |     |     |     |     |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 69...2699
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TAATAATAAC CTTAGGTTTA AAACCTTGACT AAATTTTTAG AAAAAAGTAA ATAAAAAGGC | 60  |
| TAAAAGAA ATG CTT AGA AAT CAA TTT CGT ATC GTG TTT GTC TCT TGT ATT   | 110 |
| Met Leu Arg Asn Gln Phe Arg Ile Val Phe Val Ser Cys Ile            |     |
| 1 5 10                                                             |     |
| GTC GCT AGC AAT TTG CAA GCT CAA GAA ACA ACC CAC ACT TTG GGT AAG    | 158 |
| Val Ala Ser Asn Leu Gln Ala Gln Glu Thr Thr His Thr Leu Gly Lys    |     |
| 15 20 25 30                                                        |     |
| GTA ACC ACT AAG GGT GAA AGG ACT TTT GAA TAC AAC AAT AAA ATG TAT    | 206 |
| Val Thr Thr Lys Gly Glu Arg Thr Phe Glu Tyr Asn Asn Lys Met Tyr    |     |
| 35 40 45                                                           |     |

```

AAA GAA AAC ATG GTT TTT GGT TTT GTG GTG GGG ATC CAA TTA GCG GGG 538
Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly
145 150 155 160

GAT AGT TGG GCA ACG AGC ATC AGT AAA GAA ATC GCT CAT TAT GCA AAA 586
Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys
 165 170 175

CAC CAC AGC AAT TCC AGT TAT AGC CCG GCC AAT TTC CAG TTT TTA TGG 634
His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp
 180 185 190

AAG TTT GGG GTC CGC ACC CAT ATC GCT AAA CAC AAT AGC CTA GAA TTA 682
Lys Phe Gly Val Arg Thr His Ile Ala Lys His Asn Ser Leu Glu Leu
 195 200 205

GGG ATT AAA GTG CCT ACG ATC ACA CAC CAG CTT TTC TCT CTT ACC AAC 730
Gly Ile Lys Val Pro Thr Ile Thr His Gln Leu Phe Ser Leu Thr Asn
 210 215 220

GAA AAG GGA TAC ACC TTA CAG GCT GAT GTG CGT AGA GTT TAT GCG TTT 778
Glu Lys Gly Tyr Thr Leu Gln Ala Asp Val Arg Arg Val Tyr Ala Phe
225 230 235 240

CAA ATC AGT TAC TTG AGG GAT TTT TAACCCCTTT TTAGATACAA TCACGCCTGA AA 834
Gln Ile Ser Tyr Leu Arg Asp Phe
 245

CTATCCATTT AAAGGTGTGA AA 856

```

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser
 1 5 10 15
Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met
 20 25 30
Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro
 35 40 45
Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr
 50 55 60
Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly
65 70 75 80
Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile

```

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 59...802
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

GCCATTTTAA GCTAATATAA TATAGAGCGA TTATCAAAAA ATAAAGGGAA AAGACTGA 58

ATG TTG AAA AGA ATG ATA TTA TTA GGG GCT TTG GGT GTT TTA GCG AGC 106
Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser
 1 5 10 15

GCT GAA GAG AGT GCG GCT TTT GTG GGA GTC AAT TAC CAG GTG AGC ATG 154
Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met
 20 25 30

ATA CAA AAT CAG ACT AAA ATG GTG AAT GAC AAC GGC TTG CAA AAG CCT 202
Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro
 35 40 45

TTG ATA AAG TTT CCG CCT TAC GCA GGA GCG GGT TTT GAA GTG GGC TAT 250
Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr
 50 55 60

AAG CAA TTT TTT GGT AAG AAA AAA TGG TTT GGC ATG CGT TAT TAT GGG 298
Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly
 65 70 75 80

TTT TTT GAC TAC GCG CAC AAC CGC TTT GGC GTG ATG AAA AAG GGC ATT 346
Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile
 85 90 95

CCG GTG GGC GAT AGT GGG TTT ATT TAC AAT AGT TTT AGT TTT GGA GGG 394
Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly
 100 105 110

AAC ACT TTA ACG GAA AGG GAT TCC TAT CAG GGG CAA TAC TAT GTC AAT 442
Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn
 115 120 125

TTA TTC ACT TAT GGC GTG GGG TTA GAT ACG CTG TGG AAT TTT GTG AAT 490
Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn
 130 135 140

```

```

GGG GGT GGT GTT GGT GGT GCA GTG GGG GGA GCT GTT GGT GGT CCT GCG 248
Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly Pro Ala
 55 60 65

GGT GGT TGG GCT GGC AGA TTA GTT GGT GGT TCT GTG GGG AGA GAG TTT 296
Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg Glu Phe
 70 75 80

GGT CGG GAA ATA GGC GAT AGG GTA GAA GAT TAC ATC CGT GGC GTT GAT 344
Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly Val Asp
 85 90 95

AGA GAG CCA CAA GCC CCA AGA GAA CCC ACC TAT GAT CGT CAT TTC GTG 392
Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His Phe Val
 100 105 110

TAT GAC AGG TAGCTTTGGG CGAGAAAGGA GAGAGCATGA ATGTCAAAAA TCGTTTGAG 450
Tyr Asp Arg
115

CGAT 454

```

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Lys Gly Phe Val Met Ser Gly Leu Lys Ala Phe Ser Cys Val Val
 1 5 10 15
Val Leu Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile
 20 25 30
Glu Ala Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly
 35 40 45
Ala Ile Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly
 50 55 60
Pro Ala Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg
 65 70 75 80
Glu Phe Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly
 85 90 95
Val Asp Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His
 100 105 110
Phe Val Tyr Asp Arg
 115

```

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 515 |     | 520 |     | 525 |     |     |     |     |     |     |     |     |     |     |
| Tyr | Asp | Tyr | Gln | Gly | Arg | Leu | Tyr | Asp | Ser | Val | Trp | Asn | Pro | Ser | Ser |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Ile | Leu | Pro | Ser | Asn | Ala | Ser | Asn | Lys | Thr | Val | Asp | Leu | Thr | Leu | Thr |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     | 560 |     |
| Gln | Tyr | Leu | Tyr | Gly | Leu | Gly | Gly | Gln | Glu | Leu | Leu | Tyr | Phe | Lys | Ile |
|     |     |     |     | 565 |     |     |     | 570 |     |     |     |     |     | 575 |     |
| Ser | Gln | Leu | Ile | Asn | Leu | Asp | Asp | Lys | Val | Ser | Pro | Phe | Arg | Met | Pro |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Leu | Glu | Ser | Lys | Ile | Gly | Phe | Ser | Pro | Leu | Thr | Gly | Leu | Asn | Ile | Phe |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Gly | Asn | Val | Phe | Tyr | Ser | Phe | Tyr | Gln | Asn | Arg | Leu | Glu | Glu | Ile | Ser |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Val | Asn | Ala | Asn | Tyr | Gln | Arg | Lys | Phe | Leu | Ser | Phe | Asn | Leu | Ser | Tyr |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     | 640 |     |
| Phe | Leu | Lys | Asn | Asn | Phe | Ser | Ser | Gly | Ile | Asn | Ser | Ile | Val | Glu | Asn |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Leu | Arg | Ile | Ile |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 660 |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...401
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TCAAGGTGTG CCAAACATGC CTTGAAACTC AATTTTGTGAA TCTCAATTTT ATG AAA | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| GGA TTT GTT ATG AGT GGA TTA AAA GCA TTT AGT TGT GTA GTG GTT TTA | 104 |
| Gly Phe Val Met Ser Gly Leu Lys Ala Phe Ser Cys Val Val Val Leu |     |
| 5 10 15                                                         |     |
| TGC GGT GCA ATG GCT AAT ACG GCT ATA GCT GGT CCT AAA ATA GAA GCA | 152 |
| Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile Glu Ala |     |
| 20 25 30                                                        |     |
| AGG GGT GAG TTT GGC AGA TTT TGG GGG GGA GCT GTT GGT GGT GCA ATT | 200 |
| Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly Ala Ile |     |
| 35 40 45 50                                                     |     |

Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp  
 85 90 95  
 Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe  
 100 105 110  
 Tyr Val Gln Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala  
 115 120 125  
 Ser Gly Lys Asp Gln Lys Tyr Lys Val Lys Asn Met Ser Thr Ser Gly  
 130 135 140  
 Cys Ser Ile Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser  
 145 150 155 160  
 Phe Asn Met Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr  
 165 170 175  
 Val Gly Asp Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr  
 180 185 190  
 Ser Asn Lys Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser  
 195 200 205  
 Asn Leu Asp Gly Phe Ile Tyr Leu Gln Pro Phe Tyr Leu Ala Pro Lys  
 210 215 220  
 Asn Ser Trp Asp Met Thr Phe Thr Pro Gln Ile Arg Tyr Lys Arg Gly  
 225 230 235 240  
 Phe Gly Leu Asn Phe Glu Ala Arg Tyr Ile Asn Ser Lys Asn Asp Arg  
 245 250 255  
 Phe Leu Phe Asn Ala Arg Tyr Phe Arg Asn Tyr Thr Gln Tyr Val Lys  
 260 265 270  
 Arg Tyr Asp Leu Arg Asn Gln Asn Ile Tyr Gly Phe Glu Phe Leu Ser  
 275 280 285  
 Ser Ser Arg Asp Thr Leu Gln Lys Tyr Phe His Leu Lys Ser Asn Ile  
 290 295 300  
 Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr  
 305 310 315 320  
 Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met  
 325 330 335  
 Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu  
 340 345 350  
 Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr  
 355 360 365  
 Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu  
 370 375 380  
 Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr  
 385 390 395 400  
 Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro  
 405 410 415  
 Val Gly Leu Gln Phe Ser Leu Phe Lys Lys Tyr Leu Ser Leu Gly Leu  
 420 425 430  
 Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn  
 435 440 445  
 Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe  
 450 455 460  
 Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu  
 465 470 475 480  
 Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile  
 485 490 495  
 Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala  
 500 505 510  
 Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp



```

CAA TAC CTT TAT GGC TTA GGG GGG CAA GAG TTA TTG TAT TTT AAA ATA 1787
Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile
 565 570

575

TCG CAA CTC ATC AAT CTT GAC GAT AAA GTT TCG CCC TTT AGA ATG CCA 1835
Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro
 580 585 590

CTA GAG AGC AAG ATC GGG TTT TCG CCC TTA ACG GGA TTG AAC ATC TTT 1883
Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe
 595 600 605

GGG AAT GTC TTT TAT TCG TTT TAT CAA AAC CGC TTA GAA GAA ATC TCT 1931
Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser
 610 615 620

GTG AAC GCC AAT TAC CAA CGC AAG TTT TTA AGC TTT AAC CTC TCT TAT 1979
Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr
 625 630 635 640

TTT TTA AAA AAC AAT TTT AGC AGT GGG ATT AAT AGC ATT GTA GAA AAT 2027
Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn
 645 650 655

CTG CGG ATT ATT TAAAGGCGGG TTTTAGCAAC GACTTTGGCT ATTTTCCAT GAGCGC 2085
Leu Arg Ile Ile
 660

GGATGTGGGT TATGATATTA GAAACAATGT GGTTTTAAAT TGGAATGTGG GGATTTATAA 2145
AAAAATCCGT TGTTTTGGGA TTGG
 2169

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu
 1 5 10 15
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys
 20 25 30
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile
 35 40 45
Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu
 50 55 60
Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu
 65 70 75 80

```

|                                                                 |      |
|-----------------------------------------------------------------|------|
| TCT AGG GCG AAT TAC TAT TTG CAA ACA GAA AAC AAT TAT TAC GGC TTG | 1115 |
| Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu |      |
| 340 345 350                                                     |      |
| AAT ATC AAG TAT TTT TTA AAC CTG AAT AAA ATC AAC AAT AAC CGC ACT | 1163 |
| Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr |      |
| 355 360 365                                                     |      |
| TTC CAA TCT GTC CCT AAT TTG CAA TAC CAT AAA TAT TTA AAT TCT TTG | 1211 |
| Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu |      |
| 370 375 380                                                     |      |
| TAT TTT AGA AAT TTG TTG TAT TCG GTG GAT TAT CAG TTT AGA AAC ACC | 1259 |
| Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr |      |
| 385 390 395 400                                                 |      |
| GCA AGA GAG ATT GGT TAT GGC TAT GTG CAA AAC GCT TTG AAT GTG CCG | 1307 |
| Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro |      |
| 405 410 415                                                     |      |
| GTG GGC TTG CAA TTT TCT TTG TTT AAA AAG TAT TTG TCT TTA GGG CTT | 1355 |
| Val Gly Leu Gln Phe Ser Leu Phe Lys Lys Tyr Leu Ser Leu Gly Leu |      |
| 420 425 430                                                     |      |
| TGG AAT GAT CTC CAA CTA TCT AAT GTG GCT TTA ATG CAA TCT AAA AAT | 1403 |
| Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn |      |
| 435 440 445                                                     |      |
| TCC TTC GTG CCT ACG ATC CCT AAT GAA TCA AGG GAA TTT GGG AAT TTT | 1451 |
| Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe |      |
| 450 455 460                                                     |      |
| GTG TCT TCA AAT TTT TCC ATG TAT GTC AAT ACG GAT TTG GCT AGA GAA | 1499 |
| Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu |      |
| 465 470 475 480                                                 |      |
| TAC AAC AAG CTT TTC CAC ACG ATC CAA CTA GAA GCG ATT TTC AAC ATC | 1547 |
| Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile |      |
| 485 490 495                                                     |      |
| CCT TAT TAC ACC TTT AAA AAC GGC TTA TTT TCT CAA AAC ATG TAT GCT | 1595 |
| Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala |      |
| 500 505 510                                                     |      |
| TTA AGC GCG CAA GCC TTA AAC AGC TAC ACT TCG CCT TTA TTG AGA GAT | 1643 |
| Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp |      |
| 515 520 525                                                     |      |
| TAT GAT TAT CAA GGG CGT TTG TAT GAC TCG GTG TGG AAT CCT AGC AGT | 1691 |
| Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser |      |
| 530 535 540                                                     |      |
| ATT TTA CCT AGC AAT GCG AGC AAC AAG ACG GTG GAT TTA ACC CTA ACG | 1739 |
| Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr |      |
| 545 550 555 560                                                 |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Tyr | Val | Gln | Asp | Ser | Val | Ser | Gly | Ile | Trp | Val | Ser | Ala | Asp | Ile | Ala |      |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |      |  |
| AGC | GGA | AAG | GAT | CAA | AAA | TAT | AAG | GTT | AAA | AAC | ATG | AGC | ACT | TCA | GGG | 491  |  |
| Ser | Gly | Lys | Asp | Gln | Lys | Tyr | Lys | Val | Lys | Asn | Met | Ser | Thr | Ser | Gly |      |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |      |  |
| TGC | AGC | ATT | GAT | AAC | CCC | ATT | TGG | CAT | GTC | AAT | GCG | ACT | TCA | GGC | TCA | 539  |  |
| Cys | Ser | Ile | Asp | Asn | Pro | Ile | Trp | His | Val | Asn | Ala | Thr | Ser | Gly | Ser |      |  |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |      |  |
| TTC | AAC | ATG | CAA | AAA | TCG | CAT | TTG | TCT | ATG | TGG | AAT | CCT | AAG | ATC | TAT | 587  |  |
| Phe | Asn | Met | Gln | Lys | Ser | His | Leu | Ser | Met | Trp | Asn | Pro | Lys | Ile | Tyr |      |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |      |  |
| GTC | GGT | GAT | ATT | CCT | GTA | TTG | TAT | TTG | CCC | TAT | ATT | TTC | ATG | TCC | ACG | 635  |  |
| Val | Gly | Asp | Ile | Pro | Val | Leu | Tyr | Leu | Pro | Tyr | Ile | Phe | Met | Ser | Thr |      |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |  |
| AGC | AAT | AAA | AGA | ACT | ACT | GGG | TTT | TTA | TAC | CCT | GAG | TTT | GGC | ACT | TCC | 683  |  |
| Ser | Asn | Lys | Arg | Thr | Thr | Gly | Phe | Leu | Tyr | Pro | Glu | Phe | Gly | Thr | Ser |      |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |  |
| AAC | TTA | GAC | GGC | TTT | ATT | TAT | TTG | CAA | CCC | TTT | TAT | TTA | GCC | CCC | AAA | 731  |  |
| Asn | Leu | Asp | Gly | Phe | Ile | Tyr | Leu | Gln | Pro | Phe | Tyr | Leu | Ala | Pro | Lys |      |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |  |
| AAC | TCA | TGG | GAT | ATG | ACC | TTT | ACC | CCA | CAA | ATC | CGC | TAT | AAA | AGG | GGT | 779  |  |
| Asn | Ser | Trp | Asp | Met | Thr | Phe | Thr | Pro | Gln | Ile | Arg | Tyr | Lys | Arg | Gly |      |  |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |  |
| TTT | GGC | TTG | AAT | TTT | GAA | GCG | CGC | TAC | ATT | AAC | TCT | AAA | AAC | GAC | AGG | 827  |  |
| Phe | Gly | Leu | Asn | Phe | Glu | Ala | Arg | Tyr | Ile | Asn | Ser | Lys | Asn | Asp | Arg |      |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |  |
| TTT | TTA | TTC | AAC | GCG | CGC | TAT | TTT | AGG | AAT | TAC | ACC | CAA | TAT | GTC | AAA | 875  |  |
| Phe | Leu | Phe | Asn | Ala | Arg | Tyr | Phe | Arg | Asn | Tyr | Thr | Gln | Tyr | Val | Lys |      |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |  |
| CGC | TAC | GAT | TTG | AGG | AAT | CAA | AAT | ATC | TAC | GGG | TTT | GAA | TTT | TTA | AGC | 923  |  |
| Arg | Tyr | Asp | Leu | Arg | Asn | Gln | Asn | Ile | Tyr | Gly | Phe | Glu | Phe | Leu | Ser |      |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |  |
| TCT | AGC | AGG | GAC | ACT | TTA | CAA | AAA | TAC | TTC | CAC | CTT | AAG | TCT | AAT | ATT | 971  |  |
| Ser | Ser | Arg | Asp | Thr | Leu | Gln | Lys | Tyr | Phe | His | Leu | Lys | Ser | Asn | Ile |      |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |  |
| GAC | AAC | GGG | CAT | TAC | ATT | GAC | TTT | TTA | TAC | ATG | AAC | GAT | TTG | GAC | TAT | 1019 |  |
| Asp | Asn | Gly | His | Tyr | Ile | Asp | Phe | Leu | Tyr | Met | Asn | Asp | Leu | Asp | Tyr |      |  |
|     |     | 305 |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |      |  |
| GTG | CGT | TTT | GAA | AAG | GTT | AAT | AAG | CGT | ATC | ACA | GAC | GCC | ACG | CAC | ATG | 1067 |  |
| Val | Arg | Phe | Glu | Lys | Val | Asn | Lys | Arg | Ile | Thr | Asp | Ala | Thr | His | Met |      |  |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |      |  |

Lys Leu Ser Asp Thr Tyr Glu Gln Leu Ser Arg Leu Leu Thr Asn Asp  
 50 55 60  
 Asn Gly Thr Asn Ser Lys Thr Ser Ala Gln Xaa Gln Pro Ser Gly  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...2039
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCCTATCATA GGGCGTGGCA TGAAGAAAAA AGCAAAAGTC TTTTGGTATT GTTTTAATC 59

ATG ATT TAT TGG TTG TAT TTG GCG GTC TTT TTT TTG TTG AGC GCA TTA 107  
 Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu  
 1 5 10 15

GAC GCT AAA GAA ATC GCT ATG CAA CGA TTT GAC AAA CAA AAC CAT AAG 155  
 Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys  
 20 25 30

ATT TTT GAA ATC CTT GCG GAT AAA GTG AGC GCT AAA GAC AAT GTG ATA 203  
 Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile  
 35 40 45

ACC GCA TCA GGG AAT GCG ATC TTA TTG AAT TAT GAT GTG TAT ATT CTA 251  
 Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu  
 50 55 60

GCG GAC AAG GTG CGT TAT GAC ACT AAA ACC AAA GAA GCG TTA TTA GAG 299  
 Ala Asp Lys Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu  
 65 70 75 80

GGG AAT ATC AAG GTT TAT AGG GGC GAG GGT TTG CTC GTT AAA ACC GAT 347  
 Gly Asn Ile Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp  
 85 90 95

TAC GTG AAA TTG AGT TTG AAT GAA AAA TAT GAA ATC ATT TTC CCC TTT 395  
 Tyr Val Lys Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe  
 100 105 110

TAT GTC CAA GAC AGC GTG AGC GGG ATT TGG GTG AGC GCG GAT ATT GCC 443

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 87...323  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

AAATTTATGT TATAATTAAA CGCATTGTAA ATAAATTCTC ATTTTGATAC ATTTTACAA 60
TAAACATTA CTTTAAGGAA CATCTT ATG AAA AAA ACG AAA AAA ACG ATT CTG 113
 Met Lys Lys Thr Lys Lys Thr Ile Leu
 1 5

CTT TCT CTA ACT CTC GCG GCG TCA TTG CTC CAT GCT GAA GAC AAC GGC 161
Leu Ser Leu Thr Leu Ala Ala Ser Leu Leu His Ala Glu Asp Asn Gly
10 15 20 25

GTT TTT TTA AGC GTG GGT TAT CAA ATC GGT GAA GCG GTT CAA AAA GTG 209
Val Phe Leu Ser Val Gly Tyr Gln Ile Gly Glu Ala Val Gln Lys Val
 30 35 40

AAA AAC GCC GAC AAG GTG CAA AAA CTT TCA GAC ACT TAT GAA CAA TTA 257
Lys Asn Ala Asp Lys Val Gln Lys Leu Ser Asp Thr Tyr Glu Gln Leu
 45 50 55

AGC CGG CTT TTA ACC AAC GAT AAT GGC ACA AAC TCA AAG ACA AGC GCG 305
Ser Arg Leu Leu Thr Asn Asp Asn Gly Thr Asn Ser Lys Thr Ser Ala
 60 65 70

CAA NAT CAA CCA AGC GGT TAATAATTTG AACGAACGCG CAAAACTTT AGCCGGTG 361
Gln Xaa Gln Pro Ser Gly
 75

GGACAACCAA TTCCCC 377

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Lys Lys Thr Lys Lys Thr Ile Leu Leu Ser Leu Thr Leu Ala Ala
 1 5 10 15
Ser Leu Leu His Ala Glu Asp Asn Gly Val Phe Leu Ser Val Gly Tyr
 20 25 30
Gln Ile Gly Glu Ala Val Gln Lys Val Lys Asn Ala Asp Lys Val Gln
 35 40 45

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 130 |     | 135 |     | 140 |     |     |     |     |     |     |     |     |     |     |     |
| Tyr | Leu | Glu | Tyr | Ala | Tyr | Lys | Asn | Tyr | Phe | Glu | Ile | Lys | Ala | Gly | Arg |
| 145 |     | 150 |     | 155 |     | 160 |     |     |     |     |     |     |     |     |     |
| Tyr | Leu | Ser | Thr | Met | Pro | Tyr | Lys | Ser | Gly | Gln | Thr | Gln | Gly | Phe | Gln |
|     |     | 165 |     | 170 |     | 175 |     |     |     |     |     |     |     |     |     |
| Ile | Ser | Gly | Gln | Tyr | Lys | Lys | Ala | Arg | Leu | Thr | Trp | Phe | Ser | Ser | Phe |
|     |     | 180 |     | 185 |     | 190 |     |     |     |     |     |     |     |     |     |
| Gly | Arg | Ala | Phe | Ala | Tyr | Gly | Ser | Phe | Leu | Met | Asp | Trp | Phe | Ala | Ala |
|     |     | 195 |     | 200 |     | 205 |     |     |     |     |     |     |     |     |     |
| Arg | Thr | Thr | Tyr | Ser | Gly | Gly | Phe | Thr | Lys | Asn | Asp | Lys | Gly | Gly | Tyr |
|     |     | 210 |     | 215 |     | 220 |     |     |     |     |     |     |     |     |     |
| Asp | Ser | His | Gly | Arg | Lys | Val | Leu | Tyr | Gly | Thr | His | Ala | Val | Gln | Leu |
| 225 |     | 230 |     | 235 |     | 240 |     |     |     |     |     |     |     |     |     |
| Thr | Tyr | Lys | Pro | His | Arg | Phe | Leu | Ile | Glu | Gly | Phe | Tyr | Tyr | Leu | Ser |
|     |     | 245 |     | 250 |     | 255 |     |     |     |     |     |     |     |     |     |
| Pro | Gln | Ile | Phe | Asn | Ala | Pro | Gly | Val | Lys | Ile | Gly | Trp | Asp | Ser | Asn |
|     |     | 260 |     | 265 |     | 270 |     |     |     |     |     |     |     |     |     |
| Pro | Asn | Phe | Ser | Gly | Thr | Gly | Phe | Arg | Ser | Asp | Thr | Ala | Ile | Ile | Gly |
|     |     | 275 |     | 280 |     | 285 |     |     |     |     |     |     |     |     |     |
| Phe | Phe | Pro | Ile | Tyr | Tyr | Pro | Trp | Met | Ile | Val | Lys | Ser | Asn | Gly | Ser |
|     |     | 290 |     | 295 |     | 300 |     |     |     |     |     |     |     |     |     |
| Pro | Val | Tyr | Lys | Tyr | Asp | Thr | Pro | Ala | Thr | Gln | Asn | Gly | Gln | Asn | Leu |
| 305 |     | 310 |     | 315 |     | 320 |     |     |     |     |     |     |     |     |     |
| Ile | Ile | Leu | Gln | Arg | Phe | Asp | Ile | Asn | Asn | Tyr | Asn | Val | Ser | Ile | Ala |
|     |     | 325 |     | 330 |     | 335 |     |     |     |     |     |     |     |     |     |
| Phe | Tyr | Lys | Val | Phe | Gln | Asn | Ala | Asn | Gly | Trp | Ile | Gly | Asn | Met | Gly |
|     |     | 340 |     | 345 |     | 350 |     |     |     |     |     |     |     |     |     |
| Asn | Pro | Ser | Gly | Val | Ile | Met | Gly | Ser | Asn | Ser | Val | Tyr | Ala | Gly | Phe |
|     |     | 355 |     | 360 |     | 365 |     |     |     |     |     |     |     |     |     |
| Thr | Gly | Thr | Ala | Leu | Lys | Arg | Asp | Ala | Ala | Thr | Ile | Phe | Leu | Ser | Cys |
|     |     | 370 |     | 375 |     | 380 |     |     |     |     |     |     |     |     |     |
| Gly | Gly | Thr | His | Phe | Ala | Lys | Lys | Phe | Thr | Trp | Lys | Phe | Ala | Thr | Gln |
| 385 |     | 390 |     | 395 |     | 400 |     |     |     |     |     |     |     |     |     |
| Tyr | Ser | Asn | Ser | Val | Val | Ser | Trp | Glu | Ala | Arg | Ala | Met | Ile | Ser | Leu |
|     |     | 405 |     | 410 |     | 415 |     |     |     |     |     |     |     |     |     |
| Gly | Tyr | Lys | Phe | Thr | Glu | Tyr | Leu | Ser | Gly | Ser | Val | Asp | Leu | Ala | Tyr |
|     |     | 420 |     | 425 |     | 430 |     |     |     |     |     |     |     |     |     |
| Tyr | Gly | Val | Tyr | Thr | Asn | Lys | Gly | Phe | Lys | Pro | Gly | Glu | Asn | Gly | Pro |
|     |     | 435 |     | 440 |     | 445 |     |     |     |     |     |     |     |     |     |
| Val | Pro | Lys | Asp | Phe | Pro | Ala | Leu | Tyr | Ser | Asp | Arg | Ser | Ala | Leu | Tyr |
|     |     | 450 |     | 455 |     | 460 |     |     |     |     |     |     |     |     |     |
| Thr | Ala | Leu | Val | Ala | Ser | Phe |     |     |     |     |     |     |     |     |     |
| 465 |     | 470 |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

|            |     |     |     |     |            |            |            |            |     |      |     |     |     |     |     |      |  |
|------------|-----|-----|-----|-----|------------|------------|------------|------------|-----|------|-----|-----|-----|-----|-----|------|--|
| Thr        | His | Phe | Ala | Lys | Lys        | Phe        | Thr        | Trp        | Lys | Phe  | Ala | Thr | Gln | Tyr | Ser |      |  |
|            |     |     | 390 |     |            |            |            | 395        |     |      |     |     | 400 |     |     |      |  |
| AAT        | TCA | GTG | GTT | TCT | TGG        | GAA        | GCG        | AGA        | GCG | ATG  | ATC | TCT | TTA | GGT | TAT | 1304 |  |
| Asn        | Ser | Val | Val | Ser | Trp        | Glu        | Ala        | Arg        | Ala | Met  | Ile | Ser | Leu | Gly | Tyr |      |  |
|            |     | 405 |     |     |            |            | 410        |            |     |      |     | 415 |     |     |     |      |  |
| AAA        | TTC | ACT | GAA | TAC | TTG        | AGC        | GGT        | AGC        | GTG | GAT  | CTT | GCA | TAT | TAT | GGC | 1352 |  |
| Lys        | Phe | Thr | Glu | Tyr | Leu        | Ser        | Gly        | Ser        | Val | Asp  | Leu | Ala | Tyr | Tyr | Gly |      |  |
|            |     | 420 |     |     |            | 425        |            |            |     |      | 430 |     |     |     |     |      |  |
| GTG        | TAT | ACT | AAC | AAA | GGA        | TTT        | AAA        | CCG        | GGT | GAA  | AAC | GGG | CCT | GTG | CCT | 1400 |  |
| Val        | Tyr | Thr | Asn | Lys | Gly        | Phe        | Lys        | Pro        | Gly | Glu  | Asn | Gly | Pro | Val | Pro |      |  |
| 435        |     |     |     |     | 440        |            |            |            |     | 445  |     |     |     |     | 450 |      |  |
| AAA        | GAC | TTC | CCC | GCC | CTT        | TAT        | TCT        | GAC        | AGG | AGC  | GCG | TTA | TAC | ACG | GCT | 1448 |  |
| Lys        | Asp | Phe | Pro | Ala | Leu        | Tyr        | Ser        | Asp        | Arg | Ser  | Ala | Leu | Tyr | Thr | Ala |      |  |
|            |     |     | 455 |     |            |            |            | 460        |     |      |     |     | 465 |     |     |      |  |
| CTA        | GTA | GCA | TCT | TTT | TGATGCTACC | CTATGATTAT | GGTGGGCGTC | TTTTGATGCT | G   | 1504 |     |     |     |     |     |      |  |
| Leu        | Val | Ala | Ser | Phe |            |            |            |            |     |      |     |     |     |     |     |      |  |
|            |     |     | 470 |     |            |            |            |            |     |      |     |     |     |     |     |      |  |
| TTTCTCTAGT | CT  |     |     |     |            |            |            |            |     |      |     |     |     |     |     | 1516 |  |

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Lys | Lys | Ala | Ser | Gln | Val | Leu | Phe | Phe | Gly | Ala | Phe | Leu | Ser | Ser |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser | Leu | Gln | Gly | Phe | Glu | Ala | Lys | Leu | Asn | Gly | Phe | Val | Asp | Gln | Ser |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ser | Thr | Ile | Gly | Phe | Asn | Gln | His | Lys | Ile | Asn | Lys | Glu | Arg | Gly | Ile |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Tyr | Pro | Met | Gln | Gln | Phe | Ala | Thr | Ile | Ala | Gly | Tyr | Leu | Gly | Leu | Gly |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Phe | Ser | Leu | Leu | Pro | Lys | Lys | Val | Ser | Asp | His | Val | Leu | Lys | Gly | Lys |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Ile | Gly | Gly | Met | Val | Gly | Ser | Ile | Phe | Tyr | Asp | Gly | Thr | Lys | Lys | Phe |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Glu | Asp | Ser | Ser | Val | Ala | Tyr | Asn | Leu | Phe | Gly | Tyr | Tyr | Asp | Gly | Phe |  |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Met | Gly | Gly | Tyr | Thr | Asn | Ile | Leu | Gln | Ser | Asp | Asp | Leu | Ala | Thr | Gln |  |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |
| Asn | Met | Lys | Tyr | Asn | Lys | Asn | Val | Arg | Asn | Tyr | Val | Phe | Ser | Asp | Ala |  |  |

| 165                                                             | 170 | 175 |      |
|-----------------------------------------------------------------|-----|-----|------|
| GGG CAA TAC AAG AAA GCG CGC TTG ACT TGG TTT AGC TCT TTT GGG AGG |     |     | 632  |
| Gly Gln Tyr Lys Lys Ala Arg Leu Thr Trp Phe Ser Ser Phe Gly Arg |     |     |      |
| 180                                                             | 185 | 190 |      |
| GCG TTC GCT TAC GGC TCG TTT TTG ATG GAT TGG TTT GCC GCT AGG ACC |     |     | 680  |
| Ala Phe Ala Tyr Gly Ser Phe Leu Met Asp Trp Phe Ala Ala Arg Thr |     |     |      |
| 195                                                             | 200 | 205 | 210  |
| ACT TAT AGC GGA GGT TTT ACC AAA AAC GAT AAG GGA GGT TAT GAT AGC |     |     | 728  |
| Thr Tyr Ser Gly Gly Phe Thr Lys Asn Asp Lys Gly Gly Tyr Asp Ser |     |     |      |
|                                                                 | 215 | 220 | 225  |
| CAT GGG CGA AAG GTG CTT TAT GGC ACG CAT GCG GTG CAA CTC ACC TAT |     |     | 776  |
| His Gly Arg Lys Val Leu Tyr Gly Thr His Ala Val Gln Leu Thr Tyr |     |     |      |
|                                                                 | 230 | 235 | 240  |
| AAA CCT CAT CGT TTC CTC ATA GAA GGC TTT TAT TAC CTT TCG CCT CAA |     |     | 824  |
| Lys Pro His Arg Phe Leu Ile Glu Gly Phe Tyr Tyr Leu Ser Pro Gln |     |     |      |
|                                                                 | 245 | 250 | 255  |
| ATC TTT AAC GCT CCG GGC GTT AAG ATT GGT TGG GAT TCT AAC CCT AAT |     |     | 872  |
| Ile Phe Asn Ala Pro Gly Val Lys Ile Gly Trp Asp Ser Asn Pro Asn |     |     |      |
|                                                                 | 260 | 265 | 270  |
| TTT AGC GGC ACA GGC TTT CGC TCT GAT ACA GCT ATC ATA GGG TTT TTC |     |     | 920  |
| Phe Ser Gly Thr Gly Phe Arg Ser Asp Thr Ala Ile Ile Gly Phe Phe |     |     |      |
|                                                                 | 275 | 280 | 285  |
| CCC ATT TAC TAC CCT TGG ATG ATC GTT AAA TCC AAT GGA AGC CCG GTC |     |     | 968  |
| Pro Ile Tyr Tyr Pro Trp Met Ile Val Lys Ser Asn Gly Ser Pro Val |     |     |      |
|                                                                 | 295 | 300 | 305  |
| TAT AAA TAC GAC ACG CCT GCC ACT CAA AAT GGG CAA AAC CTC ATT ATC |     |     | 1016 |
| Tyr Lys Tyr Asp Thr Pro Ala Thr Gln Asn Gly Gln Asn Leu Ile Ile |     |     |      |
|                                                                 | 310 | 315 | 320  |
| CTC CAA CGC TTT GAC ATC AAC AAT TAC AAT GTT TCC ATC GCT TTT TAT |     |     | 1064 |
| Leu Gln Arg Phe Asp Ile Asn Asn Tyr Asn Val Ser Ile Ala Phe Tyr |     |     |      |
|                                                                 | 325 | 330 | 335  |
| AAA GTC TTT CAA AAC GCT AAT GGT TGG ATA GGC AAC ATG GGG AAT CCA |     |     | 1112 |
| Lys Val Phe Gln Asn Ala Asn Gly Trp Ile Gly Asn Met Gly Asn Pro |     |     |      |
|                                                                 | 340 | 345 | 350  |
| AGC GGT GTG ATC ATG GGG AGT AAC AGC GTC TAT GCG GGT TTT ACA GGC |     |     | 1160 |
| Ser Gly Val Ile Met Gly Ser Asn Ser Val Tyr Ala Gly Phe Thr Gly |     |     |      |
|                                                                 | 355 | 360 | 365  |
| ACA GCC CTT AAA AGA GAT GCC GCT ACC ATT TTC CTT TCT TGT GGC GGC |     |     | 1208 |
| Thr Ala Leu Lys Arg Asp Ala Ala Thr Ile Phe Leu Ser Cys Gly Gly |     |     |      |
|                                                                 | 375 | 380 | 385  |
| ACT CAT TTT GCC AAA AAA TTC ACA TGG AAA TTC GCC ACG CAA TAC TCC |     |     | 1256 |



- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 51...1463  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTTATCTTTA AAAGTATTTG CATTTATCAA TCTCATTTTA GGAGGCATGC ATG AAA  | 56  |
| Met Lys                                                         |     |
| 1                                                               |     |
| AAG GCA AGT CAG GTT TTA TTC TTT GGG GCA TTT TTA AGC TCT TCT TTG | 104 |
| Lys Ala Ser Gln Val Leu Phe Phe Gly Ala Phe Leu Ser Ser Ser Leu |     |
| 5 10 15                                                         |     |
| CAA GGT TTT GAA GCT AAG CTC AAC GGC TTT GTG GAT CAA TCC AGC ACT | 152 |
| Gln Gly Phe Glu Ala Lys Leu Asn Gly Phe Val Asp Gln Ser Ser Thr |     |
| 20 25 30                                                        |     |
| ATC GGT TTT AAC CAG CAT AAA ATC AAT AAA GAA AGA GGT ATC TAC CCT | 200 |
| Ile Gly Phe Asn Gln His Lys Ile Asn Lys Glu Arg Gly Ile Tyr Pro |     |
| 35 40 45 50                                                     |     |
| ATG CAG CAA TTC GCA ACG ATT GCG GGC TAT TTA GGG CTT GGT TTT AGC | 248 |
| Met Gln Gln Phe Ala Thr Ile Ala Gly Tyr Leu Gly Leu Gly Phe Ser |     |
| 55 60 65                                                        |     |
| CTG TTA CCC AAA AAG GTT TCA GAC CAT GTT CTA AAA GGC AAA ATA GGA | 296 |
| Leu Leu Pro Lys Lys Val Ser Asp His Val Leu Lys Gly Lys Ile Gly |     |
| 70 75 80                                                        |     |
| GGC ATG GTG GGA TCT ATT TTC TAT GAT GGC ACG AAG AAG TTT GAA GAC | 344 |
| Gly Met Val Gly Ser Ile Phe Tyr Asp Gly Thr Lys Lys Phe Glu Asp |     |
| 85 90 95                                                        |     |
| AGC TCT GTA GCT TAC AAC CTC TTT GGT TAT TAT GAT GGG TTC ATG GGG | 392 |
| Ser Ser Val Ala Tyr Asn Leu Phe Gly Tyr Tyr Asp Gly Phe Met Gly |     |
| 100 105 110                                                     |     |
| GGT TAT ACA AAC ATC TTA CAA AGC GAT GAT TTA GCG ACA CAA AAC ATG | 440 |
| Gly Tyr Thr Asn Ile Leu Gln Ser Asp Asp Leu Ala Thr Gln Asn Met |     |
| 115 120 125 130                                                 |     |
| AAA TAC AAT AAA AAT GTC CGC AAC TAT GTC TTT AGC GAC GCG TAT TTA | 488 |
| Lys Tyr Asn Lys Asn Val Arg Asn Tyr Val Phe Ser Asp Ala Tyr Leu |     |
| 135 140 145                                                     |     |
| GAA TAC GCT TAT AAG AAT TAT TTT GAA ATA AAA GCC GGG CGC TAT TTA | 536 |
| Glu Tyr Ala Tyr Lys Asn Tyr Phe Glu Ile Lys Ala Gly Arg Tyr Leu |     |
| 150 155 160                                                     |     |
| TCC ACT ATG CCT TAT AAA AGC GGT CAA ACG CAA GGC TTT CAA ATT TCT | 584 |
| Ser Thr Met Pro Tyr Lys Ser Gly Gln Thr Gln Gly Phe Gln Ile Ser |     |

CAATCAACTC TCGTG

810

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Asn Lys Thr Thr Val Lys Ile Leu Met Gly Met Ala Leu Leu Ser
 1 5 10 15
Ser Leu Gln Ala Ala Glu Ala Glu Leu Asp Glu Lys Ser Lys Lys Pro
 20 25 30
Lys Phe Ala Asp Arg Asn Thr Phe Tyr Leu Gly Val Gly Tyr Gln Leu
 35 40 45
Ser Ala Ile Asn Thr Ser Phe Ser Thr Glu Ser Val Asp Lys Ser Tyr
 50 55 60
Phe Met Thr Gly Asn Gly Phe Gly Val Val Leu Gly Gly Lys Phe Val
 65 70 75 80
Ala Lys Thr Gln Ala Val Glu His Val Gly Phe Arg Tyr Gly Leu Phe
 85 90 95
Tyr Asp Gln Thr Phe Ser Ser His Lys Ser Tyr Ile Ser Thr Tyr Gly
 100 105 110
Leu Glu Phe Ser Gly Leu Trp Asp Ala Phe Asn Ser Pro Lys Met Phe
 115 120 125
Leu Gly Leu Glu Phe Gly Leu Gly Ile Ala Gly Ala Thr Tyr Met Pro
 130 135 140
Gly Gly Ala Met His Gly Ile Ile Ala Gln Asn Leu Gly Lys Glu Asn
 145 150 155 160
Ser Leu Phe Gln Leu Leu Val Lys Val Gly Phe Arg Phe Gly Phe Leu
 165 170 175
His Asn Glu Ile Thr Phe Gly Leu Lys Phe Pro Val Ile Pro Asn Lys
 180 185 190
Arg Thr Glu Ile Ile Asp Gly Leu Ser Thr Thr Thr Leu Trp His Arg
 195 200 205
Leu Pro Val Ala Tyr Phe Asn Tyr Ile Tyr Asn Phe
 210 215 220

```

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

|     |     |     |     |     |     |            |            |            |          |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|------------|------------|------------|----------|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Leu | Met | Gly | Met | Ala        | Leu        | Leu        | Ser      | Ser | Leu | Gln | Ala | Ala | Glu |     |
|     |     |     | 10  |     |     |            |            | 15         |          |     |     |     | 20  |     |     |     |
| GCA | GAG | CTT | GAT | GAA | AAA | TCA        | AAA        | AAA        | CCT      | AAA | TTT | GCG | GAC | AGG | AAT | 211 |
| Ala | Glu | Leu | Asp | Glu | Lys | Ser        | Lys        | Lys        | Pro      | Lys | Phe | Ala | Ala | Asp | Arg | Asn |
|     |     | 25  |     |     |     |            | 30         |            |          |     |     | 35  |     |     |     |     |
| ACA | TTT | TAT | TTA | GGG | GTT | GGG        | TAT        | CAA        | CTT      | AGT | GCG | ATC | AAC | ACA | TCT | 259 |
| Thr | Phe | Tyr | Leu | Gly | Val | Gly        | Tyr        | Gln        | Leu      | Ser | Ala | Ile | Asn | Thr | Ser |     |
|     | 40  |     |     |     |     | 45         |            |            |          |     | 50  |     |     |     |     |     |
| TTT | AGC | ACC | GAG | TCT | GTA | GAT        | AAA        | TCG        | TAT      | TTT | ATG | ACC | GGC | AAT | GGC | 307 |
| Phe | Ser | Thr | Glu | Ser | Val | Asp        | Lys        | Ser        | Tyr      | Phe | Met | Thr | Gly | Asn | Gly |     |
| 55  |     |     |     |     | 60  |            |            |            |          | 65  |     |     |     |     | 70  |     |
| TTT | GGT | GTG | GTG | TTA | GGG | GGG        | AAA        | TTT        | GTG      | GCT | AAA | ACG | CAA | GCT | GTA | 355 |
| Phe | Gly | Val | Val | Leu | Gly | Gly        | Lys        | Phe        | Val      | Ala | Lys | Thr | Gln | Ala | Val |     |
|     |     |     |     | 75  |     |            |            |            | 80       |     |     |     |     | 85  |     |     |
| GAG | CAT | GTG | GGT | TTC | CGT | TAC        | GGG        | TTG        | TTT      | TAT | GAT | CAG | ACC | TTT | TCT | 403 |
| Glu | His | Val | Gly | Phe | Arg | Tyr        | Gly        | Leu        | Phe      | Tyr | Asp | Gln | Thr | Phe | Ser |     |
|     |     |     | 90  |     |     |            |            | 95         |          |     |     |     | 100 |     |     |     |
| TCT | CAC | AAA | TCC | TAT | ATT | TCT        | ACC        | TAT        | GGT      | TTA | GAA | TTT | AGC | GGT | TTG | 451 |
| Ser | His | Lys | Ser | Tyr | Ile | Ser        | Thr        | Tyr        | Gly      | Leu | Glu | Phe | Ser | Gly | Leu |     |
|     |     | 105 |     |     |     |            | 110        |            |          |     |     | 115 |     |     |     |     |
| TGG | GAC | GCT | TTC | AAT | TCG | CCA        | AAG        | ATG        | TTT      | TTA | GGG | TTA | GAG | TTT | GGC | 499 |
| Trp | Asp | Ala | Phe | Asn | Ser | Pro        | Lys        | Met        | Phe      | Leu | Gly | Leu | Glu | Phe | Gly |     |
|     | 120 |     |     |     |     | 125        |            |            |          |     | 130 |     |     |     |     |     |
| TTA | GGC | ATC | GCT | GGG | GCG | ACT        | TAT        | ATG        | CCA      | GGA | GGG | GCT | ATG | CAT | GGG | 547 |
| Leu | Gly | Ile | Ala | Gly | Ala | Thr        | Tyr        | Met        | Pro      | Gly | Gly | Ala | Met | His | Gly |     |
| 135 |     |     |     |     | 140 |            |            |            |          | 145 |     |     |     |     | 150 |     |
| ATT | ATC | GCT | CAA | AAT | TTA | GGC        | AAA        | GAA        | AAT      | TCG | CTT | TTC | CAA | TTG | CTT | 595 |
| Ile | Ile | Ala | Gln | Asn | Leu | Gly        | Lys        | Glu        | Asn      | Ser | Leu | Phe | Gln | Leu | Leu |     |
|     |     |     |     | 155 |     |            |            | 160        |          |     |     |     |     | 165 |     |     |
| GTG | AAA | GTG | GGT | TTT | CGT | TTT        | GGC        | TTT        | TTG      | CAC | AAT | GAA | ATC | ACT | TTC | 643 |
| Val | Lys | Val | Gly | Phe | Arg | Phe        | Gly        | Phe        | Leu      | His | Asn | Glu | Ile | Thr | Phe |     |
|     |     |     | 170 |     |     |            |            | 175        |          |     |     |     | 180 |     |     |     |
| GGG | TTG | AAA | TTC | CCT | GTC | ATT        | CCT        | AAC        | AAA      | AGA | ACG | GAA | ATC | ATT | GAT | 691 |
| Gly | Leu | Lys | Phe | Pro | Val | Ile        | Pro        | Asn        | Lys      | Arg | Thr | Glu | Ile | Ile | Asp |     |
|     |     | 185 |     |     |     |            | 190        |            |          |     |     | 195 |     |     |     |     |
| GGC | TTG | AGC | ACG | ACT | ACT | TTA        | TGG        | CAC        | CGC      | TTA | CCG | GTA | GCT | TAT | TTC | 739 |
| Gly | Leu | Ser | Thr | Thr | Thr | Leu        | Trp        | His        | Arg      | Leu | Pro | Val | Ala | Tyr | Phe |     |
|     | 200 |     |     |     |     | 205        |            |            |          |     | 210 |     |     |     |     |     |
| AAT | TAT | ATC | TAT | AAT | TTT | TAGATATGGT | TATTTAGAGG | TTTTAGATTT | GACAAAAT |     |     |     |     |     |     | 795 |
| Asn | Tyr | Ile | Tyr | Asn | Phe |            |            |            |          |     |     |     |     |     |     |     |
| 215 |     |     |     |     | 220 |            |            |            |          |     |     |     |     |     |     |     |

```

Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln Phe Ser Pro
 260 265 270
Gly Thr Tyr Tyr Ser Pro Gly Val Val Val Gly Tyr Asp Ser Asn Pro
 275 280 285
Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala Tyr Ile Leu
 290 295 300
Leu Pro Val His Asp Pro Leu Arg Arg Asp Thr Tyr Arg Tyr Ala Ile
 305 310 315 320
Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln Arg Phe Asp
 325 330 335
Tyr Asn Glu Phe Asn Phe Gly Gly Ala Phe Tyr Lys Val Trp Lys Asn
 340 345 350
Ala Asn Ala Tyr Ile Gly Thr Thr Gly Asn Pro Leu Gly Ile Asp Phe
 355 360 365
Trp Thr Asn Ser Val Tyr Asp Ile Gly Gln Ala Leu Ser His Val Val
 370 375 380
Thr Ala Asp Ala Val Ser Gly Trp Val Phe Gly Gly Gly Val His Lys
 385 390 395 400
Lys Trp Leu Trp Gly Thr Leu Trp Arg Trp Thr Ser Gly Thr Leu Ala
 405 410 415
Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile Ser Lys Ser
 420 425 430
Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met Thr His Ala
 435 440 445
Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser Lys Ala Leu
 450 455 460
Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala Lys Phe
 465 470 475

```

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...757
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

CTAATATTTA TTTTAAACTT TGTTATTATT TAAGGTGTGA TTTGATTTTA GTCTGTATGG 60
GGCAAGTGTG GGGCAGGATA ACATAAGGAA TTGGGTT ATG AAT AAA ACA ACG GTT 115
 Met Asn Lys Thr Thr Val
 1 5

AAA ATA TTA ATG GGC ATG GCG TTA TTA TCA TCG CTT CAA GCC GCA GAG 163

```

AAA GCG CTT TAT TCA GAC AGG AGT CAT TTG ATG ACA ACT CTT AGC GCT 1503  
 Lys Ala Leu Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala  
                   465                                  470                                  475

AAA TTC TAACCAATCG CTTTAAGCTG TTTATTAAAG CGTTAAAAAT CCCTTAATAA AA 1561  
 Lys Phe

A

1562

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Ser | Thr | Pro | Leu | Lys | Asn | Gln | Val | Phe | Cys | Gly | Leu | Tyr | 1   | 5   | 10  | 15  |
| Val | Leu | Ser | Leu | Ser | Ala | Ser | Leu | Gln | Ala | Phe | Asp | Tyr | Lys | Ile | Glu | 20  | 25  | 30  |     |
| Val | Ser | Ala | Glu | Ser | Phe | Ser | Lys | Val | Gly | Phe | Asn | Lys | Lys | Lys | Ile | 35  | 40  | 45  |     |
| Asp | Ile | Ala | Arg | Gly | Ile | Tyr | Pro | Thr | Glu | Thr | Phe | Val | Thr | Ala | Val | 50  | 55  | 60  |     |
| Gly | Gln | Gly | Asn | Ile | Tyr | Ala | Asp | Phe | Leu | Pro | Lys | Gly | Leu | Lys | Asp | 65  | 70  | 75  | 80  |
| Gln | Gly | His | Val | Leu | Glu | Gly | Lys | Ile | Gly | Gly | Thr | Leu | Gly | Gly | Val | 85  | 90  | 95  |     |
| Ala | Tyr | Asp | Ser | Thr | Lys | Phe | Asn | Gln | Gly | Gly | Ser | Val | Ile | Tyr | Asn | 100 | 105 | 110 |     |
| Tyr | Ile | Gly | Tyr | Trp | Asp | Gly | Tyr | Leu | Gly | Gly | Lys | Arg | Ala | Leu | Leu | 115 | 120 | 125 |     |
| Asp | Gly | Thr | Ser | Ile | His | Glu | Cys | Ala | Leu | Gly | Ser | Asp | Gly | Lys | Val | 130 | 135 | 140 |     |
| Ile | Asp | Ser | Ile | Ala | Cys | Gly | Asn | Ala | Arg | Ala | Asn | Lys | Ile | Arg | Arg | 145 | 150 | 155 | 160 |
| Asn | Tyr | Leu | Met | Asn | Asn | Ala | Phe | Leu | Glu | Tyr | Arg | Tyr | Lys | Asp | Ile | 165 | 170 | 175 |     |
| Phe | Leu | Ala | Lys | Gly | Gly | Arg | Tyr | Gln | Ser | Asn | Ala | Pro | Tyr | Met | Ser | 180 | 185 | 190 |     |
| Gly | Tyr | Thr | Gln | Gly | Phe | Glu | Ile | Ser | Ala | Lys | Val | Lys | Asp | Lys | Asn | 195 | 200 | 205 |     |
| Glu | Gly | Ile | His | Lys | Leu | Trp | Trp | Phe | Ser | Ser | Trp | Gly | Arg | Ala | Phe | 210 | 215 | 220 |     |
| Ala | Tyr | Gly | Glu | Trp | Ile | Tyr | Asp | Phe | Tyr | Ser | Pro | Arg | Thr | Val | Val | 225 | 230 | 235 | 240 |
| Lys | Asn | Gly | Arg | Thr | Leu | Asn | Tyr | Gly | Ile | His | Leu | Val | Asn | Tyr | Thr | 245 | 250 | 255 |     |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| ACC GTG GTT AAA AAC GGG CGC ACT TTG AAT TAT GGT ATC CAT TTA GTG | 831  |
| Thr Val Val Lys Asn Gly Arg Thr Leu Asn Tyr Gly Ile His Leu Val |      |
| 240 245 250                                                     |      |
| AAT TAT ACT TAT GAA AGA AAA GGG GTT AGC GTT AGC CCT TTT TTC CAA | 879  |
| Asn Tyr Thr Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln |      |
| 255 260 265                                                     |      |
| TTT TCG CCT GGG ACT TAT TAT AGC CCT GGG GTG GTT GTA GGC TAT GAT | 927  |
| Phe Ser Pro Gly Thr Tyr Tyr Ser Pro Gly Val Val Val Gly Tyr Asp |      |
| 270 275 280 285                                                 |      |
| AGT AAC CCT AAT TTT AAC GGC GTT GGC TTT AGA TCC GAA ACA AAA GCT | 975  |
| Ser Asn Pro Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala |      |
| 290 295 300                                                     |      |
| TAT ATT TTG CTC CCT GTC CAT GAC CCC TTA AGA AGG GAT ACT TAT CGT | 1023 |
| Tyr Ile Leu Leu Pro Val His Asp Pro Leu Arg Arg Asp Thr Tyr Arg |      |
| 305 310 315                                                     |      |
| TAC GCT ATA AAG GCT GGC ACT GCC GGG CAA AGC TTG CTC ATT AGG CAA | 1071 |
| Tyr Ala Ile Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln |      |
| 320 325 330                                                     |      |
| CGA TTT GAT TAC AAT GAA TTT AAT TTT GGG GGA GCG TTT TAT AAA GTA | 1119 |
| Arg Phe Asp Tyr Asn Glu Phe Asn Phe Gly Gly Ala Phe Tyr Lys Val |      |
| 335 340 345                                                     |      |
| TGG AAA AAC GCA AAC GCT TAC ATC GGC ACG ACA GGA AAC CCT TTA GGC | 1167 |
| Trp Lys Asn Ala Asn Ala Tyr Ile Gly Thr Thr Gly Asn Pro Leu Gly |      |
| 350 355 360 365                                                 |      |
| ATT GAT TTT TGG ACC AAT AGC GTT TAT GAT ATA GGG CAA GCT TTA AGC | 1215 |
| Ile Asp Phe Trp Thr Asn Ser Val Tyr Asp Ile Gly Gln Ala Leu Ser |      |
| 370 375 380                                                     |      |
| CAT GTG GTA ACC GCT GAT GCC GTC TCT GGT TGG GTT TTT GGT GGC GGC | 1263 |
| His Val Val Thr Ala Asp Ala Val Ser Gly Trp Val Phe Gly Gly Gly |      |
| 385 390 395                                                     |      |
| GTG CAT AAA AAG TGG CTG TGG GGG ACT TTA TGG CGT TGG ACT AGC GGC | 1311 |
| Val His Lys Lys Trp Leu Trp Gly Thr Leu Trp Arg Trp Thr Ser Gly |      |
| 400 405 410                                                     |      |
| ACT TTA GCC AAT GAA GCG AGT GCG GCT GTT AAT GTG GGC TAT AAG ATC | 1359 |
| Thr Leu Ala Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile |      |
| 415 420 425                                                     |      |
| AGT AAG AGT TTG ACA GCG AGC GTG AAA TTA GAA TAT TTG GGC GTG ATG | 1407 |
| Ser Lys Ser Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met |      |
| 430 435 440 445                                                 |      |
| ACG CAT GCA GGC TTT ACG GTA GGG AGT TAC AGG CCC ACG CCC GGC TCT | 1455 |
| Thr His Ala Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser |      |
| 450 455 460                                                     |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Tyr | Val | Leu | Ser | Leu | Ser | Ala | Ser | Leu | Gln | Ala | Phe | Asp | Tyr |     |
| 15  |     |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |
| AAA | ATT | GAA | GTT | TCA | GCG | GAG | TCC | TTT | TCT | AAA | GTT | GGC | TTT | AAT | AAA | 207 |
| Lys | Ile | Glu | Val | Ser | Ala | Glu | Ser | Phe | Ser | Lys | Val | Gly | Phe | Asn | Lys |     |
| 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| AAA | AAG | ATT | GAT | ATA | GCT | AGG | GGG | ATT | TAT | CCT | ACA | GAG | ACT | TTT | GTA | 255 |
| Lys | Lys | Ile | Asp | Ile | Ala | Arg | Gly | Ile | Tyr | Pro | Thr | Glu | Thr | Phe | Val |     |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| ACC | GCT | GTA | GGG | CAG | GGC | AAT | ATC | TAT | GCG | GAT | TTT | TTA | CCC | AAA | GGC | 303 |
| Thr | Ala | Val | Gly | Gln | Gly | Asn | Ile | Tyr | Ala | Asp | Phe | Leu | Pro | Lys | Gly |     |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |
| CTT | AAA | GAT | CAA | GGG | CAT | GTT | TTA | GAG | GGA | AAA | ATC | GGT | GGC | ACG | CTA | 351 |
| Leu | Lys | Asp | Gln | Gly | His | Val | Leu | Glu | Gly | Lys | Ile | Gly | Gly | Thr | Leu |     |
|     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |
| GGA | GGG | GTC | GCT | TAT | GAT | AGC | ACG | AAA | TTC | AAT | CAA | GGC | GGA | TCG | GTT | 399 |
| Gly | Gly | Val | Ala | Tyr | Asp | Ser | Thr | Lys | Phe | Asn | Gln | Gly | Gly | Ser | Val |     |
|     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |
| ATT | TAT | AAC | TAC | ATC | GGT | TAT | TGG | GAT | GGC | TAT | TTA | GGG | GGT | AAA | AGA | 447 |
| Ile | Tyr | Asn | Tyr | Ile | Gly | Tyr | Trp | Asp | Gly | Tyr | Leu | Gly | Gly | Lys | Arg |     |
| 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| GCC | TTG | CTT | GAT | GGC | ACG | AGT | ATC | CAT | GAG | TGC | GCG | CTT | GGA | TCT | GAT | 495 |
| Ala | Leu | Leu | Asp | Gly | Thr | Ser | Ile | His | Glu | Cys | Ala | Leu | Gly | Ser | Asp |     |
|     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |
| GGC | AAG | GTG | ATT | GAT | TCT | ATA | GCG | TGC | GGG | AAC | GCT | AGG | GCC | AAT | AAA | 543 |
| Gly | Lys | Val | Ile | Asp | Ser | Ile | Ala | Cys | Gly | Asn | Ala | Arg | Ala | Asn | Lys |     |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |
| ATC | CGC | CGT | AAT | TAC | TTG | ATG | AAT | AAC | GCT | TTT | TTA | GAA | TAC | CGC | TAT | 591 |
| Ile | Arg | Arg | Asn | Tyr | Leu | Met | Asn | Asn | Ala | Phe | Leu | Glu | Tyr | Arg | Tyr |     |
|     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |
| AAA | GAT | ATT | TTT | TTA | GCT | AAG | GGA | GGG | CGT | TAT | CAA | TCC | AAT | GCT | CCT | 639 |
| Lys | Asp | Ile | Phe | Leu | Ala | Lys | Gly | Gly | Arg | Tyr | Gln | Ser | Asn | Ala | Pro |     |
|     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |
| TAT | ATG | AGC | GGT | TAC | ACG | CAA | GGC | TTT | GAA | ATC | AGC | GCT | AAA | GTC | AAG | 687 |
| Tyr | Met | Ser | Gly | Tyr | Thr | Gln | Gly | Phe | Glu | Ile | Ser | Ala | Lys | Val | Lys |     |
| 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |
| GAT | AAA | AAT | GAA | GGA | ATC | CAC | AAA | TTA | TGG | TGG | TTT | AGC | TCA | TGG | GGT | 735 |
| Asp | Lys | Asn | Glu | Gly | Ile | His | Lys | Leu | Trp | Trp | Phe | Ser | Ser | Trp | Gly |     |
|     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |
| AGG | GCG | TTC | GCT | TAT | GGG | GAG | TGG | ATT | TAT | GAT | TTT | TAT | TCT | CCA | AGA | 783 |
| Arg | Ala | Phe | Ala | Tyr | Gly | Glu | Trp | Ile | Tyr | Asp | Phe | Tyr | Ser | Pro | Arg |     |
|     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |

```

Ser Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe
 195 200 205
Val Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe
 210 215 220
Ile Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val
 225 230 235 240
Gln Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe
 245 250 255
Thr Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp
 260 265 270
Ala Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr
 275 280 285
Phe Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro
 290 295 300
Ala Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys
 305 310 315 320
Phe Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe
 325 330 335
Ala Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys
 340 345 350
Arg Val Arg Leu Asp Ala Met Val Ala Phe Gly Asp Tyr Gln Glu Tyr
 355 360 365
Ser Leu Met Ser Ser Phe Arg Val Trp Thr Tyr Arg Ser Leu Ser Phe
 370 375 380
Asp Met Gly Gly Gly Tyr Val Tyr Ala Tyr Asn Ser Lys Ala Thr Arg
 385 390 395 400
Lys Ser Leu Gly Asn Ser Ser Phe Val Phe Phe Gly Lys Phe Leu Phe
 405 410 415

```

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...1509
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

TTATGCTTCT TTGTTTTTAG ATCAGTTAAG AATTGTAGTC TTAAAGATGT ATTGGCTATT 60
AAAAGGAAAA AA ATG AAA AAT AGC ACG CCT TTA AAG AAT CAA GTT TTT TGT 111
 Met Lys Asn Ser Thr Pro Leu Lys Asn Gln Val Phe Cys
 1 5 10

GGG TTA TAT GTT TTA AGT TTG AGC GCT TCT TTG CAA GCG TTT GAT TAT 159

```



```

GTG CGT TTA GAC GCG ATG GTG GCT TTT GGG GAT TAC CAA GAA TAT TCT 1164
Val Arg Leu Asp Ala Met Val Ala Phe Gly Asp Tyr Gln Glu Tyr Ser
 355 360 365

TTA ATG AGC AGT TTT AGG GTT TGG ACT TAT AGG AGT TTG TCT TTT GAT 1212
Leu Met Ser Ser Phe Arg Val Trp Thr Tyr Arg Ser Leu Ser Phe Asp
 370 375 380 385

ATG GGT GGG GGG TAT GTG TAT GCT TAC AAT TCT AAA GCC ACG AGA AAA 1260
Met Gly Gly Gly Tyr Val Tyr Ala Tyr Asn Ser Lys Ala Thr Arg Lys
 390 395 400

AGT CTT GGA AAT AGT TCT TTT GTC TTT TTT GGG AAG TTT TTG TTT TAAAA 1310
Ser Leu Gly Asn Ser Ser Phe Val Phe Phe Gly Lys Phe Leu Phe
 405 410 415

AATACCATTT CTACAATCAA TAGTGAAGAG TTTGCAATAA AGTAAGC 1357

```

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly
 1 5 10 15
Ile Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val
 20 25 30
Lys Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys
 35 40 45
Asn Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe
 50 55 60
Ser Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp
 65 70 75 80
Asn Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly
 85 90 95
Asn Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly
 100 105 110
Asp Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile
 115 120 125
Ala Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly
 130 135 140
Gly Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg
 145 150 155 160
Tyr Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile
 165 170 175
Asn Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala
 180 185 190

```

|                                                                 |      |
|-----------------------------------------------------------------|------|
| Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly Gly |      |
| 130 135 140 145                                                 |      |
| AAT ATT CAA GGG GTT TCT GTA GCT TTT AAG CAA AAT TCC ATG CGT TAT | 540  |
| Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg Tyr |      |
| 150 155 160                                                     |      |
| TTT GGG ATT TTT ATG GAT AGC ATG CTT TAT AAT GGG CAT CAA ATC AAC | 588  |
| Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile Asn |      |
| 165 170 175                                                     |      |
| AAA GAG CAA GGG AAT CGG ATC GCT ACT TCC CTA AAC GCT CTA GCG TCT | 636  |
| Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala Ser |      |
| 180 185 190                                                     |      |
| TAT GAC CCT GTG TCT AAA CGC TTG TAT GTG GGG GGG GAA GTG TTT GTT | 684  |
| Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe Val |      |
| 195 200 205                                                     |      |
| TTA GGT GCA GAA TAC AGG CAT GAA AAT CTT AAA GTG GTG CCT TTT ATT | 732  |
| Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe Ile |      |
| 210 215 220 225                                                 |      |
| TTA ACG GAC ACC CGC TTG CCT TTA TCC ACC CAA AAT GTT TTA GTG CAA | 780  |
| Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val Gln |      |
| 230 235 240                                                     |      |
| GTG GGG GGT AAG TTG GAG TAT GAC GCT TCT TTA GCT AAG GGT TTC ACT | 828  |
| Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe Thr |      |
| 245 250 255                                                     |      |
| TCG CAC ACT CTA GTG CAT GGC ATG TAT CAA TAC GGC AAC ACT GAT GCG | 876  |
| Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp Ala |      |
| 260 265 270                                                     |      |
| GCT ACA AGC GTT AAA AAT GCC GGC TTG TTT TTG ATC GAT CAA ACT TTT | 924  |
| Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr Phe |      |
| 275 280 285                                                     |      |
| AAA TAC AAA ATT TTT AAT TTT GGA ACG GGT TTT TAT ATC GTT CCG GCA | 972  |
| Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro Ala |      |
| 290 295 300 305                                                 |      |
| AGA AAC AAT AAG GGC TAT CTA TGG ACT TTT AAT GAC AGG ACT AAA TTC | 1020 |
| Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys Phe |      |
| 310 315 320                                                     |      |
| TAT GGC CGT GGG ATC AAT GCG CCC GGC GTG CCA GCG ATT TAT TTT GCA | 1068 |
| Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe Ala |      |
| 325 330 335                                                     |      |
| AAC TCT AGC ATT TCA GGC TAT GTT TTT TTA GGG CTT AAG ACT AAA AGG | 1116 |
| Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys Arg |      |
| 340 345 350                                                     |      |

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic RNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...1305
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

CGCAATTAAA AGGAATTTTA ACTAAAATAT TGAGTTTAAA TCCACGATGA GTTTTTA ATG 60
 Met
 1

CAA TAT AAG AAA AAT AAG AAA AGA TAT TAT TAT TTA GCG TTA GGG ATC 108
Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly Ile
 5 10 15

TTT TTT TTA AAT GGT CTG TCT TTG AAA GCT TTA GAA ATC GCC GTC AAA 156
Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val Lys
 20 25 30

CCT TTT GGC TAT CTG GGG CTA TTA TAT AAT CAA GGG GCG CAA AAA AAC 204
Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys Asn
 35 40 45

CCT CAC AGC TAT GTG GGG GCT TTA GCG CGT CTT GGG GTG GAT TTT TCT 252
Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe Ser
 50 55 60 65

TAT AGC AAC GGG TGG TCC TTT GGT ATT GGA GCG ATT GGG GCT TGG AAT 300
Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp Asn
 70 75 80

ATT TAT AAC AAA CAG CGT TTG GCT AAC CTT TAT ATC AGT CTA GGG AAT 348
Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly Asn
 85 90 95

TTT TTT GGT AGT TCT AAA AAT GTT AAA CCT TAT TTG AGC GCT GGC GAT 396
Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly Asp
 100 105 110

GTT TCT GAT GCG TAT GTT CAA TAC ACT AAC CAG CGT TTT AAA ATC GCT 444
Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile Ala
 115 120 125

TTA GGG CGT TTC AAT ACC GAT TTT GTG GAT TTT GAT TGG ATA GGG GGC 492

```

Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe  
 260 265 270

TTTTTCTCTA ATTGAATTTT CAATTAGAGT TTTC

910

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Phe | Val | Val | Phe | Lys | Thr | Leu | Cys | Leu | Ser | Val | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Asn | Ser | Leu | Val | Ala | Ala | Glu | Gly | Ser | Thr | Glu | Val | Gln | Lys | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Lys | Pro | Lys | Glu | Tyr | Lys | Ala | Val | Lys | Gly | Glu | Lys | Asn | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Trp | Tyr | Leu | Gly | Ile | Ser | Tyr | Gln | Val | Gly | Gln | Ala | Ser | Gln | Ser | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Asn | Pro | Pro | Lys | Ser | Ser | Glu | Phe | Asn | Tyr | Pro | Lys | Phe | Pro | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Lys | Thr | Asp | Tyr | Leu | Ala | Val | Met | Gln | Gly | Leu | Gly | Leu | Thr | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Tyr | Lys | Gln | Phe | Phe | Gly | Glu | Lys | Arg | Trp | Phe | Gly | Ala | Arg | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Gly | Phe | Met | Asp | Tyr | Gly | His | Ala | Val | Phe | Gly | Ala | Asn | Ala | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ser | Asp | Asn | Gly | Gly | Val | Cys | Glu | Leu | His | Gln | Pro | Cys | Ala | Thr |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Val | Gly | Thr | Met | Gly | Asn | Leu | Ser | Asp | Met | Phe | Thr | Tyr | Gly | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Ile | Asp | Thr | Leu | Tyr | Asn | Val | Ile | Asn | Lys | Glu | Asp | Ala | Ser | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Phe | Phe | Phe | Gly | Ala | Gln | Ile | Ala | Gly | Asn | Ser | Trp | Gly | Asn | Thr |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Thr | Gly | Ala | Phe | Leu | Glu | Thr | Lys | Ser | Pro | Tyr | Lys | His | Thr | Ser | Tyr |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Leu | Asp | Pro | Ala | Ile | Phe | Gln | Phe | Leu | Phe | Asn | Leu | Gly | Ile | Arg |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | His | Ile | Gly | Arg | His | Gln | Glu | Phe | Asp | Phe | Gly | Val | Lys | Ile | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Ile | Asn | Val | Tyr | Phe | Asn | His | Gly | Asn | Leu | Ser | Phe | Thr | Tyr |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Arg | Arg | Gln | Tyr | Ser | Leu | Tyr | Val | Gly | Tyr | Arg | Tyr | Asn | Phe |     |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |

(2) INFORMATION FOR SEQ ID NO:11:

| 35                                                                |  |  |  |  | 40  |  |  |  |  | 45  |  |  |  |  | 50  |     |
|-------------------------------------------------------------------|--|--|--|--|-----|--|--|--|--|-----|--|--|--|--|-----|-----|
| TTG GGG ATT AGC TAT CAA GTC GGT CAG GCT TCG CAA AGC GTT AAA AAC   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 248 |
| Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val Lys Asn   |  |  |  |  | 55  |  |  |  |  | 60  |  |  |  |  | 65  |     |
| CCC CCC AAA AGC AGT GAA TTT AAC TAC CCT AAG TTC CCT GTG GGT AAA   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 296 |
| Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val Gly Lys   |  |  |  |  | 70  |  |  |  |  | 75  |  |  |  |  | 80  |     |
| ACC GAC TAT CTG GCC GTT ATG CAA GGC TTA GGG CTT ACT GTG GGT TAT   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 344 |
| Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val Gly Tyr   |  |  |  |  | 85  |  |  |  |  | 90  |  |  |  |  | 95  |     |
| AAG CAG TTT TTC GGG GAA AAG AGA TGG TTT GGT GCA CGC TAT TAC GGC   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 392 |
| Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr Tyr Gly   |  |  |  |  | 100 |  |  |  |  | 105 |  |  |  |  | 110 |     |
| TTC ATG GAT TAT GGG CAT GCC GTA TTT GGA GCG AAC GCT TTA ACA TCG   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 440 |
| Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu Thr Ser   |  |  |  |  | 115 |  |  |  |  | 120 |  |  |  |  | 125 | 130 |
| GAT AAT GGT GGG GTG TGT GAG CTT CAC CAA CCA TGT GCG ACC AAA GTA   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 488 |
| Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr Lys Val   |  |  |  |  | 135 |  |  |  |  | 140 |  |  |  |  | 145 |     |
| GGG ACA ATG GGC AAT CTG TCT GAC ATG TTC ACT TAT GGT GTG GGT ATT   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 536 |
| Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val Gly Ile   |  |  |  |  | 150 |  |  |  |  | 155 |  |  |  |  | 160 |     |
| GAC ACT TTA TAC AAT GTC ATC AAT AAA GAA GAT GCG AGT TTT GGT TTC   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 584 |
| Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe Gly Phe   |  |  |  |  | 165 |  |  |  |  | 170 |  |  |  |  | 175 |     |
| TTT TTT GGG GCT CAA ATC GCG GGT AAC TCT TGG GGT AAT ACG ACA GGG   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 632 |
| Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr Thr Gly   |  |  |  |  | 180 |  |  |  |  | 185 |  |  |  |  | 190 |     |
| GCC TTT TTG GAA ACT AAA AGC CCT TAT AAG CAC ACT TCC TAT AGC CTT   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 680 |
| Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr Ser Leu   |  |  |  |  | 195 |  |  |  |  | 200 |  |  |  |  | 205 | 210 |
| GAT CCG GCG ATT TTC CAG TTC CTT TTT AAT TTA GGG ATC CGC ACC CAT   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 728 |
| Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg Thr His   |  |  |  |  | 215 |  |  |  |  | 220 |  |  |  |  | 225 |     |
| ATT GGC CGG CAT CAA GAA TTT GAC TTT GGC GTG AAG ATT CCC ACT ATC   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 776 |
| Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro Thr Ile   |  |  |  |  | 230 |  |  |  |  | 235 |  |  |  |  | 240 |     |
| AAT GTT TAT TAT TTT AAC CAT GGG AAT TTG AGC TTC ACT TAC CGC CGT   |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 824 |
| Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr Arg Arg   |  |  |  |  | 245 |  |  |  |  | 250 |  |  |  |  | 255 |     |
| CAA TAC AGC CTT TAT GTG GGG TAT CGT TAC AAT TTC TGATTTAAAA CGCTTG |  |  |  |  |     |  |  |  |  |     |  |  |  |  |     | 876 |

```

Met His Gln Asn Asn Lys Thr Phe Leu Pro Ser Gln Ser Ala His Leu
 1 5 10 15
Ser Lys Ile Ile Leu Phe Leu Asn Thr Gly Phe Leu Ala Tyr Leu Leu
 20 25 30
Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu Val Lys Asp
 35 40 45
Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu Lys Ala Ile
 50 55 60
Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro Leu Ile Asn
65 70 75 80
Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly Phe Tyr Asn
 85 90 95
Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met Tyr Gly Gly
 100 105 110
Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met Pro Tyr Gly
 115 120 125
Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala Pro Gly Tyr
 130 135 140
Phe Pro Tyr Ala Phe Tyr
145 150

```

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...860
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

ATTATGTTAT TATTATACGA AATGTAGACT TTTAGAAGGA AAAATGTTGT ATG AAA 56
 Met Lys
 1

AAG TTT GTA GTG TTT AAA ACG CTC TGT TTA TCG GTA GTG TTA GGT AAT 104
Lys Phe Val Val Phe Lys Thr Leu Cys Leu Ser Val Val Leu Gly Asn
 5 10 15

AGT CTT GTG GCA GCA GAA GGC AGC ACA GAA GTG CAA AAG CAA TTG GAA 152
Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln Leu Glu
 20 25 30

AAG CCA AAA GAG TAT AAA GCA GTG AAA GGC GAG AAA AAC GCT TGG TAT 200
Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala Trp Tyr

```

```

CCACAAAAGC TTAATGAATA TTAAATTAAA AACATGTTAA TCTTTAGTTA TTTTAAAAAT 60
TTAGGAAATC CC ATG CAT CAA AAC AAT AAA ACT TTT TTA CCC AGC CAA TCC 111
 Met His Gln Asn Asn Lys Thr Phe Leu Pro Ser Gln Ser
 1 5 10

GCT CAC CTC TCT AAA ATC ATT CTT TTT TTA AAC ACC GGC TTT TTA GCC 159
Ala His Leu Ser Lys Ile Ile Leu Phe Leu Asn Thr Gly Phe Leu Ala
 15 20 25

TAT CTG TTA AGC GCT TGT GGG GCG AAT GTG CCT ATA GAA GAA GTG TTG 207
Tyr Leu Leu Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu
 30 35 40 45

GTT AAA GAT CCT AAA GAG ACC AAA GCC CAA GAA GTC GCC AGA GAA GAA 255
Val Lys Asp Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu
 50 55 60

AAG GCT ATC CAG CAA GAA AAC GCC ACT ATT GAT GCG CGC ACC ACG CCT 303
Lys Ala Ile Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro
 65 70 75

TTA ATC AAT CGT TTC ACT AAT TAT AGC GCT TAT GGC TCT TTA AAC GGC 351
Leu Ile Asn Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly
 80 85 90

TTT TAC AAT TCA GTG GAT AAT CTC AAT TCG CCC ATG CAA AAC GGG ATG 399
Phe Tyr Asn Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met
 95 100 105

TAT GGA GGC TAT TAC ATG CCT TAT TAT TAC ATG CCC TAT GGT TTC ATG 447
Tyr Gly Gly Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met
 110 115 120 125

CCT TAT GGG TCA GGT CTT ATG CCT TAT GGG CCT TAT GGG TAT GGA GCG 495
Pro Tyr Gly Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala
 130 135 140

CCT GGA TAC TTC CCT TAC GCT TTT TAT TGATTGAGTG GCTTTAGAAA GCGTGGT 549
Pro Gly Tyr Phe Pro Tyr Ala Phe Tyr
 145 150

GGTGTGTTGGTG TTTTACTCA AACACG 575

```

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

85 90 95

GCG GCC GGG TGT TTT GCA AGT GGG GGC GAT GTA TGC TAATGGGGTA GGGATC 396  
 Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys  
 100 105 110

CAAACCAACA GATTAAAAGC CGCTCGCTAT TATGAATG 434

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu  
 1 5 10 15  
 Ser Gly Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu  
 20 25 30  
 Leu Asn Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile  
 35 40 45  
 Thr Pro Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro  
 50 55 60  
 Glu Asn Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys  
 65 70 75 80  
 Gly Asp Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn  
 85 90 95  
 Gly Asn Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys  
 100 105 110

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...522
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:



```

Met Lys Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly
 130 135 140
Leu Gly Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys
 145 150 155 160
Ile Pro Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu
 165 170 175
Glu Ser Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe
 180 185

```

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...380
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

AGCGTGAAAA AAATTGAGTT GAATCAAAAC CTGCATTAAG GATTAAAAGA ATG CTC 56
 Met Leu
 1

AAA AAA AGT TTG TTA TTG CTT GTT TTT TTA GTC TTA CAG CTT AGC GGC 104
Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu Ser Gly
 5 10 15

GCT GAA GAA AAC AAT CAA GCC CCA AAA AAC ACG CCC CCT GAA TTA AAC 152
Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu Leu Asn
 20 25 30

CCC GCT AAC GCT AAG GGC GCG CCA AAC TCT AAC ACC CAG ATC ACC CCT 200
Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile Thr Pro
 35 40 45 50

AAA AAC GAT AAC TCT AAC CTG TTA GAC AAA TTA GGT TCG CCT GAA AAC 248
Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro Glu Asn
 55 60 65

GCT CAA ACC GAG CTT TCT GCC GGT ATT GAT TTG GCT AAA AAG GGC GAT 296
Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys Gly Asp
 70 75 80

TAT CAA GGG GCT TTC AAG CTT TTT TCC CAA TCG TGC GAT AAT GGT AAT 344
Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn Gly Asn

```

TTA AGC GAT TTT TAC ACT TAC AAA AAA TAC AGC TTT GGG GTG TAT GGG 392  
 Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val Tyr Gly  
 100 105 110

GGG CTT GGG ATA GGG TAT TTT TAT CAA AGC AAC CAT TTA GGC ATG AAA 440  
 Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly Met Lys  
 115 120 125 130

AAT AGT TCG TTT ATG GGT TAT AAC GGC TTG TTT AAT GTG GGG CTT GGC 488  
 Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly Leu Gly  
 135 140 145

AGC ACG ATC GAT CGC CAC CAC CGC ATA GAG CTT GGG GCT AAA ATC CCT 536  
 Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys Ile Pro  
 150 155 160

TTT TCA AAG ACT AGA AAT TCT TTT AAA AAT CCT TAT TTT TTA GAG AGC 584  
 Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu Glu Ser  
 165 170 175

GTT TTT ATC CAT GCG ACT TAT AGC TAT ATG TTT TAAGAGAGAA TAGCCTATTA 637  
 Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe  
 180 185

GTGGTCGTTA TCAATAAGAT AAGATCCTTA ATG 670

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Lys Ile Ala Phe Ile Leu Ala Leu Trp Val Gly Leu Leu Gly  
 1 5 10 15  
 Ala Phe Glu Pro Lys Lys Ser His Ile Tyr Phe Gly Ala Met Val Gly  
 20 25 30  
 Leu Ala Pro Ile Lys Ile Thr Pro Lys Pro Ala Ser Asp Ser Ser Tyr  
 35 40 45  
 Thr Ala Phe Leu Trp Gly Ala Lys Gly Gly Tyr Gln Phe Ala Phe Phe  
 50 55 60  
 Lys Ala Leu Ala Leu Arg Gly Glu Phe Ser Tyr Leu Met Ala Ile Lys  
 65 70 75 80  
 Pro Thr Ala Leu His Thr Ile Asn Thr Ser Leu Leu Ser Leu Asn Ile  
 85 90 95  
 Asp Val Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val  
 100 105 110  
 Tyr Gly Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly  
 115 120 125

```

Met Glu Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala
 1 5 10 15
Phe Lys Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val
 20 25 30
Val Trp Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val
 35 40 45
Leu Pro Asn Met Asn Leu
 50

```

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...617
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

CCCATAGACG ACAAATCAA GCGGTTTTAT CAAACCAAA AACTTTAGA ATG AAA 56
 Met Lys
 1

AAA ATT GCT TTC ATT TTG GCT TTA TGG GTG GGC TTG TTA GGG GCG TTT 104
Lys Ile Ala Phe Ile Leu Ala Leu Trp Val Gly Leu Leu Gly Ala Phe
 5 10 15

GAG CCT AAA AAA AGT CAT ATT TAT TTT GGG GCT ATG GTG GGT TTA GCT 152
Glu Pro Lys Lys Ser His Ile Tyr Phe Gly Ala Met Val Gly Leu Ala
 20 25 30

CCT ATT AAA ATA ACC CCA AAA CCG GCT AGT GAT TCT TCT TAT ACG GCT 200
Pro Ile Lys Ile Thr Pro Lys Pro Ala Ser Asp Ser Ser Tyr Thr Ala
 35 40 45 50

TTT TTA TGG GGG GCT AAA GGA GGG TAT CAA TTC GCT TTT TTT AAA GCT 248
Phe Leu Trp Gly Ala Lys Gly Gly Tyr Gln Phe Ala Phe Phe Lys Ala
 55 60 65

CTA GCG TTA AGG GGT GAA TTT TCC TAC CTT ATG GCA ATC AAA CCC ACC 296
Leu Ala Leu Arg Gly Glu Phe Ser Tyr Leu Met Ala Ile Lys Pro Thr
 70 75 80

GCA CTG CAC ACG ATT AAC ACT TCT TTA TTG AGC TTA AAT ATT GAT GTG 344
Ala Leu His Thr Ile Asn Thr Ser Leu Leu Ser Leu Asn Ile Asp Val
 85 90 95

```

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...212
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|                                                                   |                                                   |    |
|-------------------------------------------------------------------|---------------------------------------------------|----|
| TTTTTTAGTT TGT                                                    | TTTTTGAG TATAATCCTA CGAAAATTTT AAGGAACGGC ATG GAG | 56 |
|                                                                   | Met Glu                                           |    |
|                                                                   | 1                                                 |    |
| TTT TTG GGA CTG ATT TTA AGT CTG GCC GCT ATT TTG ATA GCG TTT AAA   | 104                                               |    |
| Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala Phe Lys   |                                                   |    |
| 5 10 15                                                           |                                                   |    |
| AAG CCT GAA AAA GAA AAT TGG GCG TTT GGG ATT TTG ATG GTG GTG TGG   | 152                                               |    |
| Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val Val Trp   |                                                   |    |
| 20 25 30                                                          |                                                   |    |
| TTA GTG GAG CTT ATT ATT TTT ATA GCC CAC AGC TCT AGC GTT TTG CCT   | 200                                               |    |
| Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val Leu Pro   |                                                   |    |
| 35 40 45 50                                                       |                                                   |    |
| AAC ATG AAT CTA TAAGGGGGAT GCATGGATAA AGAAACCCGA TTTTACAACC TTTTT | 257                                               |    |
| Asn Met Asn Leu                                                   |                                                   |    |
| TCTTTGGC                                                          | 265                                               |    |

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

## SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR  
MERIEUX SERUMS ET VACCINS S.A. HUMAN GENOME  
SCIENCES, INC.
- (ii) TITLE OF THE INVENTION: Identification of Polynucleotides  
Encoding Novel Helicobacter Polypeptides in the Helicobacter  
Genome
- (iii) NUMBER OF SEQUENCES: 1376
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Clark & Elbing LLP  
(B) STREET: 176 Federal Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: PCT/US98/----  
(B) FILING DATE: 01-APR-98  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/833,457  
(B) FILING DATE: 01-APR-1997
- (vii) PRIOR APPLICATION DATA: 08/881,227
- (A) APPLICATION NUMBER: 24-JUN-1997  
(B) FILING DATE:
- (vii) PRIOR APPLICATION DATA: 08/902,615
- (A) APPLICATION NUMBER: 29-JUL-1997  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Clark, Paul T.  
(B) REGISTRATION NUMBER: 30,162  
(C) REFERENCE/DOCKET NUMBER: 06132/041WO1
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 617-428-0200  
(B) TELEFAX: 617-428-7045  
(C) TELEX:

MISSING UPON TIME OF PUBLICATION

|                                                |      |      |                                 |                                     |       |        |        |          |       |    |       |
|------------------------------------------------|------|------|---------------------------------|-------------------------------------|-------|--------|--------|----------|-------|----|-------|
| 185                                            | 1072 | June | CGCGATCCGATGCTCAATTTTATGACA     | CCGCTCGAGTTAAAGGATATAAATAGCG        | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 186                                            | 1073 | June | CGCGATCCGATGATCGGATTATCCT       | CCGCTCGAGTTAAACCAACACATCGTTTG       | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 115                                            | 1084 | Apr  | CGCGATCCGATGAAGCAATCTTAGC       | CCGCTCGAGTTACTAGCGGCTGATCAAG        | -     | 97/30" | 55/1'  | 72/50'   | -     | 25 | Vent  |
| 13                                             | 1085 | Apr  | CGCGATCCGATGAAGGCTAAAGAAATG     | CCGCTCGAGTTAGAACTGATAGGACCTC        | -     | 97/30" | 50/1'  | 72/2'30" | -     | 25 | Vent  |
| 213                                            | 1087 | July | GGGAATTCGAATGAAGAAATCAGCGATCTT  | CCGCTCGAGTTAAATCTTAAACAAGACTC       | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 187                                            | 1088 | June | CGCGATCCGATGAAGGATATTGAA        | CCGCTCGAGTTATTTGTTCTGTGCGCA         | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 116                                            | 1089 | Apr  | CGCGATCCGATCAAGATATCTATCAA      | CCGCTCGAGCTAAAGGGGTTTTTCAATTG       | -     | 97/30" | 55/1'  | 72/50'   | -     | 25 | Vent  |
| 214                                            | 1097 | July | CGCGATCCGATGCAAAATGAAGAAATG     | CCGCTCGAGTCAACCACTAATAAACC          | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 117                                            | 1099 | Apr  | CGCGATCCGATGAATCTAAATCACT       | CCGCTCGAGTTAATCTCTCTGTGAGTG         | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 30*                                            | 1101 | Apr  | GGGATCCTTACTAAGGCTTTATG         | GGAAATCTTAACTAAATCCAAC              | 94/5' | 94/30" | 45/30" | 72/30"   | 72/7' | 30 | Pwo   |
| 118                                            | 1102 | Apr  | CGCGATCCGATGAAGAAATCCCTTTGT     | CCGCTCGAGTTAAACTTCGTGAATAATA        | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 119                                            | 1111 | Apr  | CGCGATCCGATGCTTGAAAGTGTT        | CCGCTCGAGTTAAATGTGGTGGCGAA          | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 120                                            | 1114 | Apr  | CTGAATCGAATGGCAGATATCAAGG       | CCGCTCGAGTTACGTTAGCCCATTTTC         | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 190                                            | 1115 | June | CGCGATCCGATGATCCAAATCAGGCTTATAG | CCGCTCGAGTTAACCGCGCTTAAAGAAATG      | -     | 97/30" | 55/1'  | 72/5'    | -     | 25 | Vent  |
| 21                                             | 1120 | Apr  | CGCGATCCGATTTGTATCGCATAGGGCT    | CCGCTCGAGCTATTTTTCATTAATGAATTC      | -     | 97/30" | 55/1'  | 72/2'    | -     | 25 | vent  |
| 26                                             | 1138 | Apr  | CGCGATCCGATGACAGAGAAATTTG       | CCGCTCGAGTTAGCTTTTCGTGTATCG         | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent  |
| 191                                            | 1159 | June | CGCGATCCGATGCAACATGAATCCCT      | CCGCTCGAGTTAGAACTTTTTCGAAAAATTTTGTG | -     | 97/30" | 50/1'  | 72/2'    | -     | 25 | Vent  |
| 192                                            | 1177 | June | CGCGATCCGAGAGTGAAGCGTTTATAG     | CCGCTCGAGTTAGAAAGTTTTCATGACTTTC     | -     | 97/30" | 55/50" | 72/1'30" | -     | 25 | Vent  |
| 193                                            | 1187 | June | CGCGATCCGATGTCGCTCATTTTIA       | CCGCTCGAGTTAAAAAATCCCATAAACCA       | -     | 97/30" | 55/50" | 72/1'30" | -     | 25 | Vent  |
| 194                                            | 1192 | June | CGCGATCCGATGAAGAAATACAGCACT     | CCGCTCGAGTTAGTTCTGTTTATAGTC         | -     | 97/30" | 50/1'  | 72/2'    | -     | 25 | Vent  |
| 195                                            | 1195 | June | CGCGATCCGAAATGCTTGCTCATCTT      | CCGCTCGAGTTACTTTTTTTTGTGTTAAG       | -     | 97/30" | 55/50" | 72/1'30" | -     | 25 | Vent  |
| 23                                             | 1282 | July | CGCGATCCTTTCTTCAATGTTTG         | CCGCTCGAGTCAAGTTTTTAAACAAATTC       | 94/5' | 94/30" | 45/30" | 72/30"   | 72/7' | 25 | Vent  |
| 11                                             | 1310 | Apr  | CGCGATCCGAGAGTTGTGTGAACGGATT    | CCGCTCGAGCTATTTTCAGACTTACTAGA       | -     | 97/30" | 50/1'  | 72/1'30" | -     | 25 | Taq   |
| 31*                                            | 1320 | Apr  | GGGATCCTTGAAATAACCATAGCG        | GGAAATCTTACTCATATAATC               | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 25 | Pwo   |
| 22                                             | 1375 | Apr  | CGCGATCCGATTTCTTTTAGTGGTGTG     | CCGCTCGAGTTAAAGCTCTCTTTCAGGAAG      | -     | 97/30" | 55/1'  | 72/2'    | -     | 25 | Vent  |
| 5                                              | 1432 | Apr  | CGCGATCCGAGTGCATAACTTCCATTGGAAT | CCGCTCGAGTTCTTTTCTAGGTGTTGA         | -     | 97/30" | 55/45" | 72/1'    | -     | 30 | Therm |
| 42                                             | 1608 | Apr  | CGCGATCCGAAAAAGCAGTTAAAAATG     | CCGCTCGAGCTACTTTTATTCAGCTGCT        | -     | 95/30" | 55/50" | 72/1'30" | -     | 25 | Vent  |
| 32                                             | 1754 | June | CGCGATCCGATGAATGAAGAAACGAT      | CCGCTCGAGTTAATGCCACCTTTGGGCT        | -     | 97/30" | 55/1'  | 72/2'30" | -     | 25 | Taq   |
| Therm: Thermalase, Amresco                     |      |      |                                 |                                     |       |        |        |          |       |    |       |
| Vent: Vent DNA polymerase, New England Biolabs |      |      |                                 |                                     |       |        |        |          |       |    |       |
| Pwo: Pwo DNA polymerase, Boehringer Mannheim   |      |      |                                 |                                     |       |        |        |          |       |    |       |
| Taq: Taq DNA polymerase, Appligène             |      |      |                                 |                                     |       |        |        |          |       |    |       |
| ExTaq: ExTaq DNA polymerase, TaKaRa            |      |      |                                 |                                     |       |        |        |          |       |    |       |

|     |      |        |                                |                               |       |        |        |          |       |    |      |
|-----|------|--------|--------------------------------|-------------------------------|-------|--------|--------|----------|-------|----|------|
| 167 | 885  | June   | CGCGATCCGAATGAGTATTATG         | CCCCGAGTATTGAACCAAGTC         | 94/5' | 94/30" | 50/1'  | 72/1'    | 72/7' | 30 | Vent |
| 98  | 886  | Apr    | CGCGATCCGAATGAGATTITTTTGGTIT   | CCGCTCGAGTACTTCTGCTTAAATTTT   | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 168 | 889  | June   | CGCGATCCGAGGTAAATGCCAAATG      | CCGCTCGAGTATAGCGGTGTTTTTAATG  | 94/5' | 94/30" | 50/1'  | 72/1'30" | 72/7' | 30 | Vent |
| 99  | 893  | Apr    | CGCGATCCGAGTGGGAAATCCGATGT     | CCGCTCGAGTACTAGCTGCGTGGAGAT   | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 100 | 894  | Apr    | CGCGATCCGAATGAAATTTCTCCATCT    | CCGCTCGAGTCACTCTCTTCAAGCTATA  | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 101 | 895  | Apr    | CGCGATCCGAGTGGCCCTCAGAGTIT     | CCGCTCGAGTCAITTTTTACTCGCGAAGA | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 169 | 903  | June   | CGCGATCCAGTCAATAAAG            | CCGCTCGAGTCAITTTTCTCGTAGG     | 94/5' | 94/30" | 55/1'  | 72/1'    | 72/7' | 30 | Vent |
| 170 | 912  | June   | CGCGATCCGAGTATAGACCTTTTAG      | CCGCTCGAGTAAAGCCATTTTCATG     | 94/5' | 94/30" | 55/1'  | 72/1'    | 72/7' | 30 | Vent |
| 102 | 937  | Apr    | CGCGATCCGAATCGGTTTAAACATIT     | CCGCTCGAGTACCACCAAAATTAACAC   | -     | 97/30" | 55/55" | 72/1'30" | -     | 25 | Vent |
| 171 | 946  | June   | CGCGATCCATAAATATCTTTG          | CCGCTCGAGTCAAAATACTAGGCA      | 94/5' | 94/30" | 45/1'  | 72/1'    | 72/7' | 30 | Vent |
| 172 | 958  | June   | CGCGATCCGAAATTTAGTCAAAATTTAAAC | CCGCTCGAGTCAAGTATTACCGGA      | 94/5' | 94/30" | 55/1'  | 72/1'    | 72/7' | 30 | Vent |
| 44  | 961  | July   | CGCGATCCGATTTTACTTCAAAATTTAAAC | CCGCTCGAGTATAGAAAGTAGTTCAATAC | -     | 97/30" | 55/1'  | 72/2'30" | -     | 25 | Vent |
| 173 | 968  | June   | CGCGATCCAGAGATTTTITTTATG       | CCGCTCGAGTAAATGACAGCTTGTGCG   | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 25 | Vent |
| 103 | 976  | Apr    | CGCGATCCGAAGCTTATAAAGAGGCG     | CCGCTCGAGTATATCTTTAATGCCGTTTT | -     | 97/30" | 55/50" | 72/1'30" | -     | 25 | Vent |
| 104 | 984  | Apr    | CGCGATCCGAGTGAAGATACAAAGAC     | CCGCTCGAGTCACTCTTTTAAACCTG    | -     | 97/30" | 55/1'  | 72/2'30" | -     | 25 | Vent |
| 174 | 987  | June   | CGCGATCCAACTTACAGCTTTTATG      | CCGCTCGAGTAAACAGATAAAC        | 94/5' | 94/30" | 50/60" | 72/60"   | 72/7' | 30 | Vent |
| 175 | 992  | June   | CGCGATCCAGGATACAAACCAAAAC      | CCGCTCGAGTCAAAAGATGGCATG      | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 25 | Vent |
| 176 | 996  | June   | CGCGATCCCTTTTAGATTTTACG        | CCGCTCGAGTCACTCCCTTAAACAC     | 94/5' | 94/30" | 50/30" | 72/60"   | 72/7' | 30 | Vent |
| 177 | 997  | June   | CGCGATCCCTTAGAATTTATTTTA       | CCGCTCGAGTCAAAACCAACCCG       | 94/5' | 94/30" | 50/30" | 72/60"   | 72/7' | 30 | Vent |
| 178 | 1002 | June   | CGCGATCCGAATGGCGTTTGGCATAA     | CCGCTCGAGTATAGGAATGTTGGGAA    | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 106 | 1011 | Apr    | CGCGATCCGAATCCGAACAATAAACG     | CCGCTCGAGTAAACCTTAAATGATAGTA  | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 107 | 1013 | Apr    | CGAAATCCGAGTTTGGCTTTGATTTCAAT  | CCGCTCGAGTCAATGATTTATCCATCAT  | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 108 | 1020 | Apr    | CGCGATCCGATCAAGGAAATGGCACT     | CCGCTCGAGTAAACATACGCTTATGCT   | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 109 | 1024 | Apr    | CGCGATCCGAATGAAATCCATTTTA      | CCGCTCGAGTCAAAAGAGGTTTAGGGGT  | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 179 | 1026 | June   | CGCGATCCGAAATAGGAGGAATGTTTG    | CCGCTCGAGTCAAGCGGTTTCAATA     | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 110 | 1027 | Apr    | CGCGATCCGAATGAGAGCTACGGCGTA    | CCGCTCGAGTATTTTTTAAACGGCTTAC  | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 111 | 1031 | Apr    | CGCGATCCGAATGAAGACAGAAACAA     | CCGCTCGAGTATATGTTCAACTTAGAAAA | -     | 97/30" | 55/1'  | 72/1'15" | -     | 25 | Vent |
| 112 | 1034 | A/June | CTGAATCCGAATGTTGAAGACATGATTA   | CCGCTCGAGTAAAAATCCCTCAAGTAAC  | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 182 | 1038 | June   | CGCGATCCGAATGAGCTTGATTTAAAAAC  | CCGCTCGAGTAAATACAGAGCTTTTIG   | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 41  | 1050 | Apr    | CGCGATCCGAGATGTTATGCAAGTGA     | CCGCTCGAGTAAAGCTTTTGGCTGGCGT  | -     | 95/30" | 55/50" | 72/1'30" | -     | 25 | Vent |
| 212 | 1051 | July   | CGCGATCCGAGGCGCAACGATTTTATG    | CCGCTCGAGTATGTTTTTTTAAACAGCAT | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 113 | 1052 | Apr    | CGCGATCCGAATGGGATTTTGAATGGG    | CCGCTCGAGTAAAGGCTTGACACCCAC   | -     | 97/30" | 55/1'  | 72/50"   | -     | 25 | Vent |
| 183 | 1059 | June   | CGCGATCCGAGCTGATTCGCTGCTAAT    | CCGAGTCCGAGCTGATTCGCTGCTAAT   | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 184 | 1065 | June   | CGCGATCCGAATGCAAGATTCAGTTG     | CCGCTCGAGTCAAAACTGCTTAAAG     | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |



|     |     |      |                                |                                   |       |        |        |          |       |    |      |
|-----|-----|------|--------------------------------|-----------------------------------|-------|--------|--------|----------|-------|----|------|
| 39  | 708 | Apr  | GGAAATCGCACAAACCTTGG           | CCGCTCGAGTTAGGAGTTTCTTC           | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 20 | Vent |
| 81  | 709 | Apr  | GGAAATCCAAAAAATCTTAAC          | CCGCTCGAGTTAGACCAGAAATG           | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 25 | Vent |
| 151 | 710 | June | CGCGGATCCGAATGGGTTTTTCAAGCTTA  | CCGCTCGAGTTAACGAAGATAAATACAG      | -     | 97/20" | 55/40" | 72/1'30" | -     | 25 | Taq  |
| 152 | 713 | June | CGCGGATCCGAATGACCCCTCACATCAAG  | CCGCTCGAGCTAACTCATCATCTCCAAAGC    | -     | 97/20" | 55/40" | 72/1'30" | -     | 25 | Taq  |
| 153 | 716 | June | CGCGGATCCGAATGTTTAAAGAAATTTTC  | CCGCTCGAGTTAATTTCTAAAGTTTTCGCG    | -     | 97/20" | 55/40" | 72/1'30" | -     | 25 | Taq  |
| 154 | 718 | June | CGCGGATCCCATGCGAGATTTTC        | CCGCTCGAGTCAAGCTTTTTTGTG          | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 155 | 726 | June | CGCGGATCCAGAGAGTTAGAGAAC       | CCGCTCGAGTCAAGCAATATTTTTTG        | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 40  | 731 | Apr  | GGAAATCGCATGACTTATGGG          | CCGCTCGAGCTACCAACAGCTTGC          | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 20 | Vent |
| 156 | 734 | June | CGCGGATCCCAAAATGGGTTTTG        | CCGCTCGAGTCAGCCTTTGGCCTTTTC       | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 157 | 740 | June | CGCGGATCCCTTTTAGCAACCGG        | CCGCTCGAGTCAAAATATCTCAG           | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 35  | 759 | Apr  | GGGATCCATTGTAATACGGAT          | GGAAATCTTAATGTTCCITTTT            | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 25 | Vent |
| 87  | 762 | Apr  | GGAAATCCCACTGCTCCAAATTTAG      | CCGCTCGAGTTAAACAATACCAAAAG        | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 25 | Vent |
| 158 | 770 | June | CGCGGATCCGGGCTGGGCTGTG         | CCGCTCGAGTCAATAACAGCCACAAG        | 94/5' | 94/30" | 45/60" | 72/60"   | 72/7' | 30 | Vent |
| 159 | 782 | June | CGCGGATCCGCTCTCTCTATTAG        | CCGCTCGAGCTAAAAATCCTTTAAC         | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 160 | 786 | June | CGCGGATCCGATATTCGAACGAA        | CCGCTCGAGTCATCCCTTAAGC            | 94/5' | 94/30" | 50/60" | 72/60"   | 72/7' | 30 | Vent |
| 161 | 792 | June | CGCGGATCCCTTAATAAGTGATAG       | CCGCTCGAGTTAAAGGGGATTC            | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 162 | 797 | June | CGCGGATCCAAATTAATCTTTT         | CCGCTCGAGTCAAAAACACTTCG           | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 88  | 798 | Apr  | GGAAATCCAAACTGAGATGAATC        | CCGCTCGAGTCAATCAGCCCTTTTAAAG      | 94/5' | 94/30" | 50/30" | 72/1'    | 72/7' | 25 | Vent |
| 206 | 808 | July | CGCGGATCCGAATGGCTGTGGAAAGG     | CCGCTCGAGTTAAGAAGCCATCTCTAG       | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 163 | 816 | June | CGCGGATCCAGCGCTTATATCATG       | CCGCTCGAGTTAAATTAATGATAATG        | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 91  | 827 | Apr  | CGCGATCCGAATGAGGTATCAACATG     | CCGCTCGAGTTAAAAATCATCTCTCT        | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 164 | 828 | June | CGCGATCCCTTGAAGATGAAAAATC      | CCGCTCGAGTCATTTTAAACCTCC          | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 92  | 829 | Apr  | CGCGATCCGAATCCCTAGCGGTAGAA     | CCGCTCGAGTTAATACTCTCTTAAATC       | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 93  | 836 | Apr  | CGCGATCCGAATGAAAAAGCGTTAATA    | CCGCTCGAGTTATGGCGTAAGCTCTAG       | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 165 | 839 | June | CGCGATCCCAATGTCAAAAATCGTTG     | CCGCTCGAGTCACCCCTTAATTTAG         | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 25 | Vent |
| 20  | 840 | June | CGCGATCCGAGGAAATAGCATGTTAATACC | CCGCTCGAGTCACCTGCTTGCATGACTTATCCA | -     | 97/30" | 55/1'  | 72/2'    | -     | 25 | Vent |
| 208 | 841 | July | CGCGATCCGAATGCAAGCAGTATTTA     | CCGCTCGAGTTATAAGAAATTTTGCATACAC   | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 166 | 842 | June | CGCGAATTCAGACACAAACACCGA       | CCGCTCGAGTCATCAAAATCAATGG         | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent |
| 209 | 846 | July | CGCGATCCGAATGGCAAGGATTCGTGGTA  | CCGCTCGAGTACTTCTGCTACCCAGGT       | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent |
| 25  | 847 | Apr  | CGCGATCCGAAGCAGTGATTTACGGAGCGT | CCGCTCGAGTCAATTTATATCTTAAAGTTATC  | -     | 95/30" | 55/50" | 72/1'30" | -     | 25 | Vent |
| 94  | 850 | Apr  | CGCGATCCGAGTTGAATTAAGTGGGT     | CCGCTCGAGTTAAAGCCCTACCGCTTA       | -     | 97/30" | 60/1'  | 72/1'30" | -     | 25 | Vent |
| 95  | 852 | Apr  | CTGAATTCGAATGAATAAGCTATTGCTA   | CCGCTCGAGTCAAAATATTATACGCATACC    | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 96  | 876 | Apr  | CGCGATCCGAATGACTCTAGGCATTGAT   | CCGCTCGAGTTAAATAAGCGTTGTTCCAC     | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |
| 97  | 881 | Apr  | CGCGATCCGAATGAAACGATTTATGG     | CCGCTCGAGTCAATAATCCCATTTGTTTG     | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent |

|     |     |      |                                  |                                |       |        |        |          |       |    |       |
|-----|-----|------|----------------------------------|--------------------------------|-------|--------|--------|----------|-------|----|-------|
| 140 | 544 | June | CGCGATCCGAATGAGCCGTGACTGCG       | CCGCTCGAGTCAATTCCTTATCTATCAAG  | -     | 97/30" | 52/1'  | 72/1'30" | -     | 25 | Vent  |
| 60  | 551 | Apr  | CGCGATCCGAATGAAAGTGCAAAATTTT     | CCGCTCGAGCTATTTTCATCATCAAA     | -     | 97/30" | 55/45" | 72/1'30" | -     | 25 | Vent  |
| 61  | 558 | Apr  | CGCGATCCGATTTTATCGTTTATGGG       | CCGCTCGAGCTAAAGACACTTTATC      | -     | 97/30" | 55/45" | 72/1'30" | -     | 25 | Vent  |
| 201 | 561 | July | CGCGATCCGAATGATGCAAGTTTACCAC     | CCGCTCGAGTTAAGCGTTTGAAGATTTC   | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 62  | 563 | Apr  | CGCGATCCGAGTAGACATTATGACTAC      | CCGCTCGAGCTAAGCTTGAITTTTAGG    | -     | 97/30" | 55/45" | 72/1'30" | -     | 25 | Vent  |
| 141 | 576 | June | CGCGATCCGAATGGGTTTATGACGGA       | CCGCTCGAGTAGAACACATATTGATCCC   | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 142 | 578 | June | CGCGATCCGAATGAAGAACGGAATAGTCA    | CCGCTCGAGTTAAATTAAGTTTGGGGTT   | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 143 | 580 | June | CGCGATCCGAATGTTTGAAGATTTAAAC     | CCGCTCGAGCTACGACTCGCTCTTTGTATT | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 144 | 585 | June | CGCGATCCGAATGAGTTTATAATATTTAAATG | CCGCTCGAGTTAAATGCGCACGAATGCGA  | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 145 | 599 | June | CGCGATCCGAATGCCAGATAAAGAAATAC    | CCGCTCGAGTTAGAAAATTTAGGATTGT   | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 65  | 602 | Apr  | CGCGATCCGAATGAAGATTTGCAITTT      | CCGCTCGAGTCACTCTTTTCGTTCAA     | -     | 97/30" | 55/45" | 72/1'30" | -     | 25 | Vent  |
| 66  | 607 | Apr  | GGGAATCAAAATAGCACGCC             | CCGCTCGAGTTAGAAATTTAGCGC       | 94/5' | 94/30" | 55/30" | 72/1'    | 72/7' | 25 | Vent  |
| 67  | 610 | Apr  | GGGAATTCGGCTTGAATAATCTC          | CCGCTCGAGTTAAATTTAGGTTAG       | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 25 | Vent  |
| 19  | 615 | July | CGCGATCCGAAGACATGTGCAACCGATG     | CCGCTCGAGCTAAAGTTTTCGAAATCAC   | -     | 97/30" | 55/1'  | 72/2'    | -     | 25 | Vent  |
| 68  | 616 | Apr  | GGGAATTCGGGTTACTGGGCTAAG         | CCGCTCGAGTTACCTTAAAGAAAC       | 94/5' | 94/30" | 45/30" | 72/30"   | 72/7' | 25 | Vent  |
| 204 | 625 |      | CGCGATCCGAAGGGTGGCGCACTTAGG      | CCGCTCGAGCTAAATTTGAACACCTCCGC  | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 14  | 626 | Apr  | CGCGATCCGACAAAAGATCATGGCATTTTG   | CCGCTCGAGCTAAGTCGCGCACCTTCAGC  | -     | 97/30" | 55/45" | 72/1'30" | -     | 25 | Vent  |
| 205 | 633 | July | CGCGATCCGAATGACTTCAGCTTCAAGC     | CCGCTCGAGCTAGCTCTTTTAAAGAG     | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 69  | 635 | Apr  | GGGAATCAATAAACACCGTT             | CCGCTCGAGCTAAATAATATAGAT       | 94/5' | 94/30" | 45/30" | 72/30"   | 72/7' | 30 | Vent  |
| 146 | 639 | June | CGCGATCCGAATGGCAAAAGATTTGAAT     | CCGCTCGAGTTAAAAAGCTCATTTTAGG   | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 147 | 642 | June | CTGAATTCGAGTTTAAAGGGTTTITGAA     | CCGCTCGAGTTAAAAATATAAGTTAGTT   | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 70  | 646 | Apr  | CGGATCCGATACGCAAGCAAAATTAG       | CCGCTCGAGTTATCGGCTTGAAGTG      | 94/5' | 94/30" | 45/30" | 72/30"   | 72/7' | 30 | Vent  |
| 148 | 647 | June | GGAAATCGAATGAGCGGAGTTTITGAAA     | CCGCTCGAGTTAAATTTCTTCTTGGAT    | -     | 97/30" | 55/1'  | 72/1'30" | -     | 25 | Vent  |
| 149 | 654 | June | CGCGATCCGAATGCAAAACCATGATTIA     | CCGCTCGAGCTACCCATGCGAACATGAGCA | -     | 97/30" | 55/1'  | 72/1'    | -     | 25 | Vent  |
| 72  | 655 | Apr  | GGGAATCAAAAGGCTTTTITATCCC        | CCGCTCGAGTCATGGTTTTCATGGTG     | 94/5' | 94/30" | 55/30" | 72/30"   | 72/7' | 30 | Vent  |
| 150 | 669 | June | CGCGATCCGAATCTCTTAAGCGTTTGG      | CCGCTCGAGTCAAGATTGAGCGTTTTCG   | -     | 97/20" | 55/40" | 72/1'30" | -     | 25 | Taq   |
| 73  | 670 | Apr  | GGGAATCAATATATCGGTTAACCCC        | CCGCTCGAGTCAACTCCCTTAACC       | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 20 | Vent  |
| 74  | 675 | Apr  | GGGAATTCAGCGTGAATAGTATGG         | CCGCTCGAGTCACTTCATCTCATC       | 94/5' | 94/30" | 55/30" | 72/1'    | 72/7' | 25 | Vent  |
| 34  | 678 | Apr  | CGCGATCCGAAGACAAAGAGTCTTGATCTA   | CCGCTCGAGTTAGTCTTCTTAAAGATTG   | -     | 97/30" | 55/45" | 72/1'30" | -     | 25 | Vent  |
| 75  | 690 | Apr  | CGGATCCATTAATAAAGCTAG            | CCGCTCGAGTTAAACCCCATGATG       | 94/5' | 94/30" | 50/30" | 72/1'    | 72/7' | 25 | ExTaq |
| 76  | 695 | Apr  | CGGATCCCGTGAACGTAGCGC            | CCGCTCGAGTTAAACCCCATTTTG       | 94/5' | 94/30" | 50/30" | 72/30"   | 72/7' | 30 | Vent  |
| 77  | 699 |      | CGGATCCCTTAAGGAAAAACATTTAG       | CCGCTCGAGTCACTCATCAACCG        | 94/5' | 94/30" | 50/30" | 72/1'    | 72/7' | 25 | Vent  |
| 78  | 701 | Apr  | CGGATCCAAAAGGCAAGTCAG            | CCGCTCGAGTCAAAAAGATGCTAC       | 94/5' | 94/30" | 50/30" | 72/1'    | 72/7' | 25 | Vent  |
| 79  | 702 | Apr  | CGGGAATTCATTAACCAATCATTAAATG     | CCGCTCGAGTCAAGGCTTTTGATG       | 94/5' | 94/30" | 50/30" | 72/1'    | 72/7' | 25 | ExTaq |

| ORF HP | GHP  | Priority | oligo 5'                        | oligo 3'                          | PCR Conditions |        |        |          |           |        |            |  |
|--------|------|----------|---------------------------------|-----------------------------------|----------------|--------|--------|----------|-----------|--------|------------|--|
|        |      |          |                                 |                                   | Dén. inil.     | Dén.   | Hyb.   | Elong.   | Elong fin | cycles | Polymérase |  |
| PMO    | TIGR |          |                                 |                                   |                |        |        |          |           |        |            |  |
| 43     | 147  | July     | CTGAATTCGAATGAAAGAAATTTTAGTGCT  | CCGCTCGAGTTAAAGCTCATAATTCAAAT     | -              | 97/30" | 55/1'  | 72/2'30" | -         | 25     | Vent       |  |
| 24*    | 282  | Apr      | CGGGATCCGAAAGGTTATCACAATG       | CCGCTCGAGTCACATAGCGCTGTGATG       | 94/5'          | 94/30" | 50/30" | 72/1'    | 72/7'     | 30     | Vent       |  |
| 12     | 359  | Apr      | CCGGATCCGAATTAGGAGAGTTGTGCGATG  | CCGCTCGAGCTACCAATTTGTAGCCACTTC    | -              | 97/30" | 50/1'  | 72/2'30" | -         | 25     | Vent       |  |
| 123    | 409  | June     | CCGGATCCGAATGTGGAATTTTAAACACC   | CCGCTCGAGTTAAAACTTATAGGAATTTTC    | -              | 97/20" | 55/40" | 72/1'30" | -         | 25     | Taq        |  |
| 124    | 422  | June     | CCGGATCCGAATGAATTTTAAATTTTATG   | CCGCTCGAGTCAAAATTCGTCATATTTTC     | -              | 97/20" | 55/40" | 72/1'30" | -         | 25     | Taq        |  |
| 121    | 430  | June     | CTGAATTCGAATGAAACTCCCGGTGCTTGAG | CCGCTCGAGTTAAAGCCCTTTTGTATTATC    | -              | 97/20" | 55/40" | 72/1'30" | -         | 25     | Taq        |  |
| 46     | 442  | Apr      | CTGAATTCGAATGAAAAAGAGGTCGTG     | CCGCTCGAGTTAATCCCTAAAAAATGCA      | -              | 97/30" | 55/45" | 72/1'30" | -         | 25     | Vent       |  |
| 47     | 445  | Apr      | CCGGATCCGACTCAGTGGTAGACACGA     | CCGCTCGAGTAGTCGCGCTTGAACGAT       | -              | 97/30" | 55/45" | 72/1'30" | -         | 25     | Vent       |  |
| 122    | 446  | June     | CCGGATCCGAATGGTGGTTTTACTAAAAAG  | CCGCTCGAGTCAAGTTTTTAGATTTTCACC    | -              | 97/20" | 55/40" | 72/1'30" | -         | 25     | Taq        |  |
| 125    | 447  | June     | CCGGATCCGAATTCCTTATCTGTGTTAAACA | CCGCTCGAGTTAAAAACGCCACCACATAGT    | -              | 97/30" | 55/50" | 72/1'30" | -         | 25     | Vent       |  |
| 126    | 450  | June     | CCGGATCCGAATCGCTGCGTGGTGAT      | CCGCTCGAGCTATTTATGGTATGGATGCTT    | -              | 97/30" | 55/50" | 72/1'30" | -         | 25     | Vent       |  |
| 127    | 451  | June     | CCGGATCCGAATGGGATTTGCAGATTTC    | CCGCTCGAGTTAAAAAATCTTTGAAGTCTT    | -              | 97/30" | 55/50" | 72/1'30" | -         | 25     | Vent       |  |
| 128    | 452  | June     | CCGGATCCGAATGCAAGGTTCTTTTAC     | CCGCTCGAGTCAAAACCCCTAAATTCAGGCT   | -              | 97/30" | 55/50" | 72/1'30" | -         | 25     | Vent       |  |
| 48     | 454  | Apr      | CCGGATCCGAATGGTTTTATCGCTCTT     | CCGCTCGAGCTACCTTAAACGCACAAC       | -              | 97/30" | 55/45" | 72/1'30" | -         | 25     | Vent       |  |
| 129    | 456  | June     | CCGGATCCGAATGAACGCTTGGAAATACG   | CCGCTCGAGTCATGATTTTCTCTTATTTTTTAG | -              | 97/30" | 55/50" | 72/1'30" | -         | 25     | Vent       |  |
| 130    | 461  | June     | CCGGATCCGAATGCAGATTTTTCAGT      | CCGCTCGAGTTAACTAAACCCATTTTCAGC    | -              | 97/30" | 55/50" | 72/1'30" | -         | 25     | Vent       |  |
| 131    | 476  | June     | CCGGATCCGAATGGCGCAAAAAAAGCTTT   | CCGCTCGAGTTAAAAATAGGGTTTCACCTA    | -              | 97/30" | 55/50" | 72/1'30" | -         | 25     | Vent       |  |
| 132    | 478  | June     | CCGGATCCGAATGAATTTTCAAGAAAT     | CCGCTCGAGTCAGCCTTTTCTTAACTCATC    | -              | 97/30" | 55/50" | 72/2'    | -         | 25     | Vent       |  |
| 52     | 479  | Apr      | CCGGATCCGATTTTAAAGGGAITAGA      | CCGCTCGAGTTATGAAATGATTTGAC        | -              | 97/30" | 55/45" | 72/1'30" | -         | 25     | Vent       |  |
| 53     | 480  | Apr      | CCGGATCCGAATGCAAGGGGAAATCATG    | CCGCTCGAGTTAAAGAAATTTAGAAAT       | -              | 97/30" | 55/45" | 72/1'30" | -         | 25     | Vent       |  |
| 196    | 483  |          | CCGGATCCGACCACTTTCAGGGAAGCG     | CCGCTCGAGTACCCAAATAGTATCCATAG     | -              | 97/30" | 55/50" | 72/1'30" | -         | 25     | Vent       |  |
| 134    | 511  | June     | CCGGATCCGAAGACATAGAAACAGAGCT    | CCGCTCGAGTTAAAAATCCATTCATAG       | -              | 97/20" | 55/40" | 72/1'30" | -         | 25     | Taq        |  |
| 55     | 515  | Apr      | CCGGATCCGACAAAGGGTGGTTTCACTG    | CCGCTCGAGTCAAAACACTTCTTCATTG      | -              | 97/30" | 55/45" | 72/1'30" | -         | 25     | Vent       |  |
| 198    | 517  | July     | CCGGATCCGAAGACTTCCCTCAATTTTAAAG | CCGCTCGAGTACTCGTATATGTGGG         | -              | 97/30" | 55/1'  | 72/1'    | -         | 25     | Vent       |  |
| 135    | 519  | June     | CCGGATCCGAATGAAAAAATGATGAT      | CCGCTCGAGTTAATCGGTGTTTCTTGATC     | -              | 97/20" | 55/40" | 72/1'30" | -         | 25     | Taq        |  |
| 56     | 523  | Apr      | CCGGATCCGATTTAAGGATTTCTATTG     | CCGCTCGAGTTAAAGGTTTAAAGGGC        | -              | 97/30" | 55/45" | 72/1'30" | -         | 25     | Vent       |  |
| 137    | 526  | June     | CCGGATCCGAATGCAATTTTCAATCATCT   | CCGCTCGAGTCAATTAACCTCATATTG       | -              | 97/20" | 55/40" | 72/1'30" | -         | 25     | Taq        |  |
| 138    | 534  | June     | CCGGATCCGAATGCTTTTGTATGCTT      | CCGCTCGAGTATCAAAATCTTTTTTG        | -              | 97/30" | 55/1'  | 72/1'30" | -         | 25     | Vent       |  |
| 59     | 541  | Apr      | CCGGATCCGAATGCAATATAGAAAAAT     | CCGCTCGAGTTAAACAAAAAATCTCCC       | -              | 97/30" | 55/45" | 72/1'30" | -         | 25     | Vent       |  |
| 139    | 542  | June     | CCGGATCCGAATGAGTAAGAGTTTATAG    | CCGCTCGAGTTACAAATCTTTTTCTAATAAC   | -              | 97/30" | 55/1'  | 72/1'    | -         | 25     | Vent       |  |

-87-

phosphate buffer, containing 500 mM NaCl (pH 7.5). The gel is then transferred to a tube, mixed with 100 mM ethanolamine (pH 7.5) for 4 hours at room temperature, and washed twice with 2 column volumes of PBS. The gel is then stored in 1/10,000 PBS/merthiolate. The amount of IgG antibodies coupled to the gel is determined by measuring the optical density (OD) at 280 nm of the IgG solution and the direct eluate, plus washings.

#### 4.C. Adsorption and elution of the antigen

An antigen solution in 50 mM Tris-HCl (pH 8.0), 2 mM EDTA, for example, the supernatant or the solubilized pellet obtained using the methods described in 3.E., after centrifugation and filtration through a 0.45  $\mu$ m membrane, is applied to a column equilibrated with 50 mM Tris-HCl (pH 8.0), 2 mM EDTA, at a flow rate of about 10 ml/hour. The column is then washed with 20 volumes of 50 mM Tris-HCl (pH 8.0), 2 mM EDTA. Alternatively, adsorption can be achieved by mixing overnight at  $5\pm 3^{\circ}\text{C}$ .

The adsorbed gel is washed with 2 to 6 volumes of 10 mM sodium phosphate buffer (pH 6.8) and the antigen is eluted with 100 mM glycine buffer (pH 2.5). The eluate is recovered in 3 ml fractions, to each of which is added 150  $\mu$ l of 1 M sodium phosphate buffer (pH 8.0). Absorption is measured at 280 nm for each fraction; those fractions containing the antigen are pooled and stored at  $-20^{\circ}\text{C}$ .

-86-

**EXAMPLE 4: Purification of the polypeptides of the invention by immunoaffinity****4.A. Purification of specific IgGs**

An immune serum, as prepared as is described in section 2.G., is applied to a protein A Sepharose Fast Flow column (Pharmacia) equilibrated in 100 mM Tris-HCl (pH 8.0). The resin is washed by applying 10 column volumes of 100 mM Tris-HCl and 10 volumes of 10 mM Tris-HCl (pH 8.0) to the column. IgG antibodies are eluted with 0.1 M glycine buffer (pH 3.0) and are collected as 5 ml fractions to each of which is added 0.25 ml 1 M Tris-HCl (pH 8.0). The optical density of the eluate is measured at 280 nm and fractions containing the IgG antibodies are pooled, dialyzed against 50 mM Tris-HCl (pH 8.0), and, if necessary, stored frozen at -70°C.

**4.B. Preparation of the column**

An appropriate amount of CNBr-activated Sepharose 4B gel (1 g of dried gel provides for approximately 3.5 ml of hydrated gel; gel capacity is from 5 to 10 mg coupled IgG/ml of gel) manufactured by Pharmacia (17-0430-01) is suspended in 1 mM HCl buffer and washed with a buchner by adding small quantities of 1 mM HCl buffer. The total volume of buffer is 200 ml per gram of gel.

Purified IgG antibodies are dialyzed for 4 hours at  $20 \pm 5^\circ\text{C}$  against 50 volumes of 500 mM sodium phosphate buffer (pH 7.5). The antibodies are then diluted in 500 mM phosphate buffer (pH 7.5) to a final concentration of 3 mg/ml.

IgG antibodies are mixed with the gel overnight at  $5 \pm 3^\circ\text{C}$ . The gel is packed into a chromatography column and is washed with 2 column volumes of 500 mM phosphate buffer (pH 7.5), and 1 column volume of 50 mM sodium

-85-

The N-terminal primers are designed to include the ribosome binding site of the target gene, the ATG start site, and any signal sequence and cleavage site. The N-terminal primers can include a 5' clamp and a restriction endonuclease recognition site, such as that for *Bam*HI (GGATCC), which facilitates subsequent cloning. Similarly, the C-terminal primers can include a restriction endonuclease recognition site, such as that for *Xho*I (CTCGAG), which can be used in subsequent cloning, and a TAA stop codon.

Amplification of genes encoding the polypeptides of the invention can be carried out using Thermalase DNA Polymerase under the conditions described above in Example 2. Alternatively, Vent DNA polymerase (New England Biolabs), Pwo DNA polymerase (Boehringer Mannheim), or Taq DNA polymerase (Appligene) can be used, according to instructions provided by the manufacturers.

A single PCR product for each clone is amplified and cloned into appropriately cleaved pET 24 (*e.g.*, *Bam*HI-*Xho*I cleaved pET 24), resulting in the construction of a transcriptional fusion that permits expression of the proteins without His-tags. The expressed products can be purified as denatured proteins that are refolded by dialysis into 1 M arginine.

Cloning into pET 24 allows transcription of the genes from the T7 promoter, which is supplied by the vector, but relies upon binding of the RNA-specific DNA polymerase to the intrinsic ribosome binding sites of the genes, and thereby expression of the complete ORF. The amplification, digestion, and cloning protocols that can be used in this method are as described above for constructing translational fusions.

-84-

same way. Fifteen days after the last injection, animal serum is recovered, decomplexed, and filtered through a 0.45 µm membrane.

### 2.G.2. Mouse hyperimmune ascites fluid

Ten mice are injected subcutaneously with 10-50 µg of a purified fusion polypeptide as obtained using the methods described in 2.E.1. or 2.E.2., in the presence of Freund's complete adjuvant and in a volume of approximately 200 µl. Seven and 14 days after the initial injection, booster doses, which are identical to the priming doses, except that Freund's incomplete adjuvant is used, are administered in the same way. Twenty one and 28 days after the initial infection, mice receive 50 µg of the antigen alone intraperitoneally. On day 21, mice are also injected intraperitoneally with sarcoma 180/TG cells CM26684 (Lennette *et al.*, *Diagnostic Procedures for Viral, Rickettsial, and Chlamydial Infections*, 5th Ed. Washington DC, American Public Health Association, 1979). Ascites fluid is collected 10-13 days after the last injection.

### EXAMPLE 3: Methods for producing transcriptional fusions lacking His-tags

Methods for amplification and cloning of DNA encoding the polypeptides of the invention as transcriptional fusions lacking His-tags are described as follows. Two PCR primers for each clone are designed based upon the sequences of the polynucleotides that encode them (see the attached sequence listing, odd numbers, up to SEQ ID NO:1363). These primers can be used to amplify DNA encoding the polypeptides of the invention from any *H. pylori* strain, including, for example, ORV2001 and the strain deposited as ATCC deposit number 43579, as well as from other *Helicobacter* species.

-83-

$\beta$ -mercaptoethanol is added to the eluted protein to a final concentration of 1 mM, and then the eluted protein is passed through a Sephadex G-25 column equilibrated in 0.1 M acetic acid. Protein eluted from the column is slowly added to 4 volumes of 50 mM phosphate buffer (pH 7.0), and the protein remains in solution.

5

## 2.F. Evaluation of the protective activity of the purified protein

Groups of 10 OF1 mice (IFFA Credo) are immunized rectally with 25  $\mu$ g of the purified recombinant protein, admixed with 1  $\mu$ g of cholera toxin (Berna) in physiological buffer. Mice are immunized on days 0, 7, 14, and 21. Fourteen days after the last immunization, the mice are challenged with *H. pylori* strain ORV2001, grown in liquid media (the cells are grown on agar plates, as described in 2.A., and, after harvest, are resuspended in Brucella broth; the flasks are then incubated overnight at 37°C). Fourteen days after challenge, the mice are sacrificed and their stomachs are removed. The amount of *H. pylori* is determined by measuring the urease activity in the stomach and by culture.

10

15

## 2.G. Production of monospecific polyclonal antibodies

### 2.G.1. Hyperimmune rabbit antiserum

20

25

New Zealand rabbits are injected both subcutaneously and intramuscularly with 100  $\mu$ g of a purified fusion polypeptide, as obtained using the methods described in 2.E.1. or 2.E.2., in the presence of Freund's complete adjuvant and in a total volume of approximately 2 ml. Twenty one and 42 days after the initial injection, booster doses, which are identical to the priming doses, except that Freund's incomplete adjuvant is used, are administered in the



-82-

The protein fractions eluted from the IMAC column with buffer D (buffer C containing 500 mM imidazole) are pooled. Arginine is added to the solution to a final concentration of 0.5 M, and the mixture is dialyzed against PBS containing 0.5 M arginine and various concentrations of urea (4 M, 3 M, 2 M, 1 M, and 0.5 M) to progressively decrease the concentration of urea. The final dialysate is filtered through a 0.22  $\mu$ m membrane and stored at -45°C.

Alternatively, when the above-described purification process is not as efficient as it should be, two other processes can be used and are described as follows. A first alternative involves the use of a mild denaturant, N-octyl glucoside (NOG). Briefly, a pellet obtained as is described in 2.E. is homogenized in a solution of 5 mM imidazole, 500 mM sodium chloride, and 20 mM Tris-HCl (pH 7.9) by microfluidization at a pressure of 15,000 psi, and is clarified by centrifugation at 4,000-5,000 x g. The pellet is recovered, resuspended in 50 mM NaPO<sub>4</sub> (pH 7.5) containing 1-2% weight /volume NOG, and homogenized. The NOG-soluble impurities are removed by centrifugation. The pellet is extracted once more by repeating the preceding extraction step. The pellet is dissolved in 8 M urea, 50 mM Tris (pH 8.0). The urea-solubilized protein is diluted with an equal volume of 2 M arginine, 50 mM Tris (pH 8.0), and is dialyzed against 1 M arginine for 24-48 hours to remove the urea. The final dialysate is filtered through a 0.22  $\mu$ m membrane and stored at -45°C.

A second alternative involves the use of a strong denaturant, such as guanidine hydrochloride. Briefly, a pellet obtained as is described in 2.E. is homogenized in a solution of 5 mM imidazole, 500 mM sodium chloride, and 20 mM Tris-HCl (pH 7.9) by microfluidization at a pressure of 15,000 psi, and is clarified by centrifugation at 4,000-5,000 x g. The pellet is recovered, resuspended in 6 M guanidine hydrochloride, and passed through an IMAC column charged with Ni<sup>++</sup>. The bound antigen is eluted with 8 M urea (pH 8.5).

-81-

location of the target protein in the soluble or insoluble fractions, as is described further below.

#### 2.E.1. Soluble fraction

If the target protein is produced in a soluble form (*i.e.*, in the supernatant obtained using the methods described in 2.E.) NaCl and imidazole are added to the supernatant to final concentrations of 50 mM Tris-HCl (pH 8.0), 0.5 M NaCl, and 10 mM imidazole (buffer A). The mixture is filtered through a 0.45  $\mu$ m membrane and loaded onto an IMAC column (Pharmacia HiTrap chelating Sepharose; 1 ml), which has been charged with nickel ions according to the manufacturer's recommendations. After loading, the column is washed with 50 column volumes of buffer A and the recombinant protein is eluted with 5 ml of buffer B (50 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 500 mM imidazole).

The elution profile is monitored by measuring the absorbance of the fractions at 280 nm. Fractions corresponding to the protein peak are pooled, dialyzed against PBS containing 0.5 M arginine, filtered through a 0.22  $\mu$ m membrane, and stored at -45°C.

#### 2.E.2. Insoluble fraction

If the target protein is expressed in the insoluble fraction (pellets obtained using the methods described in 2.E.), purification is conducted under denaturing conditions. NaCl, imidazole, and urea are added to the resuspended pellet to final concentrations of 50 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 10 mM imidazole, and 6 M urea (buffer C). After complete solubilization, the mixture is filtered through a 0.45  $\mu$ m membrane and loaded onto an IMAC column.

The purification procedures on the IMAC column are the same as are described in 2.E.1., except that 6 M urea is included in all of the buffers used and 10 column volumes of buffer C are used to wash the column after protein loading, instead of 50 column volumes.

-80-

absorbance at 600 nm ( $OD_{600}$ ) reaches 0.4-1.0. The culture is stopped from growing by placing the flask at 4°C overnight. The following day, 10 ml of the overnight culture is used to inoculate 240 ml LB medium containing kanamycin (25 µg/ml), with the initial  $OD_{600}$  being about 0.02-0.04. Four flasks are inoculated for each ORF. The cells are grown to an  $OD_{600}$  of 1.0 (about 2 hours at 37°C), a 1 ml sample is harvested by centrifugation, and the sample is analyzed by SDS-PAGE to detect any leaky expression. The remaining culture is induced with 1 mM IPTG and the induced cultures are grown for an additional 2 hours at 37°C.

The final  $OD_{600}$  reading is taken and the cells are harvested by centrifugation at 5,000 x g for 15 minutes at 4°C. The supernatant is discarded and the pellets are resuspended in 50 mM Tris-HCl (pH 8.0), 2 mM EDTA. Two hundred and fifty ml of buffer are used for each 1 L of culture and the cells are recovered by centrifugation at 12,000 x g for 20 minutes. The supernatant is discarded and the pellets are stored at -45°C.

## 2. E. Protein purification

Pellets obtained using the methods described in 2.D. are thawed and resuspended in 95 ml of 50 mM Tris-HCl (pH 8.0). Pefabloc and lysozyme are added to final concentrations of 100 µM and 100 µg/ml, respectively. The mixture is homogenized with magnetic stirring at 5°C for 30 minutes. Benzonase (Merck) is added to a final concentration of 1 U/ml, in the presence of 10 mM  $MgCl_2$ , to ensure total digestion of the DNA. The suspension is sonicated (Branson Sonifier 450) for 3 cycles of 2 minutes each at maximum output. The homogenate is centrifuged at 19,000 x g for 15 minutes and both the supernatant and the pellet are analyzed by SDS-PAGE to detect the cellular

-79-

presence of histidine residues at the N-terminus of the fusion protein, which are encoded by the vector.

The ligation reaction (20  $\mu$ l) is carried out at 14°C overnight and then is used to transform 100  $\mu$ l fresh *E. coli* XL1-blue competent cells (Novagen).

The cells are incubated on ice for 2 hours, heat-shocked at 42°C for

30 seconds, and returned to ice for 90 seconds. The samples are then added to 1 ml LB broth in the absence of selection and grown at 37°C for 2 hours. The cells are plated out on LB agar containing kanamycin (50  $\mu$ g/ml) at a 10x and neat dilution and incubated overnight at 37°C. The following day, 50 colonies are picked, plated onto secondary plates, and incubated at 37°C overnight.

Five colonies are picked, grown in 3 ml LB broth supplemented with kanamycin (100  $\mu$ g/ml), and grown overnight at 37°C. Plasmid DNA is extracted using the Quiagen mini-prep method and is quantitated by agarose gel electrophoresis.

PCR is performed with the gene-specific primers under the conditions set forth above and transformant DNA is confirmed to contain the desired insert. If PCR-positive, one of the five plasmid DNA samples (500 ng) extracted from the *E. coli* XL1-blue cells is used to transform competent BL21 ( $\lambda$ DE3) *E. coli* competent cells (Novagen; as described previously).

Transformants (10) are picked, plated onto selective kanamycin (50  $\mu$ g/ml)-containing LB agar plates, and stored as a research stock in LB containing 50% glycerol.

## 2.D. Purification of recombinant proteins

One ml of frozen glycerol stock prepared as described in 2.C. is used to inoculate 50 ml of LB medium containing 25  $\mu$ g/ml kanamycin in a 250 ml Erlenmeyer flask. The flask is incubated at 37°C for 2 hours or until the

-78-

|                            |             |
|----------------------------|-------------|
| dNTPs mix                  | 200 $\mu$ M |
| 10x ThermoPol buffer       | 10 $\mu$ l  |
| primers                    | 300 nM each |
| DNA template               | 50 ng       |
| Heat-stable DNA polymerase | 2 units     |

Appropriate amplification reaction conditions can readily be determined by one skilled in the art. For example, the following conditions can be used for amplification of DNA encoding GHPO 615 using the primers set forth above: initial denaturation at 94°C for 5 minutes, 25 cycles of denaturation at 97°C for 30 seconds, hybridization at 55°C for 1 minute, and elongation at 72°C for 2 minutes, using Vent DNA polymerase. In the case of amplifying DNA encoding GHPO 1282 with the primers set forth above, the following conditions can be used: initial denaturation at 94°C for 5 minutes, 25 cycles of denaturation at 94°C for 30 seconds, hybridization at 45°C for 30 seconds, and elongation at 72°C for 30 seconds, followed by a final elongation at 72°C for 7 minutes, using Vent DNA polymerase. The following conditions can be used for amplification of DNA encoding GHPO 840 using the primers set forth above: 25 cycles of denaturation at 97°C for 30 seconds, hybridization at 55°C for 1 minute, and elongation at 72°C for 2 minutes using Vent DNA polymerase. Table 1 sets forth conditions for using the primers listed therein.

## 2.C. Transformation and selection of transformants

A single PCR product is thus amplified and then is digested at 37°C for 2 hours with *Bam*HI and *Xho*I together in a 20  $\mu$ l reaction volume. The digested product is ligated to similarly cleaved pET28a (Novagen) that is dephosphorylated prior to the ligation by treatment with Calf Intestinal Alkaline Phosphatase (CIP). The gene fusion constructed in this manner allows one-step affinity purification of the resulting fusion protein because of the

-77-

NO:1367), and

5'-CCGCTCGAGCTAAAAGTTTTGCAAATCAC-3' (SEQ ID  
NO:1368).

GHPO 961: 5'-CGCGGATCCGATTTTACTTGAAAAATTTAAAC-3' (SEQ  
ID NO:1369), and

5'-CCGCTCGAGTTAGAAAGTGTAAGTTCAAATAC-3' (SEQ ID  
NO:1370).

GHPO 1282: 5'-GCGGATCCTTTTCTTCAATGTTTG-3' (SEQ ID NO:1371),  
and

5'-CCGCTCGAGTCAAAGTTTAAACAAATTC-3' (SEQ ID  
NO:1372).

GHPO 296: 5'-CCGAATTCGGTTATAAAGCCCCT-3' (SEQ ID NO:1373),  
and

5'-CCGCTCGAGTTAAGGCTGATTAA-3' (SEQ ID NO:1374).

GHPO 840: 5'-CGCGGATCCGAGGAAATAGCATGTTAATAACC-3' (SEQ  
ID NO:1375), and

5'-CCGCTCGAGTCACTGCTTGCATGACTTATTCCA-3' (SEQ ID  
NO:1376).

The N-terminal and C-terminal primers for each clone can each include  
a 5' clamp and a restriction enzyme recognition sequence for cloning purposes  
(for example, *Bam*HI (GGATCC) and *Xho*I (CTCGAG) recognition  
sequences).

Amplification of gene-specific DNA is carried out using Vent DNA  
Polymerase (New England Biolabs) or Taq DNA polymerase (Appligene),  
according to the manufacturer's instructions. The reaction mixture, which is  
brought to a final volume of 100 µl with distilled water, is as follows:

-76-

associated with insertion of signal sequences in the membrane of the host strain carrying the hybrid construct are avoided.

**EXAMPLE 2: Preparation of isolated DNA encoding the polypeptides of the invention, and production of these polypeptides as histidine-tagged fusion proteins**

**2.A. Preparation of genomic DNA from *Helicobacter pylori***

*H. pylori* strain ORV2001, stored in LB medium containing 50% glycerol at -70°C, is grown on Colombia agar containing 7% sheep blood for 48 hours under microaerophilic conditions (8-10% CO<sub>2</sub>, 5-7% O<sub>2</sub>, 85-87% N<sub>2</sub>). Cells are harvested, washed with phosphate buffer saline (PBS) (pH 7.2), and DNA is then extracted from the cells using the Rapid Prep Genomic DNA Isolation kit (Pharmacia Biotech).

**2.B. PCR amplification**

DNA molecules encoding the polypeptides of the invention are amplified from genomic DNA, as can be prepared as is described above, by the Polymerase Chain Reaction (PCR) using primers that can readily be designed by one skilled in the art. Specific examples of primers that can be used in the invention are shown in Table 1. As specific examples, to amplify genes encoding GHPO 147, GHPO 615, GHPO 961, GHPO 1282, GHPO 296, and GHPO 840 the following primers can be used:

GHPO 147: 5'-CTGAATTCGAATGAAAAGAATTTTAGTCTCT-3' (SEQ ID NO:1365), and

5'-CCGCTCGAGTTAAACTCATAATTCAAAT-3' (SEQ ID NO:1366).

GHPO 615: 5'-CGCGGATCCGAAGACATGTGCAACCGATG-3' (SEQ ID

-75-

### 1.D. Identification of signal sequences

The deduced protein encoded by a target gene sequence is analyzed using the PROTEAN software package (DNASar, Inc.). This analysis predicts those areas of the protein that are hydrophobic by using the Kyte-Doolittle algorithm, and identifies any potential polar residues preceding the hydrophobic core region, which is typical for many signal sequences. For confirmation, the target protein is then searched against a PROSITE database (DNASar, Inc.) consisting of motifs and signatures. Characteristic of many signal sequences and hydrophobic regions in general, is the identification of predicted prokaryotic lipid attachment sites. Where confirmation between the two approaches is apparent at the N-terminus of any protein, putative cleavage sites are sought. Specifically, this includes the presence of either an Alanine (A), Serine (S), or Glycine (G) residue immediately after the core hydrophobic region. In the case of lipoproteins, a Cysteine (C) residue would be identified as the +1 residue, post-cleavage.

### 1.E. Rational design of PCR primers based on the identification of signal sequences

In order to clone gene sequences as N-terminus translational fusions for the generation of recombinant proteins with N-terminal Histidine tags, the gene sequence that specifies the signal sequence is omitted. The 5'-end of the gene-specific portion of the N-terminal primer is designed to start at the first codon beyond the cleavage site. In the case of lipoproteins, the 5'-end of the N-terminal primer begins at the second codon, immediately after the modifiable residue at position +1 post-cleavage. The omission of the signal sequence from the recombinant allows for one-step purification, and potential problems



-74-

by the *H. pylori* genome for both the plus and minus strands, and was given the designation "O." Each ORF was assigned a number indicating its location on the genome and its position relative to other genes. No manipulation of the text file was required.

### 5      **1.B. Searching the *H. pylori* databases**

10      The databases constructed as is described above were searched using the program FASTA (Pearson *et al.*, Proc. Natl. Acad. Sci. USA 85:2444-2448, 1988). FASTA was used for searching either a DNA sequence against either of the gene databases ("H" and/or "N"), or a peptide sequence against the ORF library ("O"). TFASTX was used to search a peptide sequence against all possible reading frames of a DNA database ("H" and/or "N" libraries). Potential frameshifts also being resolved, FASTX was used for searching the translated reading frames of a DNA sequence against either a DNA database, or a peptide sequence against the protein database.

### 15      **1.C. Isolation of DNA sequences from the *H. pylori* genome**

20      The FASTA searches against the constructed DNA databases identified exact nucleotide coordinates on one or more of the isolated contigs, and therefore the location of the target DNA. Once the exact location of the target sequence was known, the contig identified to carry the gene was exported into the software package MapDraw (DNASTar, Inc.) and the gene was isolated. Gene sequences with flanking DNA was then excised and copied into the EditSeq. Software package (DNASTar, Inc.) for further analysis.

25

-73-

the invention so that they can be produced without his-tags, and Example 4 describes methods for purifying recombinantly produced polypeptides of the invention.

**EXAMPLE 1: Identification of genes in the *H. pylori* genome,  
identification of signal sequences, and primer design for amplification of  
genes lacking signal sequences**

**1.A. Creating *H. pylori* genomic databases**

The *H. pylori* genome was provided as a text file containing a single contiguous string of nucleotides that had been determined to be 1.76  
Megabases in length. The complete genome was split into 17 separate files using the program SPLIT (Creativity in Action), giving rise to 16 contigs, each containing 100,000 nucleotides, and a 17<sup>th</sup> contig containing the remaining 76,000 nucleotides. A header was added to each of the 17 files using the format: >hpg0.txt (representing contig 1), .hpg1.txt (representing contig 2), etc.  
The resulting 17 files, named hpg0 through hpg16, were then copied together to form one file that represented the plus strand of the complete *H. pylori* genome. The constructed database was given the designation "H." A negative strand database of the *H. pylori* genome was created similarly by first creating a reverse complement of the positive strand using the program SeqPup (D.G. Gilbert, Indiana University Biology Department) and then performing the same procedure as described above for the plus strand. This database was given the designation "N."

The regions predicted to encode open reading frames (ORFs) were defined for the complete *H. pylori* genome using the program GENEMARK™ (Borodovsky *et al.*, Comp. Chem. 17:123, 1993). A database was created from a text file containing an annotated version of all ORFs predicted to be encoded

-72-

pepto-bismol (see, *e.g.*, Goodwin *et al.*, *Helicobacter pylori, Biology and Clinical Practice*, CRC Press, Boca Raton, FL, pp 366-395, 1993; Physicians' Desk Reference, 49<sup>th</sup> edn., Medical Economics Data Production Company, Montvale, New Jersey, 1995). In addition, compounds containing more than one of the above-listed components coupled together, *e.g.*, ranitidine coupled to bismuth subcitrate, can be used. The invention also includes compositions for carrying out these methods, *i.e.*, compositions containing a *Helicobacter* antigen (or antigens) of the invention, an adjuvant, and one or more of the above-listed compounds, in a pharmaceutically acceptable carrier or diluent.

Amounts of the above-listed compounds used in the methods and compositions of the invention can readily be determined by one skilled in the art. In addition, one skilled in the art can readily design treatment/immunization schedules. For example, the non-vaccine components can be administered on days 1-14, and the vaccine antigen + adjuvant can be administered on days 7, 14, 21, and 28.

Methods and pharmaceutical compositions of the invention can be used to treat or to prevent *Helicobacter* infections and, accordingly, gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, *e.g.*, gastric and duodenal ulcers.

The invention is further illustrated by the following examples. Example 1 describes identification of genes, such as genes that encode the polypeptides of the invention, in the *Helicobacter* genome, as well as identification of signal sequences, and primer design for amplification of genes lacking signal sequences. Example 2 describes cloning of DNA molecules encoding polypeptides of the invention into a vector that provides a histidine tag, and production and purification of the resulting his-tagged fusion proteins. Example 3 describes methods for cloning DNA encoding the polypeptides of

-71-

with a pharmaceutically acceptable diluent or carrier, *e.g.*, water or a saline solution, such as phosphate buffer saline, optionally, including a bicarbonate salt, such as sodium bicarbonate, *e.g.*, 0.1 to 0.5 M. Bicarbonate can advantageously be added to compositions intended for oral or intragastric administration. In general, a diluent or carrier can be selected on the basis of the mode and route of administration, and standard pharmaceutical practice. Suitable pharmaceutical carriers and diluents, as well as pharmaceutical necessities for their use in pharmaceutical formulations, are described in *Remington's Pharmaceutical Sciences*, a standard reference text in this field and in the USP/NF.

The invention also includes methods in which gastroduodenal infections, such as *Helicobacter* infection, are treated by oral administration of a *Helicobacter* polypeptide of the invention and a mucosal adjuvant, in combination with an antibiotic, an antisecretory agent, a bismuth salt, an antacid, sucralfate, or a combination thereof. Examples of such compounds that can be administered with the vaccine antigen and an adjuvant are antibiotics, including, *e.g.*, macrolides, tetracyclines,  $\beta$ -lactams, aminoglycosides, quinolones, penicillins, and derivatives thereof (specific examples of antibiotics that can be used in the invention include, *e.g.*, amoxicillin, clarithromycin, tetracycline, metronidazole, erythromycin, cefuroxime, and erythromycin); antisecretory agents, including, *e.g.*,  $H_2$ -receptor antagonists (*e.g.*, cimetidine, ranitidine, famotidine, nizatidine, and roxatidine), proton pump inhibitors (*e.g.*, omeprazole, lansoprazole, and pantoprazole), prostaglandin analogs (*e.g.*, misoprostil and enprostil), and anticholinergic agents (*e.g.*, pirenzepine, telenzepine, carbenoxolone, and proglumide); and bismuth salts, including colloidal bismuth subcitrate, tripotassium dicitrate bismuthate, bismuth subsalicylate, bicitropeptide, and

-70-

Adjuvants that can be used in any of the vaccine compositions described above are described as follows. Adjuvants for parenteral administration include, for example, aluminum compounds, such as aluminum hydroxide, aluminum phosphate, and aluminum hydroxy phosphate. The antigen can be precipitated with, or adsorbed onto, the aluminum compound using standard methods. Other adjuvants, such as RIBI (ImmunoChem, Hamilton, MT), can also be used in parenteral administration.

Adjuvants that can be used for mucosal administration include, for example, bacterial toxins, *e.g.*, the cholera toxin (CT), the *E. coli* heat-labile toxin (LT), the *Clostridium difficile* toxin A, the *pertussis* toxin (PT), and combinations, subunits, toxoids, or mutants thereof. For example, a purified preparation of native cholera toxin subunit B (CTB) can be used. Fragments, homologs, derivatives, and fusions to any of these toxins can also be used, provided that they retain adjuvant activity. Preferably, a mutant having reduced toxicity is used. Suitable mutants are described, *e.g.*, in WO 95/17211 (Arg-7-Lys CT mutant), WO 96/6627 (Arg-192-Gly LT mutant), and WO 95/34323 (Arg-9-Lys and Glu-129-Gly PT mutant). Additional LT mutants that can be used in the methods and compositions of the invention include, *e.g.*, Ser-63-Lys, Ala-69-Gly, Glu-110-Asp, and Glu-112-Asp mutants. Other adjuvants, such as the bacterial monophosphoryl lipid A (MPLA) of, *e.g.*, *E. coli*, *Salmonella minnesota*, *Salmonella typhimurium*, or *Shigella flexneri*; saponins, and polylactide glycolide (PLGA) microspheres, can also be used in mucosal administration. Adjuvants useful for both mucosal and parenteral administrations, such as polyphosphazene (WO 95/2415), can also be used.

Any pharmaceutical composition of the invention, containing a polynucleotide, polypeptide, polypeptide derivative, or antibody of the invention, can be manufactured using standard methods. It can be formulated

-69-

least one additional monospecific antibody specific for a different *Helicobacter* polypeptide. The amount of antibody and the particular regimen used can be readily determined by one skilled in the art. For example, daily administration of about 100 to 1,000 mg of antibody over one week, or three doses per day of about 100 to 1,000 mg of antibody over two or three days, can be effective regimens for most purposes.

Therapeutic or prophylactic efficacy can be evaluated using standard methods in the art, *e.g.*, by measuring induction of a mucosal immune response or induction of protective and/or therapeutic immunity, using, *e.g.*, the *H. felis* mouse model and the procedures described by Lee *et al.* (Eur. J. Gastroenterology & Hepatology 7:303, 1995) or Lee *et al.* (J. Infect. Dis. 172:161, 1995). Those skilled in the art will recognize that the *H. felis* strain of the model can be replaced with another *Helicobacter* strain. For example, the efficacy of polynucleotide molecules and polypeptides from *H. pylori* is, preferably, evaluated in a mouse model using an *H. pylori* strain. Protection can be determined by comparing the degree of *Helicobacter* infection in the gastric tissue assessed by, for example, urease activity, bacterial counts, or gastritis, to that of a control group. Protection is shown when infection is reduced by comparison to the control group. Such an evaluation can be made for polynucleotides, vaccine vectors, polypeptides, and polypeptide derivatives, as well as for antibodies of the invention.

For example, various doses of an antibody of the invention can be administered to the gastric mucosa of mice previously challenged with an *H. pylori* strain, as described, *e.g.*, by Lee *et al.* (*supra*). Then, after an appropriate period of time, the bacterial load of the mucosa can be estimated by assessing urease activity, as compared to a control. Reduced urease activity indicates that the antibody is therapeutically effective.

-68-

allowed to adsorb onto the material. The chromatography material, such as a gel or a resin coupled to an antibody of the invention, can be in batch form or in a column. The unbound components are washed off and the antigen is eluted with an appropriate elution buffer, such as a glycine buffer, a buffer containing a chaotropic agent, *e.g.*, guanidine HCl, or a buffer having high salt concentration (*e.g.*, 3 M MgCl<sub>2</sub>). Eluted fractions are recovered and the presence of the antigen is detected, *e.g.*, by measuring the absorbance at 280 nm.

An antibody of the invention can be screened for therapeutic efficacy as follows. According to an eleventh aspect of the invention, there is provided (i) a composition of matter containing a monospecific antibody of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a monospecific antibody of the invention, and (iii) a method for treating or preventing *Helicobacter* (*e.g.*, *H. pylori*, *H. felis*, *H. mustelae*, or *H. heilmanii*) infection, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an individual in need of such treatment. In addition, the eleventh aspect of the invention includes the use of a monospecific antibody of the invention in the preparation of a medicament for treating or preventing *Helicobacter* infection.

The monospecific antibody can be polyclonal or monoclonal, and is, preferably, predominantly of the IgA isotype. In passive immunization methods, the antibody is administered to a mucosal surface of a mammal, *e.g.*, the gastric mucosa, *e.g.*, orally or intragastrically, optionally, in the presence of a bicarbonate buffer. Alternatively, systemic administration, not requiring a bicarbonate buffer, can be carried out. A monospecific antibody of the invention can be administered as a single active agent or as a mixture with at

-67-

that interacts with the reagent is first attached to the solid support. For example, if a polypeptide reagent is used, an antibody that binds to it can serve as an anti-reagent, provided that it binds to an epitope that is not involved in recognition of antibodies in biological samples. Indirect means can also employ a ligand-receptor system, for example, a molecule, such as a vitamin, can be grafted onto the polypeptide reagent and the corresponding receptor can be immobilized on the solid phase. This concept is illustrated by the well known biotin-streptavidin system. Alternatively, indirect means can be used, *e.g.*, by adding to the reagent a peptide tail, chemically or by genetic engineering, and immobilizing the grafted or fused product by passive adsorption or covalent linkage of the peptide tail.

According to a tenth aspect of the invention, there is provided a process for purifying, from a biological sample, a polypeptide or polypeptide derivative of the invention, which involves carrying out antibody-based affinity chromatography with the biological sample, wherein the antibody is a monospecific antibody of the invention.

For use in a purification process of the invention, the antibody can be polyclonal or monospecific, and preferably is of the IgG type. Purified IgGs can be prepared from an antiserum using standard methods (see, *e.g.*, Coligan *et al.*, *supra*). Conventional chromatography supports, as well as standard methods for grafting antibodies, are described, for example, by Harlow *et al.* (*Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1988).

Briefly, a biological sample, such as an *H. pylori* extract, preferably in a buffer solution, is applied to a chromatography material, which is, preferably, equilibrated with the buffer used to dilute the biological sample, so that the polypeptide or polypeptide derivative of the invention (*i.e.*, the antigen) is



-66-

methods to detect the presence of *Helicobacter* antigens in a sample, such as a biological sample. The antibodies can also be used in affinity chromatography methods for purifying a polypeptide or polypeptide derivative of the invention. As is discussed further below, the antibodies can also be used in prophylactic and therapeutic passive immunization methods.

5           Accordingly, a ninth aspect of the invention provides (i) a reagent for detecting the presence of *Helicobacter* in a biological sample that contains an antibody, polypeptide, or polypeptide derivative of the invention; and (ii) a diagnostic method for detecting the presence of *Helicobacter* in a biological sample, by contacting the biological sample with an antibody, a polypeptide, or  
10           a polypeptide derivative of the invention, so that an immune complex is formed, and detecting the complex as an indication of the presence of *Helicobacter* in the sample or the organism from which the sample was derived. The immune complex is formed between a component of the sample and the antibody, polypeptide, or polypeptide derivative, and that any unbound  
15           material can be removed prior to detecting the complex. A polypeptide reagent can be used for detecting the presence of anti-*Helicobacter* antibodies in a sample, *e.g.*, a blood sample, while an antibody of the invention can be used for screening a sample, such as a gastric extract or biopsy sample, for the presence of *Helicobacter* polypeptides.

20           For use in diagnostic methods, the reagent (*e.g.*, the antibody, polypeptide, or polypeptide derivative of the invention) can be in a free state or can be immobilized on a solid support, such as, for example, on the interior surface of a tube or on the surface, or within pores, of a bead. Immobilization can be achieved using direct or indirect means. Direct means include passive  
25           adsorption (*i.e.*, non-covalent binding) or covalent binding between the support and the reagent. By "indirect means" is meant that an anti-reagent compound

-65-

unlabeled, depending upon the diagnostic method. Diagnostic methods involving such a reagent are described below.

Upon expression of a polynucleotide molecule of the invention, a polypeptide or polypeptide derivative is produced and can be purified using known methods. For example, the polypeptide or polypeptide derivative can be produced as a fusion protein containing a fused tail that facilitates purification. The fusion product can be used to immunize a small mammal, *e.g.*, a mouse or a rabbit, in order to raise monospecific antibodies against the polypeptide or polypeptide derivative. The eighth aspect of the invention thus provides a monospecific antibody that binds to a polypeptide or polypeptide derivative of the invention.

By "monospecific antibody" is meant an antibody that is capable of reacting with a unique, naturally-occurring *Helicobacter* polypeptide. An antibody of the invention can be polyclonal or monoclonal. Monospecific antibodies can be recombinant, *e.g.*, chimeric (*e.g.*, consisting of a variable region of murine origin and a human constant region), humanized (*e.g.*, a human immunoglobulin constant region and a variable region of animal, *e.g.*, murine, origin), and/or single chain. Both polyclonal and monospecific antibodies can also be in the form of immunoglobulin fragments, *e.g.*, F(ab)'<sub>2</sub> or Fab fragments. The antibodies of the invention can be of any isotype, *e.g.*, IgG or IgA, and polyclonal antibodies can be of a single isotype or can contain a mixture of isotypes.

The antibodies of the invention, which can be raised to a polypeptide or polypeptide derivative of the invention, can be produced and identified using standard immunological assays, *e.g.*, Western blot assays, dot blot assays, or ELISA (see, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology*, John Wiley & Sons, Inc., New York, NY, 1994). The antibodies can be used in diagnostic

-64-

Administration can be achieved in a single dose or repeated as necessary at intervals that can be determined by one skilled in the art. For example, a priming dose can be followed by three booster doses at weekly or monthly intervals. An appropriate dose depends on various parameters, including the nature of the recipient (*e.g.*, whether the recipient is an adult or an infant), the particular vaccine antigen, the route and frequency of administration, the presence/absence or type of adjuvant, and the desired effect (*e.g.*, protection and/or treatment), and can be readily determined by one skilled in the art. In general, a vaccine antigen of the invention can be administered mucosally in an amount ranging from about 10  $\mu$ g to about 500 mg, preferably from about 1 mg to about 200 mg. For a parenteral route of administration, the dose usually should not exceed about 1 mg, and is, preferably, about 100  $\mu$ g.

When used as components of a vaccine, the polynucleotides and polypeptides of the invention can be used sequentially as part of a multi-step immunization process. For example, a mammal can be initially primed with a vaccine vector of the invention, such as a pox virus, *e.g.*, *via* a parenteral route, and then boosted twice with a polypeptide encoded by the vaccine vector, *e.g.*, *via* the mucosal route. In another example, liposomes associated with a polypeptide or polypeptide derivative of the invention can be used for priming, with boosting being carried out mucosally using a soluble polypeptide or polypeptide derivative of the invention, in combination with a mucosal adjuvant (*e.g.*, LT).

Polypeptides and polypeptide derivatives of the invention can also be used as diagnostic reagents for detecting the presence of anti-*Helicobacter* antibodies, *e.g.*, in blood samples. Such polypeptides can be about 5 to about 80, preferably, about 10 to about 50 amino acids in length and can be labeled or

-63-

the invention in the preparation of a medicament for preventing and/or treating *Helicobacter* infection.

The immunogenic compositions of the invention can be administered by any conventional route in use in the vaccine field, for example, to a mucosal (*e.g.*, ocular, intranasal, pulmonary, oral, gastric, intestinal, rectal, vaginal, or urinary tract) surface or *via* a parenteral (*e.g.*, subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. The choice of the administration route depends upon a number of parameters, such as the adjuvant used. For example, if a mucosal adjuvant is used, the intranasal or oral route will be preferred, and if a lipid formulation or an aluminum compound is used, a parenteral route will be preferred. In the latter case, the subcutaneous or intramuscular route is most preferred. The choice of administration route can also depend upon the nature of the vaccine agent. For example, a polypeptide of the invention fused to CTB or to LTB will be best administered to a mucosal surface.

A composition of the invention can contain one or several polypeptides or derivatives of the invention. It can also contain at least one additional *Helicobacter* antigen, such as the urease apoenzyme, or a subunit, fragment, homolog, mutant, or derivative thereof.

For use in a composition of the invention, a polypeptide or polypeptide derivative can be formulated into or with liposomes, such as neutral or anionic liposomes, microspheres, ISCOMS, or virus-like particles (VLPs), to facilitate delivery and/or enhance the immune response. These compounds are readily available to those skilled in the art; for example, see *Liposomes: A Practical Approach* (*supra*). Adjuvants other than liposomes can also be used in the invention and are well known in the art (see, for example, the list provided below).

-62-

addition of 50 mM Tris-HCl (pH 7.5) and the membrane is air-dried. The membrane is saturated in blocking buffer (50 mM Tris-HCl (pH 7.5), 0.15 M NaCl, 10 g/L skim milk) and incubated with an antiserum diluted from about 1:50 to about 1:5000, preferably about 1:500. The reaction is detected using standard methods. For example, a goat anti-rabbit peroxidase conjugate can be added to the wells when rabbit antibodies are used. Incubation is carried out for about 90 minutes at 37°C and the blot is washed. The reaction is developed with the appropriate substrate and stopped. The reaction is then measured visually by the appearance of a colored spot, *e.g.*, by colorimetry. Under these experimental conditions, a positive reaction is associated with detection of a colored spot for reactions carried out with a dilution of at least about 1:50, preferably, of at least about 1:500. Therapeutic or prophylactic efficacy of a polypeptide or polypeptide derivative of the invention can be evaluated as described below.

According to a seventh aspect of the invention, there is provided (i) a composition of matter containing a polypeptide of the invention together with a diluent or carrier; (ii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a polypeptide of the invention; (iii) a method for inducing an immune response against *Helicobacter* in a mammal by administering to the mammal an immunogenically effective amount of a polypeptide of the invention to elicit an immune response, *e.g.*, a protective immune response to *Helicobacter*; and (iv) a method for preventing and/or treating a *Helicobacter* (*e.g.*, *H. pylori*, *H. felis*, *H. mustelae*, or *H. heilmanii*) infection, by administering a prophylactic or therapeutic amount of a polypeptide of the invention to an individual in need of such treatment. Additionally, this aspect of the invention includes the use of a polypeptide of

-61-

corresponding to the product exhibits reactivity at any of the dilutions in the range.

In an ELISA assay, the product to be screened can be used as the coating antigen. A purified preparation is preferred, but a whole cell extract can also be used. Briefly, about 100  $\mu$ l of a preparation of about 10  $\mu$ g protein/ml is distributed into wells of a 96-well ELISA plate. The plate is incubated for about 2 hours at 37°C, then overnight at 4°C. The plate is washed with phosphate buffer saline (PBS) containing 0.05% Tween 20 (PBS/Tween buffer) and the wells are saturated with 250  $\mu$ l PBS containing 1% bovine serum albumin (BSA), to prevent non-specific antibody binding. After 1 hour of incubation at 37°C, the plate is washed with PBS/Tween buffer. The antiserum is serially diluted in PBS/Tween buffer containing 0.5% BSA, and 100  $\mu$ l dilutions are added to each well. The plate is incubated for 90 minutes at 37°C, washed, and evaluated using standard methods. For example, a goat anti-rabbit peroxidase conjugate can be added to the wells when the specific antibodies used were raised in rabbits. Incubation is carried out for about 90 minutes at 37°C and the plate is washed. The reaction is developed with the appropriate substrate and the reaction is measured by colorimetry (absorbance measured spectrophotometrically). Under these experimental conditions, a positive reaction is shown once an O.D. value of 1.0 is detected with a dilution of at least about 1:50, preferably of at least about 1:500.

In a dot blot assay, a purified product is preferred, although a whole cell extract can be used. Briefly, a solution of the product at a concentration of about 100  $\mu$ g/ml is serially diluted two-fold with 50 mM Tris-HCl (pH 7.5). One hundred  $\mu$ l of each dilution is applied to a filter, such as a 0.45  $\mu$ m nitrocellulose membrane, set in a 96-well dot blot apparatus (Biorad). The buffer is removed by applying vacuum to the system. Wells are washed by

-60-

A "substantially purified polypeptide" is defined as a polypeptide that is separated from the environment in which it naturally occurs and/or a polypeptide that is free of most of the other polypeptides that are present in the environment in which it was synthesized. The polypeptides of the invention can be purified from a natural source, such as a *Helicobacter* strain, or can be produced using recombinant methods.

Homologous polypeptides or polypeptide derivatives encoded by polynucleotides of the invention can be screened for specific antigenicity by testing cross-reactivity with an antiserum raised against a polypeptide having an amino acid sequence as shown in the sequence listing (even numbers, up to SEQ ID NO:1364). Briefly, a monospecific hyperimmune antiserum can be raised against a purified reference polypeptide as such or as a fusion polypeptide, for example, an expression product of MBP, GST, or His-tag systems, or a synthetic peptide predicted to be antigenic. The homologous polypeptide or derivative that is screened for specific antigenicity can be produced as such or as a fusion polypeptide. In the latter case, and if the antiserum is also raised against a fusion polypeptide, two different fusion systems are employed. Specific antigenicity can be determined using a number of methods, including Western blot (Towbin *et al.*, Proc. Natl. Acad. Sci. USA 76:4350, 1979), dot blot, and ELISA methods, as described below.

In a Western blot assay, the product to be screened, either as a purified preparation or a total *E. coli* extract, is fractionated by SDS-PAGE, as described, for example, by Laemmli (Nature 227:680, 1970). After being transferred to a filter, such as a nitrocellulose membrane, the material is incubated with the monospecific hyperimmune antiserum, which is diluted in a range of dilutions from about 1:50 to about 1:5000, preferably from about 1:100 to about 1:500. Specific antigenicity is shown once a band

-59-

exception that RNA is used as a target), or a sandwich method (Dunn *et al.*, Cell 12:23, 1977). As is known in the art, the latter technique involves the use of a specific capture probe and a specific detection probe that have nucleotide sequences that are at least partially different from each other.

Primers used in the invention usually contain about 10 to 40 nucleotides and are used to initiate enzymatic polymerization of DNA in an amplification process (*e.g.*, PCR), an elongation process, or a reverse transcription method. In a diagnostic method involving PCR, the primers can be labeled.

Thus, the invention also encompasses (i) a reagent containing a probe of the invention for detecting and/or identifying the presence of *Helicobacter* in a biological material; (ii) a method for detecting and/or identifying the presence of *Helicobacter* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA or RNA is extracted from the material and denatured, and (c) the sample is exposed to a probe of the invention, for example, a capture probe, a detection probe, or both, under stringent hybridization conditions, so that hybridization is detected; and (iii) a method for detecting and/or identifying the presence of *Helicobacter* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA is extracted therefrom, (c) the extracted DNA is contacted with at least one, or, preferably two, primers of the invention, and amplified by the polymerase chain reaction, and (d) an amplified DNA molecule is produced.

As mentioned above, polypeptides that can be produced by expression of the polynucleotides of the invention can be used as vaccine antigens.

Accordingly, a sixth aspect of the invention features a substantially purified polypeptide or polypeptide derivative having an amino acid sequence encoded by a polynucleotide of the invention.



-58-

listing. For example, they can contain from about 5 to about 100, preferably from about 10 to about 80 nucleotides. In particular, probes have sequences that are at least 75%, preferably at least 85%, more preferably 95% homologous to a portion of a sequence as shown in the sequence listing (odd numbers, up to SEQ ID NO:1363), or a sequence complementary to any of such sequences.

Probes can contain modified bases, such as inosine, methyl-5-deoxycytidine, deoxyuridine, dimethylamino-5-deoxyuridine, or diamino-2, 6-purine. Sugar or phosphate residues can also be modified or substituted. For example, a deoxyribose residue can be replaced by a polyamide (Nielsen *et al.*, Science 254:1497, 1991) and phosphate residues can be replaced by ester groups such as diphosphate, alkyl, arylphosphonate, and phosphorothioate esters. In addition, the 2'-hydroxyl group on ribonucleotides can be modified by addition of, *e.g.*, alkyl groups.

Probes of the invention can be used in diagnostic tests, or as capture or detection probes. Such capture probes can be immobilized on solid supports, directly or indirectly, by covalent means or by passive adsorption. A detection probe can be labeled by a detectable label, for example a label selected from radioactive isotopes; enzymes, such as peroxidase and alkaline phosphatase; enzymes that are able to hydrolyze a chromogenic, fluorogenic, or luminescent substrate; compounds that are chromogenic, fluorogenic, or luminescent; nucleotide base analogs; and biotin.

Probes of the invention can be used in any conventional hybridization method, such as in dot blot methods (Maniatis *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1982), Southern blot methods (Southern, J. Mol. Biol. 98:503, 1975), northern blot methods (identical to Southern blot to the

-57-

intestinal, rectal, vaginal, or urinary tract surface, or *via* a parenteral route, *e.g.*, by an intravenous, subcutaneous, intraperitoneal, intradermal, intraepidermal, or intramuscular route. The choice of administration route will depend on, *e.g.*, the formulation that is selected. A polynucleotide formulated in association with bupivacaine is advantageously administered into muscle. When a neutral or anionic liposome or a cationic lipid, such as DOTMA, is used, the formulation can be advantageously injected *via* intravenous, intranasal (for example, by aerosolization), intramuscular, intradermal, and subcutaneous routes. A polynucleotide in a naked form can advantageously be administered *via* the intramuscular, intradermal, or subcutaneous routes. Although not absolutely required, such a composition can also contain an adjuvant. A systemic adjuvant that does not require concomitant administration in order to exhibit an adjuvant effect is preferable.

The sequence information provided in the present application enables the design of specific nucleotide probes and primers that can be used in diagnostic methods. Accordingly, in a fifth aspect of the invention, there is provided a nucleotide probe or primer having a sequence found in, or derived by degeneracy of the genetic code from, a sequence shown in the sequence listing (odd numbers, up to SEQ ID NO:1363).

The term "probe" as used in the present application refers to DNA (preferably single stranded) or RNA molecules (or modifications or combinations thereof) that hybridize under the stringent conditions, as defined above, to polynucleotide molecules having sequences homologous to any of those shown in the sequence listing (odd numbers, up to SEQ ID NO:1363), or to a complementary or anti-sense sequence of any of those shown in the sequence listing (odd numbers, up to SEQ ID NO:1363). Generally, probes are significantly shorter than the full-length sequences shown in the sequence

-56-

for gene delivery are preferably used in association with a neutral lipid such as DOPE (dioleoyl phosphatidylethanolamine; WO 90/11092). Other transfection-facilitating compounds can be added to a formulation containing cationic liposomes. A number of them are described in, *e.g.*, WO 93/18759, WO 93/19768, WO 94/25608, and WO 95/2397. They include, *e.g.*, spermine derivatives useful for facilitating the transport of DNA through the nuclear membrane (see, for example, WO 93/18759) and membrane-permeabilizing compounds such as GALA, Gramicidine S, and cationic bile salts (see, for example, WO 93/19768).

Gold or tungsten microparticles can also be used for gene delivery, as described in WO 91/359, WO 93/17706, and by Tang *et al.* (Nature 356:152, 1992). In this case, the microparticle-coated polynucleotides can be injected *via* intradermal or intraepidermal routes using a needleless injection device ("gene gun"), such as those described in U.S. Patent No. 4,945,050, U.S. Patent No. 5,015,580, and WO 94/24263.

The amount of DNA to be used in a vaccine recipient depends, *e.g.*, on the strength of the promoter used in the DNA construct, the immunogenicity of the expressed gene product, the condition of the mammal intended for administration (*e.g.*, the weight, age, and general health of the mammal), the mode of administration, and the type of formulation. In general, a therapeutically or prophylactically effective dose from about 1  $\mu$ g to about 1 mg, preferably, from about 10  $\mu$ g to about 800  $\mu$ g, and, more preferably, from about 25  $\mu$ g to about 250  $\mu$ g, can be administered to human adults. The administration can be achieved in a single dose or repeated at intervals.

The route of administration can be any conventional route used in the vaccine field. As general guidance, a polynucleotide of the invention can be administered *via* a mucosal surface, *e.g.*, an ocular, intranasal, pulmonary, oral,

-55-

Standard methods can be used in the preparation of therapeutic polynucleotides of the invention. For example, a polynucleotide can be used in a naked form, free of any delivery vehicles, such as anionic liposomes, cationic lipids, microparticles, *e.g.*, gold microparticles, precipitating agents, *e.g.*, calcium phosphate, or any other transfection-facilitating agent. In this case, the polynucleotide can be simply diluted in a physiologically acceptable solution, such as sterile saline or sterile buffered saline, with or without a carrier. When present, the carrier preferably is isotonic, hypotonic, or weakly hypertonic, and has a relatively low ionic strength, such as provided by a sucrose solution, *e.g.*, a solution containing 20% sucrose.

Alternatively, a polynucleotide can be associated with agents that assist in cellular uptake. It can be, *e.g.*, (i) complemented with a chemical agent that modifies cellular permeability, such as bupivacaine (see, *e.g.*, WO 94/16737), (ii) encapsulated into liposomes, or (iii) associated with cationic lipids or silica, gold, or tungsten microparticles.

Anionic and neutral liposomes are well-known in the art (see, *e.g.*, *Liposomes: A Practical Approach*, RPC New Ed, IRL Press, 1990, for a detailed description of methods for making liposomes) and are useful for delivering a large range of products, including polynucleotides.

Cationic lipids can also be used for gene delivery. Such lipids include, for example, Lipofectin<sup>TM</sup>, which is also known as DOTMA (N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium chloride), DOTAP (1,2-bis(oleyloxy)-3-(trimethylammonio)propane), DDAB (dimethyldioctadecylammonium bromide), DOGS (dioctadecylamidologlycyl spermine), and cholesterol derivatives. A description of these cationic lipids can be found in EP 187,702, WO 90/11092, U.S. Patent No. 5,283,185, WO 91/15501, WO 95/26356, and U.S. Patent No. 5,527,928. Cationic lipids

-54-

unable to replicate in a mammalian cell and unable to integrate into the mammalian genome. Typically, a DNA molecule is placed under the control of a promoter suitable for expression in a mammalian cell. The promoter can function ubiquitously or tissue-specifically. Examples of non-tissue specific promoters include the early Cytomegalovirus (CMV) promoter (U.S. Patent No. 4,168,062) and the Rous Sarcoma Virus promoter (Norton *et al.*, Molec. Cell Biol. 5:281, 1985). The desmin promoter (Li *et al.*, Gene 78:243, 1989; Li *et al.*, J. Biol. Chem. 266:6562, 1991; Li *et al.*, J. Biol. Chem. 268:10403, 1993) is tissue-specific and drives expression in muscle cells. More generally, useful promoters and vectors are described, *e.g.*, in WO 94/21797 and by Hartikka *et al.* (Human Gene Therapy 7:1205, 1996).

For DNA/RNA vaccination, the polynucleotide of the invention can encode a precursor or a mature form of a polypeptide of the invention. When it encodes a precursor form, the precursor sequence can be homologous or heterologous. In the latter case, a eucaryotic leader sequence can be used, such as the leader sequence of the tissue-type plasminogen factor (tPA).

A composition of the invention can contain one or several polynucleotides of the invention. It can also contain at least one additional polynucleotide encoding another *Helicobacter* antigen, such as urease subunit A, B, or both, or a fragment, derivative, mutant, or analog thereof. A polynucleotide encoding a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12), can also be added to the composition so that the immune response is enhanced. These additional polynucleotides are placed under appropriate control for expression. Advantageously, DNA molecules of the invention and/or additional DNA molecules to be included in the same composition are carried in the same plasmid.

-53-

invention can be inserted into the bacterial genome or it can remain in a free state, for example, carried on a plasmid.

An adjuvant can also be added to a composition containing a bacterial vector vaccine. A number of adjuvants that can be used are known to those skilled in the art. For example, preferred adjuvants can be selected from the list provided below.

According to a fourth aspect of the invention, there is also provided (i) a composition of matter containing a polynucleotide of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a polynucleotide of the invention; (iii) a method for inducing an immune response against *Helicobacter*, in a mammal, by administering to the mammal an immunogenically effective amount of a polynucleotide of the invention to elicit an immune response, *e.g.*, a protective immune response to *Helicobacter*; and (iv) a method for preventing and/or treating a *Helicobacter* (*e.g.*, *H. pylori*, *H. felis*, *H. mustelae*, or *H. heilmanii*) infection, by administering a prophylactic or therapeutic amount of a polynucleotide of the invention to an individual in need of such treatment. Additionally, the fourth aspect of the invention encompasses the use of a polynucleotide of the invention in the preparation of a medicament for preventing and/or treating *Helicobacter* infection. The fourth aspect of the invention preferably includes the use of a polynucleotide molecule placed under conditions for expression in a mammalian cell, *e.g.*, in a plasmid that is unable to replicate in mammalian cells and to substantially integrate into a mammalian genome.

Polynucleotides (for example, DNA or RNA molecules) of the invention can also be administered as such to a mammal as a vaccine. When a DNA molecule of the invention is used, it can be in the form of a plasmid that is

-52-

Non-toxicogenic *Vibrio cholerae* mutant strains that can be used in live oral vaccines are described by Mekalanos *et al.* (Nature 306:551, 1983) and in U.S. Patent No. 4,882,278 (strain in which a substantial amount of the coding sequence of each of the two *ctxA* alleles has been deleted so that no functional *cholerae* toxin is produced); WO 92/11354 (strain in which the *irgA* locus is inactivated by mutation; this mutation can be combined in a single strain with *ctxA* mutations); and WO 94/1533 (deletion mutant lacking functional *ctxA* and *attRS1* DNA sequences). These strains can be genetically engineered to express heterologous antigens, as described in WO 94/19482. An effective vaccine dose of a *V. cholerae* strain capable of expressing a polypeptide or polypeptide derivative encoded by a polynucleotide molecule of the invention can contain, *e.g.*, about  $1 \times 10^5$  to about  $1 \times 10^9$ , preferably about  $1 \times 10^6$  to about  $1 \times 10^8$  viable bacteria in an appropriate volume for the selected route of administration. Preferred routes of administration include all mucosal routes, but, most preferably, these vectors are administered intranasally or orally.

Attenuated *Salmonella typhimurium* strains, genetically engineered for recombinant expression of heterologous antigens, and their use as oral vaccines, are described by Nakayama *et al.* (Bio/Technology 6:693, 1988) and in WO 92/11361. Preferred routes of administration for these vectors include all mucosal routes. Most preferably, the vectors are administered intranasally or orally.

Others bacterial strains useful as vaccine vectors are described by High *et al.* (EMBO 11:1991, 1992) and Sizemore *et al.* (Science 270:299, 1995; *Shigella flexneri*); Medaglini *et al.* (Proc. Natl. Acad. Sci. USA 92:6868, 1995; *Streptococcus gordonii*); Flynn (Cell. Mol. Biol. 40 (suppl. I):31, 1194), and in WO 88/6626, WO 90/0594, WO 91/13157, WO 92/1796, and WO 92/21376 (Bacille Calmette Guerin). In bacterial vectors, a polynucleotide of the

-51-

intervals. The appropriate dosage depends on various parameters that are understood by those skilled in the art, such as the nature of the vaccine vector itself, the route of administration, and the condition of the mammal to be vaccinated (*e.g.*, the weight, age, and general health of the mammal).

Live vaccine vectors that can be used in the invention include viral  
5 vectors, such as adenoviruses and poxviruses, as well as bacterial vectors, *e.g.*,  
*Shigella*, *Salmonella*, *Vibrio cholerae*, *Lactobacillus*, Bacille bilié de Calmette-  
Guérin (BCG), and *Streptococcus*. An example of an adenovirus vector, as  
well as a method for constructing an adenovirus vector capable of expressing a  
polynucleotide molecule of the invention, is described in U.S. Patent No.  
10 4,920,209. Poxvirus vectors that can be used in the invention include, *e.g.*,  
vaccinia and canary pox viruses, which are described in U.S. Patent No.  
4,722,848 and U.S. Patent No. 5,364,773, respectively (also see, *e.g.*, Tartaglia  
*et al.*, Virology 188:217, 1992, for a description of a vaccinia virus vector, and  
Taylor *et al.*, Vaccine 13:539, 1995, for a description of a canary poxvirus  
15 vector). Poxvirus vectors capable of expressing a polynucleotide of the  
invention can be obtained by homologous recombination, as described in Kieny  
*et al.* (Nature 312:163, 1984) so that the polynucleotide of the invention is  
inserted in the viral genome under appropriate conditions for expression in  
mammalian cells. Generally, the dose of viral vector vaccine, for therapeutic  
20 or prophylactic use, can be from about  $1 \times 10^4$  to about  $1 \times 10^{11}$ , advantageously  
from about  $1 \times 10^7$  to about  $1 \times 10^{10}$ , or, preferably, from about  $1 \times 10^7$  to about  
 $1 \times 10^9$  plaque-forming units per kilogram. Preferably, viral vectors are  
administered parenterally, for example, in 3 doses that are 4 weeks apart.  
Those skilled in the art will recognize that it is preferable to avoid adding a  
25 chemical adjuvant to a composition containing a viral vector of the invention  
and thereby minimizing the immune response to the viral vector itself.



-50-

administering a prophylactic or therapeutic amount of a vaccine vector of the invention to an individual in need. Additionally, the third aspect of the invention encompasses the use of a vaccine vector of the invention in the preparation of a medicament for preventing and/or treating *Helicobacter* infection.

5           A vaccine vector of the invention can express one or several polypeptides or derivatives of the invention, as well as at least one additional *Helicobacter* antigen such as a urease apoenzyme or a subunit, fragment, homolog, mutant, or derivative thereof. In addition, it can express a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12), that enhances the  
10       immune response. Thus, a vaccine vector can include an additional polynucleotide molecules encoding, *e.g.*, urease subunit A, B, or both, or a cytokine, placed under the control of elements required for expression in a mammalian cell.

          Alternatively, a composition of the invention can include several vaccine  
15       vectors, each of which being capable of expressing a polypeptide or derivative of the invention. A composition can also contain a vaccine vector capable of expressing an additional *Helicobacter* antigen such as urease apoenzyme, a subunit, fragment, homolog, mutant, or derivative thereof, or a cytokine such as IL-2 or IL-12.

20           In vaccination methods for treating or preventing infection in a mammal, a vaccine vector of the invention can be administered by any conventional route in use in the vaccine field, for example, to a mucosal (*e.g.*, ocular, intranasal, oral, gastric, pulmonary, intestinal, rectal, vaginal, or urinary tract) surface or  
      *via* a parenteral (*e.g.*, subcutaneous, intradermal, intramuscular, intravenous, or  
25       intraperitoneal) route. Preferred routes depend upon the choice of the vaccine vector. The administration can be achieved in a single dose or repeated at

-49-

from the supernatant after centrifugation of the cell culture. Typically, the recombinant polypeptide can be purified by antibody-based affinity purification or by any other method known to a person skilled in the art, such as by genetic fusion to a small affinity-binding domain. Antibody-based affinity purification methods are also available for purifying a polypeptide of the invention  
5 extracted from a *Helicobacter* strain. Antibodies useful for immunoaffinity purification of the polypeptides of the invention can be obtained using methods described below.

Polynucleotides of the invention can also be used in DNA vaccination methods, using either a viral or bacterial host as gene delivery vehicle (live  
10 vaccine vector) or administering the gene in a free form, *e.g.*, inserted into a plasmid. Therapeutic or prophylactic efficacy of a polynucleotide of the invention can be evaluated as is described below.

Accordingly, in a third aspect of the invention, there is provided (i) a vaccine vector such as a poxvirus, containing a polynucleotide molecule of the  
15 invention placed under the control of elements required for expression; (ii) a composition of matter containing a vaccine vector of the invention, together with a diluent or carrier; (iii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a vaccine vector of the invention; (iv) a method for inducing an immune response against *Helicobacter*  
20 in a mammal (*e.g.*, a human; alternatively, the method can be used in veterinary applications for treating or preventing *Helicobacter* infection of animals, *e.g.*, cats or birds), which involves administering to the mammal an immunogenically effective amount of a vaccine vector of the invention to elicit an immune response, *e.g.*, a protective or therapeutic immune response to  
25 *Helicobacter*; and (v) a method for preventing and/or treating a *Helicobacter* (*e.g.*, *H. pylori*, *H. felis*, *H. mustelae*, or *H. heilmanii*) infection, which involves

-48-

be homologous or heterologous to the polynucleotide molecule encoding the mature polypeptide and it can be specific to the secretion apparatus of the host used for expression. The open reading frame constituted by the polynucleotide molecule of the invention, alone or together with the signal peptide, is placed under the control of the promoter so that transcription and translation occur in the host system. Promoters and signal peptide-encoding regions are widely known and available to those skilled in the art and include, for example, the promoter of *Salmonella typhimurium* (and derivatives) that is inducible by arabinose (promoter araB) and is functional in Gram-negative bacteria such as *E. coli* (U.S. Patent No. 5,028,530; Cagnon *et al.*, Protein Engineering 4(7):843, 1991); the promoter of the bacteriophage T7 RNA polymerase gene, which is functional in a number of *E. coli* strains expressing T7 polymerase (U.S. Patent No. 4,952,496); the OspA lipidation signal peptide; and RlpB lipidation signal peptide (Takase *et al.*, J. Bact. 169:5692, 1987).

The expression cassette is typically part of an expression vector, which is selected for its ability to replicate in the chosen expression system. Expression vectors (*e.g.*, plasmids or viral vectors) can be chosen from, for example, those described in Pouwels *et al.* (*Cloning Vectors: A Laboratory Manual*, 1985, Supp. 1987) and can be purchased from various commercial sources. Methods for transforming or transfecting host cells with expression vectors are well known in the art and will depend on the host system selected, as described in Ausubel *et al.* (*supra*).

Upon expression, a recombinant polypeptide of the invention (or a polypeptide derivative) is produced and remains in the intracellular compartment, is secreted/excreted in the extracellular medium or in the periplasmic space, or is embedded in the cellular membrane. The polypeptide can then be recovered in a substantially purified form from the cell extract or

-47-

invention; (iii) a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, as well as (iv) a process for producing a polypeptide or polypeptide derivative encoded by a polynucleotide of the invention, which involves culturing a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, under conditions that allow expression of the polynucleotide molecule of the invention and, recovering the encoded polypeptide or polypeptide derivative from the cell culture.

A recombinant expression system can be selected from procaryotic and eucaryotic hosts. Eucaryotic hosts include, for example, yeast cells (*e.g.*, *Saccharomyces cerevisiae* or *Pichia Pastoris*), mammalian cells (*e.g.*, COS1, NIH3T3, or JEG3 cells), arthropods cells (*e.g.*, *Spodoptera frugiperda* (SF9) cells), and plant cells. Preferably, a procaryotic host such as *E. coli* is used. Bacterial and eucaryotic cells are available from a number of different sources that are known to those skilled in the art, *e.g.*, the American Type Culture Collection (ATCC; Rockville, Maryland).

The choice of the expression cassette will depend on the host system selected, as well as the features desired for the expressed polypeptide. For example, it may be useful to produce a polypeptide of the invention in a particular lipidated form or any other form. Typically, an expression cassette includes a constitutive or inducible promoter that is functional in the selected host system; a ribosome binding site; a start codon (ATG); if necessary, a region encoding a signal peptide, *e.g.*, a lipidation signal peptide; a polynucleotide molecule of the invention; a stop codon; and, optionally, a 3' terminal region (translation and/or transcription terminator). The signal peptide-encoding region is adjacent to the polynucleotide of the invention and is placed in the proper reading frame. The signal peptide-encoding region can

-46-

calculated  $T_m$ . Those skilled in the art will understand that optimal temperature and salt conditions can be readily determined empirically in preliminary experiments using conventional procedures. For example, stringent conditions can be achieved, both for pre-hybridizing and hybridizing incubations, (i) within 4-16 hours at 42°C, in 6 x SSC containing  
5 50% formamide or (ii) within 4-16 hours at 65°C in an aqueous 6 x SSC solution (1 M NaCl, 0.1 M sodium citrate (pH 7.0)). For polynucleotides containing 30 to 600 nucleotides, the above formula is used and then is corrected by subtracting (600/polynucleotide size in base pairs). Stringency conditions are defined by a  $T_h$  that is 5 to 10°C below  $T_m$ .

10 Hybridization conditions with oligonucleotides shorter than 20-30 bases do not precisely follow the rules set forth above. In such cases, the formula for calculating the  $T_m$  is as follows:  $T_m = 4 \times (G+C) + 2 (A+T)$ . For example, an 18 nucleotide fragment of 50% G+C would have an approximate  $T_m$  of 54°C.

15 A polynucleotide molecule of the invention, containing RNA, DNA, or modifications or combinations thereof, can have various applications. For example, a polynucleotide molecule can be used (i) in a process for producing the encoded polypeptide in a recombinant host system, (ii) in the construction of vaccine vectors such as poxviruses, which are further used in methods and compositions for preventing and/or treating *Helicobacter* infection, (iii) as a  
20 vaccine agent, in a naked form or formulated with a delivery vehicle and, (iv) in the construction of attenuated *Helicobacter* strains that can over-express a polynucleotide of the invention or express it in a non-toxic, mutated form.

According to a second aspect of the invention, there is therefore provided (i) an expression cassette containing a polynucleotide molecule of the  
25 invention placed under the control of elements (e.g., a promoter) required for expression; (ii) an expression vector containing an expression cassette of the

-45-

toxin or *E. coli* heat-labile toxin. Several possibilities can be used for producing such fusion proteins. First, the polypeptide of the invention can be fused to the N-terminal end or, preferably, to the C-terminal end of the polypeptide having adjuvant activity. Second, a polypeptide fragment of the invention can be fused within the amino acid sequence of the polypeptide having adjuvant activity. Spacer sequences can also be included, if desired.

As stated above, the polynucleotides of the invention encode *Helicobacter* polypeptides in precursor or mature form. They can also encode hybrid precursors containing heterologous signal peptides, which can mature into polypeptides of the invention. By "heterologous signal peptide" is meant a signal peptide that is not found in the naturally-occurring precursor of a polypeptide of the invention.

A polynucleotide of the invention hybridizes, preferably under stringent conditions, to a polynucleotide having a sequence as shown in the sequence listing (odd numbers, up to SEQ ID NO:1363). Hybridization procedures are, *e.g.*, described by Ausubel *et al.* (*supra*); Silhavy *et al.* (*Experiments with Gene Fusions*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1984); and Davis *et al.* (*A Manual for Genetic Engineering: Advanced Bacterial Genetics*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1980). Important parameters that can be considered for optimizing hybridization conditions are reflected in the following formula, which facilitates calculation of the melting temperature ( $T_m$ ), which is the temperature above which two complementary DNA strands separate from one another (Casey *et al.*, Nucl. Acid Res. 4:1539, 1977):  $T_m = 81.5 + 0.5 \times (\% G+C) + 1.6 \log (\text{positive ion concentration}) - 0.6 \times (\% \text{ formamide})$ . Under appropriate stringency conditions, hybridization temperature ( $T_h$ ) is approximately 20 to 40°C, 20 to 25°C, or, preferably, 30 to 40°C below the

-44-

as murine mammary tumor virus (peptide containing 11 amino acids; Dion *et al.*, Virology 179:474-477, 1990), Semliki Forest virus (peptide containing 16 amino acids; Snijders *et al.*, J. Gen. Virol. 72:557-565, 1991), and canine parvovirus (2 overlapping peptides, each containing 15 amino acids; Langeveld *et al.*, Vaccine 12(15):1473-1480, 1994) have been shown to be effective vaccine antigens against their respective pathogens.

Polynucleotides encoding polypeptide fragments and polypeptides having large internal deletions can be constructed using standard methods (see, *e.g.*, Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons Inc., 1994), for example, by PCR, including inverse PCR, by restriction enzyme treatment of the cloned DNA molecules, or by the method of Kunkel *et al.* (Proc. Natl. Acad. Sci. USA 82:448, 1985; biological material available at Stratagene).

A polypeptide derivative can also be produced as a fusion polypeptide that contains a polypeptide or a polypeptide derivative of the invention fused, *e.g.*, at the N- or C-terminal end, to any other polypeptide (hereinafter referred to as a peptide tail). Such a product can be easily obtained by translation of a genetic fusion, *i.e.*, a hybrid gene. Vectors for expressing fusion polypeptides are commercially available, and include the pMal-c2 or pMal-p2 systems of New England Biolabs, in which the peptide tail is a maltose binding protein, the glutathione-S-transferase system of Pharmacia, or the His-Tag system available from Novagen. These and other expression systems provide convenient means for further purification of polypeptides and derivatives of the invention.

Another particular example of fusion polypeptides included in invention includes a polypeptide or polypeptide derivative of the invention fused to a polypeptide having adjuvant activity, such as, *e.g.*, subunit B of either cholera

-43-

at least 20 amino acids, preferably at least 50 amino acids, more preferably at least 75 amino acids, and most preferably at least 100 amino acids in length.

Useful polypeptide derivatives, *e.g.*, polypeptide fragments, can be designed using computer-assisted analysis of amino acid sequences in order to identify sites in protein antigens having potential as surface-exposed, antigenic regions (Hughes *et al.*, Infect. Immun. 60(9):3497, 1992). For example, the Laser Gene Program from DNA Star can be used to obtain hydrophilicity, antigenic index, and intensity index plots for the polypeptides of the invention. This program can also be used to obtain information about homologies of the polypeptides with known protein motifs. One skilled in the art can readily use the information provided in such plots to select peptide fragments for use as vaccine antigens. For example, fragments spanning regions of the plots in which the antigenic index is relatively high can be selected. One can also select fragments spanning regions in which both the antigenic index and the intensity plots are relatively high. Fragments containing conserved sequences, particularly hydrophilic conserved sequences, can also be selected.

Polypeptide fragments and polypeptides having large internal deletions can be used for revealing epitopes that are otherwise masked in the parent polypeptide and that may be of importance for inducing a protective T cell-dependent immune response. Deletions can also remove immunodominant regions of high variability among strains.

It is an accepted practice in the field of immunology to use fragments and variants of protein immunogens as vaccines, as all that is required to induce an immune response to a protein is a small (*e.g.*, 8 to 10 amino acids) immunogenic region of the protein. This has been done for a number of vaccines against pathogens other than *Helicobacter*. For example, short synthetic peptides corresponding to surface-exposed antigens of pathogens such



-42-

Those skilled in the art can readily design primers that can be used to isolate the polynucleotides of the invention from different *Helicobacter* strains. Experimental conditions for carrying out PCR can readily be determined by one skilled in the art and an illustration of carrying out PCR is provided in Example 2. As is well known in the art, restriction endonuclease recognition sites that contain, typically, 4 to 6 nucleotides (for example, the sequences 5'-GGATCC-3' (*Bam*HI) or 5'-CTCGAG-3' (*Xho*I)), can be included on the 5' ends of the primers. Restriction sites can be selected by those skilled in the art so that the amplified DNA can be conveniently cloned into an appropriately digested vector, such as a plasmid.

Useful homologs that do not occur naturally can be designed using known methods for identifying regions of an antigen that are likely to be tolerant of amino acid sequence changes and/or deletions. For example, sequences of the antigen from different species can be compared to identify conserved sequences.

Polypeptide derivatives that are encoded by polynucleotides of the invention include, *e.g.*, fragments, polypeptides having large internal deletions derived from full-length polypeptides, and fusion proteins. Polypeptide fragments of the invention can be derived from a polypeptide having a sequence homologous to any of the sequences of the sequence listing (even numbers, up to SEQ ID NO:1364), to the extent that the fragments retain the substantial antigenicity of the parent polypeptide (specific antigenicity). Polypeptide derivatives can also be constructed by large internal deletions that remove a substantial part of the parent polypeptide, while retaining specific antigenicity. Generally, polypeptide derivatives should be about at least 12 amino acids in length to maintain antigenicity. Advantageously, they can be

-41-

UreA + UreB apoenzyme expressed from pORV214 (UreA and UreB sequences differ from *H. pylori* strain CPM630 by one and two amino acid changes, respectively; Lee *et al.*, *supra*, 1995); a UreA-glutathione-S-transferase fusion protein (UreA sequence from *H. pylori* strain ATCC 43504; Thomas *et al.*, *Acta Gastro-Enterologica Belgica* 56:54, 1993); UreA + UreB holoenzyme purified from *H. pylori* strain NCTC11637 (Marchetti *et al.*, *Science* 267:1655, 1995); a UreA-MBP fusion protein (UreA from *H. pylori* strain 85P; Ferrero *et al.*, *Infection and Immunity* 62:4981, 1994); a UreB-MBP fusion protein (UreB from *H. pylori* strain 85P; Ferrero *et al.*, *supra*); a UreA-MBP fusion protein (UreA from *H. felis* strain ATCC 49179; Ferrero *et al.*, *supra*); a UreB-MBP fusion protein (UreB from *H. felis* strain ATCC 49179; Ferrero *et al.*, *supra*); and a 37 kDa fragment of UreB containing amino acids 220-569 (Dore-Davin *et al.*, "A 37 kD fragment of UreB is sufficient to confer protection against *Helicobacter felis* infection in mice"). Finally, Thomas *et al.* (*supra*) showed that oral immunization of mice with crude sonicates of *H. pylori* protected mice from subsequent challenge with *H. felis*.

Polynucleotides, *e.g.*, DNA molecules, encoding allelic variants can easily be obtained by polymerase chain reaction (PCR) amplification of genomic bacterial DNA extracted by conventional methods. This involves the use of synthetic oligonucleotide primers matching sequences that are upstream and downstream of the 5' and 3' ends of the coding region. Suitable primers can be designed based on the nucleotide sequence information provided in the sequence listing (odd numbers, up to SEQ ID NO:1363). Typically, a primer consists of 10 to 40, preferably 15 to 25 nucleotides. It can also be advantageous to select primers containing C and G nucleotides in proportions sufficient to ensure efficient hybridization, *e.g.*, an amount of C and G nucleotides of at least 40%, preferably 50%, of the total nucleotide amount.

-40-

Allelic variants are very common in nature. For example, a bacterial species, *e.g.*, *H. pylori*, is usually represented by a variety of strains that differ from each other by minor allelic variations. Indeed, a polypeptide that fulfills the same biological function in different strains can have an amino acid sequence that is not identical in each of the strains. Such an allelic variation can be equally reflected at the polynucleotide level.

Support for the use of allelic variants of polypeptide antigens comes from, *e.g.*, studies of the *Helicobacter* urease antigen. The amino acid sequence of *Helicobacter* urease varies widely from species to species, yet cross-species protection occurs, indicating that the urease molecule, when used as an immunogen, is highly tolerant of amino acid variations. Even among different strains of the single species *H. pylori*, there are amino acid sequence variations.

For example, although the amino acid sequences of the UreA and UreB subunits of *H. pylori* and *H. felis* ureases differ from one another by 26.5% and 11.8%, respectively (Ferrero *et al.*, Molecular Microbiology 9(2):323-333, 1993), it has been shown that *H. pylori* urease protects mice from *H. felis* infection (Michetti *et al.*, Gastroenterology 107:1002, 1994). In addition, it has been shown that the individual structural subunits of urease, UreA and UreB, which contain distinct amino acid sequences, are both protective antigens against *Helicobacter* infection (Michetti *et al.*, *supra*). Similarly, Cuenca *et al.* (Gastroenterology 110:1770, 1996) showed that therapeutic immunization of *H. mustelae*-infected ferrets with *H. pylori* urease was effective at eradicating *H. mustelae* infection. Further, several urease variants have been reported to be effective vaccine antigens, including, *e.g.*, recombinant UreA + UreB apoenzyme expressed from pORV142 (UreA and UreB sequences derived from *H. pylori* strain CPM630; Lee *et al.*, J. Infect. Dis. 172:161, 1995); recombinant

-39-

University of Wisconsin Biotechnology Center, 1710 University Avenue,  
Madison, WI 53705). Similar amino acid sequences are aligned to obtain the  
maximum degree of homology (*i.e.*, identity). To this end, it may be necessary  
to artificially introduce gaps into the sequence. Once the optimal alignment has  
been set up, the degree of homology (*i.e.*, identity) is established by recording  
all of the positions in which the amino acids of both sequences are identical,  
relative to the total number of positions.

Homologous polynucleotide sequences are defined in a similar way.  
Preferably, a homologous sequence is one that is at least 45%, more preferably  
at least 60%, and most preferably at least 85% identical to a coding sequence of  
any of the nucleotide sequences set forth in the sequence listing (odd numbers,  
up to SEQ ID NO:1363).

Polypeptides having a sequence homologous to any one of the sequences  
shown in the sequence listing (even numbers, up to SEQ ID NO:1364), include  
naturally-occurring allelic variants, as well as mutants or any other non-  
naturally occurring variants that are analogous in terms of antigenicity, to a  
polypeptide having a sequence as shown in the sequence listing (even numbers,  
up to SEQ ID NO:1364).

As is known in the art, an allelic variant is an alternate form of a  
polypeptide that is characterized as having a substitution, deletion, or addition  
of one or more amino acids that does not alter the biological function of the  
polypeptide. By "biological function" is meant a function of the polypeptide in  
the cells in which it naturally occurs, even if the function is not necessary for  
the growth or survival of the cells. For example, the biological function of a  
porin is to allow the entry into cells of compounds present in the extracellular  
medium. The biological function is distinct from the antigenic function. A  
polypeptide can have more than one biological function.

-38-

By "homologous amino acid sequence" is meant an amino acid sequence that differs from an amino acid sequence shown in the sequence listing (even numbers, up to SEQ ID NO:1364), or an amino acid sequence encoded by a nucleotide sequence shown in the sequence listing (odd numbers, up to SEQ ID NO:1363), by one or more non-conservative amino acid substitutions, deletions, or additions located at positions at which they do not destroy the specific antigenicity of the polypeptide. Preferably, such a sequence is at least 75%, more preferably at least 80%, and most preferably at least 90% identical to an amino acid sequence shown in the sequence listing (even numbers, up to SEQ ID NO:1364). Homologous amino acid sequences include sequences that are identical or substantially identical to an amino acid sequence as shown in the sequence listing (even numbers, up to SEQ ID NO:1364). By "amino acid sequence that is substantially identical" is meant a sequence that is at least 90%, preferably at least 95%, more preferably at least 97%, and most preferably at least 99% identical to an amino acid sequence of reference and that differs from the sequence of reference, if at all, by a majority of conservative amino acid substitutions.

Conservative amino acid substitutions typically include substitutions among amino acids of the same class. These classes include, for example, amino acids having uncharged polar side chains, such as asparagine, glutamine, serine, threonine, and tyrosine; amino acids having basic side chains, such as lysine, arginine, and histidine; amino acids having acidic side chains, such as aspartic acid and glutamic acid; and amino acids having nonpolar side chains, such as glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and cysteine.

Homology can be measured using sequence analysis software (*e.g.*, Sequence Analysis Software Package of the Genetics Computer Group,

-37-

naturally-occurring DNA molecule present in the genome of a living bacteria or as part of a gene bank is not isolated, but the same molecule, separated from the remaining part of the bacterial genome, as a result of, *e.g.*, a cloning event (amplification), is "isolated." Typically, an isolated DNA molecule is free from DNA regions (*e.g.*, coding regions) with which it is immediately contiguous, at the 5' or 3' ends, in the naturally occurring genome. Such isolated polynucleotides can be part of a vector or a composition and still be isolated, as such a vector or composition is not part of its natural environment.

A polynucleotide of the invention can consist of RNA or DNA (*e.g.*, cDNA, genomic DNA, or synthetic DNA), or modifications or combinations of RNA or DNA. The polynucleotide can be double-stranded or single-stranded and, if single-stranded, can be the coding (sense) strand or the non-coding (anti-sense) strand. The sequences that encode polypeptides of the invention, as shown in the sequence listing (even numbers, up to SEQ ID NO:1364), can be (a) the coding sequence as shown in any of the nucleotide sequences of the sequence listing (odd numbers, up to SEQ ID NO:1363); (b) a ribonucleotide sequence derived by transcription of (a); or (c) a different coding sequence that, as a result of the redundancy or degeneracy of the genetic code, encodes the same polypeptides as the polynucleotide molecules having the sequences illustrated in any of the nucleotide sequences of the sequence listing (odd numbers, up to SEQ ID NO:1363). The polypeptide can be one that is naturally secreted or excreted by, *e.g.*, *H. felis*, *H. mustelae*, *H. heilmanii*, or *H. pylori*.

By "polypeptide" or "protein" is meant any chain of amino acids, regardless of length or post-translational modification (*e.g.*, glycosylation or phosphorylation). Both terms are used interchangeably in the present application.

-36-

NO:1299), GHPO 1613 (SEQ ID NO:1301), GHPO 1614 (SEQ ID NO:1303), GHPO 1626 (SEQ ID NO:1305), GHPO 1628 (SEQ ID NO:1307), GHPO 1639 (SEQ ID NO:1309), GHPO 1640 (SEQ ID NO:1311), GHPO 1641 (SEQ ID NO:1313), GHPO 1646 (SEQ ID NO:1315), GHPO 1662 (SEQ ID NO:1317), GHPO 1667 (SEQ ID NO:1319), GHPO 1668 (SEQ ID NO:1321), GHPO 1670 (SEQ ID NO:1323), GHPO 1671 (SEQ ID NO:1325), GHPO 1672 (SEQ ID NO:1327), GHPO 1678 (SEQ ID NO:1329), GHPO 1684 (SEQ ID NO:1331), GHPO 1695 (SEQ ID NO:1333), GHPO 1697 (SEQ ID NO:1335), GHPO 1701 (SEQ ID NO:1337), GHPO 1719 (SEQ ID NO:1339), GHPO 1723 (SEQ ID NO:1341), GHPO 1732 (SEQ ID NO:1343), GHPO 1739 (SEQ ID NO:1345), GHPO 1741 (SEQ ID NO:1347), GHPO 1747 (SEQ ID NO:1349), GHPO 1749 (SEQ ID NO:1351), GHPO 1750 (SEQ ID NO:1353), GHPO 1751 (SEQ ID NO:1355), GHPO 1755 (SEQ ID NO:1357), GHPO 1771 (SEQ ID NO:1359), GHPO 1786 (SEQ ID NO:1361), and GHPO 1789 (SEQ ID NO:1363).

An isolated polynucleotide of the invention encodes (i) a polypeptide having an amino acid sequence that is homologous to a *Helicobacter* amino acid sequence of a polypeptide, the *Helicobacter* amino acid sequence being selected from the group consisting of the amino acid sequences shown in the sequence listing (even numbers, up to SEQ ID NO:1364), or (ii) a derivative of the polypeptide.

In addition to the full-length polypeptides encoded by the polynucleotides of the invention, as set forth above, polynucleotides included in the invention can also encode polypeptides that lack signal sequences, as well as other polypeptide or peptide fragments of the full-length polypeptides.

The term "isolated polynucleotide" is defined as a polynucleotide that is removed from the environment in which it naturally occurs. For example, a

-35-

GHPO 1240 (SEQ ID NO:1179), GHPO 1246 (SEQ ID NO:1181), GHPO  
1251 (SEQ ID NO:1183), GHPO 1252 (SEQ ID NO:1185), GHPO 1261 (SEQ  
ID NO:1187), GHPO 1265 (SEQ ID NO:1189), GHPO 1267 (SEQ ID  
NO:1191), GHPO 1278 (SEQ ID NO:1193), GHPO 1282 (SEQ ID NO:1195),  
GHPO 1283 (SEQ ID NO:1197), GHPO 1287 (SEQ ID NO:1199), GHPO  
5 1292 (SEQ ID NO:1201), GHPO 1293 (SEQ ID NO:1203), GHPO 1302 (SEQ  
ID NO:1205), GHPO 1309 (SEQ ID NO:1207), GHPO 1317 (SEQ ID  
NO:1209), GHPO 1318 (SEQ ID NO:1211), GHPO 1321 (SEQ ID NO:1213),  
GHPO 1325 (SEQ ID NO:1215), GHPO 1341 (SEQ ID NO:1217), GHPO  
1351 (SEQ ID NO:1219), GHPO 1354 (SEQ ID NO:1221), GHPO 1363 (SEQ  
10 ID NO:1223), GHPO 1371 (SEQ ID NO:1225), GHPO 1381 (SEQ ID  
NO:1227), GHPO 1401 (SEQ ID NO:1229), GHPO 1402 (SEQ ID NO:1231),  
GHPO 1403 (SEQ ID NO:1233), GHPO 1408 (SEQ ID NO:1235), GHPO  
1416 (SEQ ID NO:1237), GHPO 1420 (SEQ ID NO:1239), GHPO 1428 (SEQ  
ID NO:1241), GHPO 1437 (SEQ ID NO:1243), GHPO 1439 (SEQ ID  
15 NO:1245), GHPO 1460 (SEQ ID NO:1247), GHPO 1463 (SEQ ID NO:1249),  
GHPO 1472 (SEQ ID NO:1251), GHPO 1474 (SEQ ID NO:1253), GHPO  
1484 (SEQ ID NO:1255), GHPO 1489 (SEQ ID NO:1257), GHPO 1494 (SEQ  
ID NO:1259), GHPO 1495 (SEQ ID NO:1261), GHPO 1498 (SEQ ID  
NO:1263), GHPO 1499 (SEQ ID NO:1265), GHPO 1500 (SEQ ID NO:1267),  
20 GHPO 1503 (SEQ ID NO:1269), GHPO 1504 (SEQ ID NO:1271), GHPO  
1510 (SEQ ID NO:1273), GHPO 1518 (SEQ ID NO:1275), GHPO 1533 (SEQ  
ID NO:1277), GHPO 1541 (SEQ ID NO:1279), GHPO 1544 (SEQ ID  
NO:1281), GHPO 1548 (SEQ ID NO:1283), GHPO 1565 (SEQ ID NO:1285),  
GHPO 1575 (SEQ ID NO:1287), GHPO 1582 (SEQ ID NO:1289), GHPO  
25 1595 (SEQ ID NO:1291), GHPO 1597 (SEQ ID NO:1293), GHPO 1599 (SEQ  
ID NO:1295), GHPO 1601 (SEQ ID NO:1297), GHPO 1609 (SEQ ID



-34-

NO:1055), GHPO 904 (SEQ ID NO:1057), GHPO 906 (SEQ ID NO:1059),  
GHPO 908 (SEQ ID NO:1061), GHPO 921 (SEQ ID NO:1063), GHPO 923  
(SEQ ID NO:1065), GHPO 926 (SEQ ID NO:1067), GHPO 933 (SEQ ID  
NO:1069), GHPO 939 (SEQ ID NO:1071), GHPO 940 (SEQ ID NO:1073),  
GHPO 943 (SEQ ID NO:1075), GHPO 951 (SEQ ID NO:1077), GHPO 961  
5 (SEQ ID NO:1079), GHPO 965 (SEQ ID NO:1081), GHPO 990 (SEQ ID  
NO:1083), GHPO 991 (SEQ ID NO:1085), GHPO 998 (SEQ ID NO:1087),  
GHPO 1001 (SEQ ID NO:1089), GHPO 1005 (SEQ ID NO:1091), GHPO  
1033 (SEQ ID NO:1093), GHPO 1039 (SEQ ID NO:1095), GHPO 1041 (SEQ  
ID NO:1097), GHPO 1043 (SEQ ID NO:1099), GHPO 1044 (SEQ ID  
10 NO:1101), GHPO 1051 (SEQ ID NO:1103), GHPO 1058 (SEQ ID NO:1105),  
GHPO 1060 (SEQ ID NO:1107), GHPO 1075 (SEQ ID NO:1109), GHPO  
1077 (SEQ ID NO:1111), GHPO 1082 (SEQ ID NO:1113), GHPO 1083 (SEQ  
ID NO:1115), GHPO 1086 (SEQ ID NO:1117), GHPO 1087 (SEQ ID  
NO:1119), GHPO 1090 (SEQ ID NO:1121), GHPO 1097 (SEQ ID NO:1123),  
15 GHPO 1098 (SEQ ID NO:1125), GHPO 1103 (SEQ ID NO:1127), GHPO  
1113 (SEQ ID NO:1129), GHPO 1116 (SEQ ID NO:1131), GHPO 1123 (SEQ  
ID NO:1133), GHPO 1125 (SEQ ID NO:1135), GHPO 1129 (SEQ ID  
NO:1137), GHPO 1130 (SEQ ID NO:1139), GHPO 1134 (SEQ ID NO:1141),  
GHPO 1161 (SEQ ID NO:1143), GHPO 1166 (SEQ ID NO:1145), GHPO  
20 1170 (SEQ ID NO:1147), GHPO 1175 (SEQ ID NO:1149), GHPO 1181 (SEQ  
ID NO:1151), GHPO 1186 (SEQ ID NO:1153), GHPO 1188 (SEQ ID  
NO:1155), GHPO 1191 (SEQ ID NO:1157), GHPO 1193 (SEQ ID NO:1159),  
GHPO 1196 (SEQ ID NO:1161), GHPO 1204 (SEQ ID NO:1163), GHPO  
1210 (SEQ ID NO:1165), GHPO 1211 (SEQ ID NO:1167), GHPO 1216 (SEQ  
25 ID NO:1169), GHPO 1218 (SEQ ID NO:1171), GHPO 1220 (SEQ ID  
NO:1173), GHPO 1223 (SEQ ID NO:1175), GHPO 1226 (SEQ ID NO:1177),

-33-

487 (SEQ ID NO:925), GHPO 488 (SEQ ID NO:927), GHPO 489 (SEQ ID NO:929), GHPO 498 (SEQ ID NO:931), GHPO 501 (SEQ ID NO:933), GHPO 504 (SEQ ID NO:935), GHPO 512 (SEQ ID NO:937), GHPO 517 (SEQ ID NO:939), GHPO 520 (SEQ ID NO:941), GHPO 528 (SEQ ID NO:943), GHPO 530 (SEQ ID NO:945), GHPO 532 (SEQ ID NO:947), GHPO 548 (SEQ ID NO:949), GHPO 561 (SEQ ID NO:951), GHPO 564 (SEQ ID NO:953), GHPO 572 (SEQ ID NO:955), GHPO 573 (SEQ ID NO:957), GHPO 574 (SEQ ID NO:959), GHPO 577 (SEQ ID NO:961), GHPO 579 (SEQ ID NO:963), GHPO 583 (SEQ ID NO:965), GHPO 588 (SEQ ID NO:967), GHPO 593 (SEQ ID NO:969), GHPO 597 (SEQ ID NO:971), GHPO 598 (SEQ ID NO:973), GHPO 604 (SEQ ID NO:975), GHPO 606 (SEQ ID NO:977), GHPO 611 (SEQ ID NO:979), GHPO 612 (SEQ ID NO:981), GHPO 615 (SEQ ID NO:983), GHPO 632 (SEQ ID NO:985), GHPO 633 (SEQ ID NO:987), GHPO 637 (SEQ ID NO:989), GHPO 651 (SEQ ID NO:991), GHPO 663 (SEQ ID NO:993), GHPO 686 (SEQ ID NO:995), GHPO 693 (SEQ ID NO:997), GHPO 698 (SEQ ID NO:999), GHPO 703 (SEQ ID NO:1001), GHPO 704 (SEQ ID NO:1003), GHPO 705 (SEQ ID NO:1005), GHPO 707 (SEQ ID NO:1007), GHPO 721 (SEQ ID NO:1009), GHPO 727 (SEQ ID NO:1011), GHPO 728 (SEQ ID NO:1013), GHPO 733 (SEQ ID NO:1015), GHPO 758 (SEQ ID NO:1017), GHPO 763 (SEQ ID NO:1019), GHPO 771 (SEQ ID NO:1021), GHPO 774 (SEQ ID NO:1023), GHPO 776 (SEQ ID NO:1025), GHPO 783 (SEQ ID NO:1027), GHPO 800 (SEQ ID NO:1029), GHPO 806 (SEQ ID NO:1031), GHPO 807 (SEQ ID NO:1033), GHPO 808 (SEQ ID NO:1035), GHPO 809 (SEQ ID NO:1037), GHPO 811 (SEQ ID NO:1039), GHPO 815 (SEQ ID NO:1041), GHPO 819 (SEQ ID NO:1043), GHPO 841 (SEQ ID NO:1045), GHPO 843 (SEQ ID NO:1047), GHPO 846 (SEQ ID NO:1049), GHPO 875 (SEQ ID NO:1051), GHPO 892 (SEQ ID NO:1053), GHPO 902 (SEQ ID

-32-

NO:789), GHPO 123 (SEQ ID NO:791), GHPO 124 (SEQ ID NO:793), GHPO  
126 (SEQ ID NO:795), GHPO 127 (SEQ ID NO:797), GHPO 128 (SEQ ID  
NO:799), GHPO 131 (SEQ ID NO:801), GHPO 133 (SEQ ID NO:803), GHPO  
140 (SEQ ID NO:805), GHPO 141 (SEQ ID NO:807), GHPO 145 (SEQ ID  
NO:809), GHPO 147 (SEQ ID NO:811), GHPO 166 (SEQ ID NO:813), GHPO  
5 181 (SEQ ID NO:815), GHPO 187 (SEQ ID NO:817), GHPO 188 (SEQ ID  
NO:819), GHPO 192 (SEQ ID NO:821), GHPO 202 (SEQ ID NO:823), GHPO  
204 (SEQ ID NO:825), GHPO 205 (SEQ ID NO:827), GHPO 212 (SEQ ID  
NO:829), GHPO 218 (SEQ ID NO:831), GHPO 226 (SEQ ID NO:833), GHPO  
231 (SEQ ID NO:835), GHPO 236 (SEQ ID NO:837), GHPO 239 (SEQ ID  
10 NO:839), GHPO 245 (SEQ ID NO:841), GHPO 246 (SEQ ID NO:843), GHPO  
248 (SEQ ID NO:845), GHPO 253 (SEQ ID NO:847), GHPO 265 (SEQ ID  
NO:849), GHPO 266 (SEQ ID NO:851), GHPO 271 (SEQ ID NO:853), GHPO  
272 (SEQ ID NO:855), GHPO 286 (SEQ ID NO:857), GHPO 291 (SEQ ID  
NO:859), GHPO 292 (SEQ ID NO:861), GHPO 297 (SEQ ID NO:863), GHPO  
15 304 (SEQ ID NO:865), GHPO 307 (SEQ ID NO:867), GHPO 324 (SEQ ID  
NO:869), GHPO 326 (SEQ ID NO:871), GHPO 331 (SEQ ID NO:873), GHPO  
343 (SEQ ID NO:875), GHPO 345 (SEQ ID NO:877), GHPO 346 (SEQ ID  
NO:879), GHPO 352 (SEQ ID NO:881), GHPO 355 (SEQ ID NO:883), GHPO  
363 (SEQ ID NO:885), GHPO 369 (SEQ ID NO:887), GHPO 376 (SEQ ID  
20 NO:889), GHPO 378 (SEQ ID NO:891), GHPO 388 (SEQ ID NO:893), GHPO  
396 (SEQ ID NO:895), GHPO 403 (SEQ ID NO:897), GHPO 410 (SEQ ID  
NO:899), GHPO 415 (SEQ ID NO:901), GHPO 421 (SEQ ID NO:903), GHPO  
439 (SEQ ID NO:905), GHPO 441 (SEQ ID NO:907), GHPO 443 (SEQ ID  
NO:909), GHPO 453 (SEQ ID NO:911), GHPO 455 (SEQ ID NO:913), GHPO  
25 464 (SEQ ID NO:915), GHPO 467 (SEQ ID NO:917), GHPO 468 (SEQ ID  
NO:919), GHPO 470 (SEQ ID NO:921), GHPO 486 (SEQ ID NO:923), GHPO

-31-

NO:659), GHPO 1444 (SEQ ID NO:661), GHPO 1449 (SEQ ID NO:663),  
GHPO 1465 (SEQ ID NO:665), GHPO 1475 (SEQ ID NO:667), GHPO 1479  
(SEQ ID NO:669), GHPO 1483 (SEQ ID NO:671), GHPO 1488 (SEQ ID  
NO:673), GHPO 1496 (SEQ ID NO:675), GHPO 1524 (SEQ ID NO:677),  
GHPO 1536 (SEQ ID NO:679), GHPO 1539 (SEQ ID NO:681), GHPO 1540  
5 (SEQ ID NO:683), GHPO 1542 (SEQ ID NO:685), GHPO 1555 (SEQ ID  
NO:687), GHPO 1560 (SEQ ID NO:689), GHPO 1564 (SEQ ID NO:691),  
GHPO 1570 (SEQ ID NO:693), GHPO 1588 (SEQ ID NO:695), GHPO 1604  
(SEQ ID NO:697), GHPO 1605 (SEQ ID NO:699), GHPO 1619 (SEQ ID  
NO:701), GHPO 1629 (SEQ ID NO:703), GHPO 1642 (SEQ ID NO:705),  
10 GHPO 1654 (SEQ ID NO:707), GHPO 1661 (SEQ ID NO:709), GHPO 1673  
(SEQ ID NO:711), GHPO 1687 (SEQ ID NO:713), GHPO 1692 (SEQ ID  
NO:715), GHPO 1693 (SEQ ID NO:717), GHPO 1699 (SEQ ID NO:719),  
GHPO 1738 (SEQ ID NO:721), GHPO 1745 (SEQ ID NO:723), GHPO 1746  
(SEQ ID NO:725), GHPO 1754 (SEQ ID NO:727), GHPO 1792 (SEQ ID  
15 NO:729), GHPO 1795 (SEQ ID NO:731), GHPO 1796 (SEQ ID NO:733),  
GHPO 7 (SEQ ID NO:735), GHPO 8 (SEQ ID NO:737), GHPO 9 (SEQ ID  
NO:739), GHPO 10 (SEQ ID NO:741), GHPO 12 (SEQ ID NO:743), GHPO  
25 (SEQ ID NO:745), GHPO 27 (SEQ ID NO:747), GHPO 29 (SEQ ID  
NO:749), GHPO 30 (SEQ ID NO:751), GHPO 37 (SEQ ID NO:753), GHPO  
20 49 (SEQ ID NO:755), GHPO 51 (SEQ ID NO:757), GHPO 54 (SEQ ID  
NO:759), GHPO 65 (SEQ ID NO:761), GHPO 66 (SEQ ID NO:763), GHPO  
68 (SEQ ID NO:765), GHPO 70 (SEQ ID NO:767), GHPO 77 (SEQ ID  
NO:769), GHPO 83 (SEQ ID NO:771), GHPO 85 (SEQ ID NO:773), GHPO  
87 (SEQ ID NO:775), GHPO 91 (SEQ ID NO:777), GHPO 92 (SEQ ID  
25 NO:779), GHPO 96 (SEQ ID NO:781), GHPO 97 (SEQ ID NO:783), GHPO  
111 (SEQ ID NO:785), GHPO 115 (SEQ ID NO:787), GHPO 117 (SEQ ID

-30-

782 (SEQ ID NO:531), GHPO 786 (SEQ ID NO:533), GHPO 792 (SEQ ID NO:535), GHPO 797 (SEQ ID NO:537), GHPO 816 (SEQ ID NO:539), GHPO 828 (SEQ ID NO:541), GHPO 839 (SEQ ID NO:543), GHPO 840 (SEQ ID NO:545), GHPO 842 (SEQ ID NO:547), GHPO 885 (SEQ ID NO:549), GHPO 889 (SEQ ID NO:551), GHPO 903 (SEQ ID NO:553), GHPO 912 (SEQ ID NO:555), GHPO 946 (SEQ ID NO:557), GHPO 958 (SEQ ID NO:559), GHPO 968 (SEQ ID NO:561), GHPO 987 (SEQ ID NO:563), GHPO 992 (SEQ ID NO:565), GHPO 996 (SEQ ID NO:567), GHPO 997 (SEQ ID NO:569), GHPO 1002 (SEQ ID NO:571), GHPO 1026 (SEQ ID NO:573), GHPO 1028 (SEQ ID NO:575), GHPO 1034 (SEQ ID NO:577), GHPO 1038 (SEQ ID NO:579), GHPO 1059 (SEQ ID NO:581), GHPO 1065 (SEQ ID NO:583), GHPO 1072 (SEQ ID NO:585), GHPO 1073 (SEQ ID NO:587), GHPO 1088 (SEQ ID NO:589), GHPO 1091 (SEQ ID NO:591), GHPO 1105 (SEQ ID NO:593), GHPO 1115 (SEQ ID NO:595), GHPO 1159 (SEQ ID NO:597), GHPO 1177 (SEQ ID NO:599), GHPO 1187 (SEQ ID NO:601), GHPO 1192 (SEQ ID NO:603), GHPO 1195 (SEQ ID NO:605), GHPO 1224 (SEQ ID NO:607), GHPO 1225 (SEQ ID NO:609), GHPO 1228 (SEQ ID NO:611), GHPO 1229 (SEQ ID NO:613), GHPO 1231 (SEQ ID NO:615), GHPO 1236 (SEQ ID NO:617), GHPO 1242 (SEQ ID NO:619), GHPO 1248 (SEQ ID NO:621), GHPO 1270 (SEQ ID NO:623), GHPO 1271 (SEQ ID NO:625), GHPO 1298 (SEQ ID NO:627), GHPO 1301 (SEQ ID NO:629), GHPO 1304 (SEQ ID NO:631), GHPO 1315 (SEQ ID NO:633), GHPO 1319 (SEQ ID NO:635), GHPO 1323 (SEQ ID NO:637), GHPO 1331 (SEQ ID NO:639), GHPO 1332 (SEQ ID NO:641), GHPO 1347 (SEQ ID NO:643), GHPO 1373 (SEQ ID NO:645), GHPO 1376 (SEQ ID NO:647), GHPO 1380 (SEQ ID NO:649), GHPO 1394 (SEQ ID NO:651), GHPO 1407 (SEQ ID NO:653), GHPO 1415 (SEQ ID NO:655), GHPO 1425 (SEQ ID NO:657), GHPO 1427 (SEQ ID

-29-

NO:395), GHPO 122 (SEQ ID NO:397), GHPO 128 (SEQ ID NO:399), GHPO 138 (SEQ ID NO:401), GHPO 153 (SEQ ID NO:403), GHPO 160 (SEQ ID NO:405), GHPO 168 (SEQ ID NO:407), GHPO 179 (SEQ ID NO:409), GHPO 189 (SEQ ID NO:411), GHPO 229 (SEQ ID NO:413), GHPO 243 (SEQ ID NO:415), GHPO 244 (SEQ ID NO:417), GHPO 251 (SEQ ID NO:419), GHPO 267 (SEQ ID NO:421), GHPO 269 (SEQ ID NO:423), GHPO 279 (SEQ ID NO:425), GHPO 284 (SEQ ID NO:427), GHPO 296 (SEQ ID NO:429), GHPO 300 (SEQ ID NO:431), GHPO 305 (SEQ ID NO:433), GHPO 319 (SEQ ID NO:435), GHPO 330 (SEQ ID NO:437), GHPO 340 (SEQ ID NO:439), GHPO 342 (SEQ ID NO:441), GHPO 344 (SEQ ID NO:443), GHPO 358 (SEQ ID NO:445), GHPO 373 (SEQ ID NO:447), GHPO 382 (SEQ ID NO:449), GHPO 384 (SEQ ID NO:451), GHPO 398 (SEQ ID NO:453), GHPO 409 (SEQ ID NO:455), GHPO 422 (SEQ ID NO:457), GHPO 430 (SEQ ID NO:459), GHPO 446 (SEQ ID NO:461), GHPO 447 (SEQ ID NO:463), GHPO 450 (SEQ ID NO:465), GHPO 451 (SEQ ID NO:467), GHPO 452 (SEQ ID NO:469), GHPO 456 (SEQ ID NO:471), GHPO 461 (SEQ ID NO:473), GHPO 476 (SEQ ID NO:475), GHPO 478 (SEQ ID NO:477), GHPO 491 (SEQ ID NO:479), GHPO 511 (SEQ ID NO:481), GHPO 519 (SEQ ID NO:483), GHPO 526 (SEQ ID NO:485), GHPO 534 (SEQ ID NO:487), GHPO 536 (SEQ ID NO:489), GHPO 542 (SEQ ID NO:491), GHPO 544 (SEQ ID NO:493), GHPO 576 (SEQ ID NO:495), GHPO 578 (SEQ ID NO:497), GHPO 580 (SEQ ID NO:499), GHPO 585 (SEQ ID NO:501), GHPO 599 (SEQ ID NO:503), GHPO 639 (SEQ ID NO:505), GHPO 642 (SEQ ID NO:507), GHPO 647 (SEQ ID NO:509), GHPO 654 (SEQ ID NO:511), GHPO 669 (SEQ ID NO:513), GHPO 710 (SEQ ID NO:515), GHPO 713 (SEQ ID NO:517), GHPO 716 (SEQ ID NO:519), GHPO 718 (SEQ ID NO:521), GHPO 726 (SEQ ID NO:523), GHPO 734 (SEQ ID NO:525), GHPO 740 (SEQ ID NO:527), GHPO 770 (SEQ ID NO:529), GHPO

-28-

GHPO 1689 (SEQ ID NO:265), GHPO 1733 (SEQ ID NO:267), GHPO 18  
(SEQ ID NO:269), GHPO 139 (SEQ ID NO:271), GHPO 142 (SEQ ID  
NO:273), GHPO 250 (SEQ ID NO:275), GHPO 257 (SEQ ID NO:277), GHPO  
325 (SEQ ID NO:279), GHPO 355 (SEQ ID NO:281), GHPO 357 (SEQ ID  
NO:283), GHPO 454 (SEQ ID NO:285), GHPO 475 (SEQ ID NO:287), GHPO  
5 515 (SEQ ID NO:289), GHPO 527 (SEQ ID NO:291), GHPO 551 (SEQ ID  
NO:293), GHPO 602 (SEQ ID NO:295), GHPO 626 (SEQ ID NO:297), GHPO  
646 (SEQ ID NO:299), GHPO 653 (SEQ ID NO:301), GHPO 655 (SEQ ID  
NO:303), GHPO 670 (SEQ ID NO:305), GHPO 739 (SEQ ID NO:307), GHPO  
798 (SEQ ID NO:309), GHPO 1102 (SEQ ID NO:311), GHPO 1114 (SEQ ID  
10 NO:313), GHPO 1152 (SEQ ID NO:315), GHPO 1272 (SEQ ID NO:317),  
GHPO 1345 (SEQ ID NO:319), GHPO 1377 (SEQ ID NO:321), GHPO 1424  
(SEQ ID NO:323), GHPO 1430 (SEQ ID NO:325), GHPO 1502 (SEQ ID  
NO:327), GHPO 1600 (SEQ ID NO:329), GHPO 1714 (SEQ ID NO:331),  
GHPO 359 (SEQ ID NO:333), GHPO 678 (SEQ ID NO:335), GHPO 708  
15 (SEQ ID NO:337), GHPO 759 (SEQ ID NO:339), GHPO 847 (SEQ ID  
NO:341), GHPO 1050 (SEQ ID NO:343), GHPO 1101 (SEQ ID NO:345),  
GHPO 1120 (SEQ ID NO:347), GHPO 1138 (SEQ ID NO:349), GHPO 1310  
(SEQ ID NO:351), GHPO 1320 (SEQ ID NO:353), GHPO 1375 (SEQ ID  
NO:355), GHPO 1432 (SEQ ID NO:357), GHPO 21 (SEQ ID NO:359), GHPO  
20 282 (SEQ ID NO:361), GHPO 1089 (SEQ ID NO:363), GHPO 1141 (SEQ ID  
NO:365), GHPO 1280 (SEQ ID NO:367), GHPO 1608 (SEQ ID NO:369),  
GHPO 15 (SEQ ID NO:371), GHPO 16 (SEQ ID NO:373), GHPO 36 (SEQ ID  
NO:375), GHPO 38 (SEQ ID NO:377), GHPO 52 (SEQ ID NO:379), GHPO  
57 (SEQ ID NO:381), GHPO 64 (SEQ ID NO:383), GHPO 79 (SEQ ID  
25 NO:385), GHPO 84 (SEQ ID NO:387), GHPO 86 (SEQ ID NO:389), GHPO  
99 (SEQ ID NO:391), GHPO 106 (SEQ ID NO:393), GHPO 118 (SEQ ID

-27-

(SEQ ID NO:135), GHPO 374 (SEQ ID NO:137), GHPO 442 (SEQ ID NO:139), GHPO 480 (SEQ ID NO:141), GHPO 523 (SEQ ID NO:143), GHPO 610 (SEQ ID NO:145), GHPO 675 (SEQ ID NO:147), GHPO 690 (SEQ ID NO:149), GHPO 829 (SEQ ID NO:151), GHPO 850 (SEQ ID NO:153), GHPO 876 (SEQ ID NO:155), GHPO 984 (SEQ ID NO:157), GHPO 989 (SEQ ID NO:159), GHPO 1111 (SEQ ID NO:161), GHPO 1145 (SEQ ID NO:163), GHPO 1256 (SEQ ID NO:165), GHPO 1264 (SEQ ID NO:167), GHPO 1316 (SEQ ID NO:169), GHPO 1368 (SEQ ID NO:171), GHPO 1442 (SEQ ID NO:173), GHPO 1506 (SEQ ID NO:175), GHPO 1543 (SEQ ID NO:177), GHPO 1574 (SEQ ID NO:179), GHPO 1627 (SEQ ID NO:181), GHPO 1657 (SEQ ID NO:183), GHPO 1664 (SEQ ID NO:185), GHPO 1694 (SEQ ID NO:187), GHPO 1704 (SEQ ID NO:189), GHPO 1763 (SEQ ID NO:191), GHPO 616 (SEQ ID NO:193), GHPO 76 (SEQ ID NO:195), GHPO 109 (SEQ ID NO:197), GHPO 163 (SEQ ID NO:199), GHPO 169 (SEQ ID NO:201), GHPO 208 (SEQ ID NO:203), GHPO 219 (SEQ ID NO:205), GHPO 445 (SEQ ID NO:207), GHPO 479 (SEQ ID NO:209), GHPO 525 (SEQ ID NO:211), GHPO 535 (SEQ ID NO:213), GHPO 731 (SEQ ID NO:215), GHPO 836 (SEQ ID NO:217), GHPO 879 (SEQ ID NO:219), GHPO 881 (SEQ ID NO:221), GHPO 886 (SEQ ID NO:223), GHPO 893 (SEQ ID NO:225), GHPO 894 (SEQ ID NO:227), GHPO 976 (SEQ ID NO:229), GHPO 1011 (SEQ ID NO:231), GHPO 1024 (SEQ ID NO:233), GHPO 1084 (SEQ ID NO:235), GHPO 1329 (SEQ ID NO:237), GHPO 1330 (SEQ ID NO:239), GHPO 1346 (SEQ ID NO:241), GHPO 1360 (SEQ ID NO:243), GHPO 1388 (SEQ ID NO:245), GHPO 1411 (SEQ ID NO:247), GHPO 1419 (SEQ ID NO:249), GHPO 1446 (SEQ ID NO:251), GHPO 1469 (SEQ ID NO:253), GHPO 1501 (SEQ ID NO:255), GHPO 1505 (SEQ ID NO:257), GHPO 1522 (SEQ ID NO:259), GHPO 1525 (SEQ ID NO:261), GHPO 1615 (SEQ ID NO:263),



-26-

encoding GHPO 35 (SEQ ID NO:1), GHPO 55 (SEQ ID NO:3), GHPO 78  
(SEQ ID NO:5), GHPO 89 (SEQ ID NO:7), GHPO 129 (SEQ ID NO:9),  
GHPO 541 (SEQ ID NO:11), GHPO 607 (SEQ ID NO:13), GHPO 635 (SEQ  
ID NO:15), GHPO 701 (SEQ ID NO:17), GHPO 712 (SEQ ID NO:19), GHPO  
761 (SEQ ID NO:21), GHPO 838 (SEQ ID NO:23), GHPO 1034 (SEQ ID  
5 NO:25), GHPO 1085 (SEQ ID NO:27), GHPO 1213 (SEQ ID NO:29), GHPO  
1255 (SEQ ID NO:31), GHPO 1308 (SEQ ID NO:33), GHPO 1389 (SEQ ID  
NO:35), GHPO 1706 (SEQ ID NO:37), GHPO 234 (SEQ ID NO:39), GHPO  
314 (SEQ ID NO:41), GHPO 510 (SEQ ID NO:43), GHPO 603 (SEQ ID  
NO:45), GHPO 937 (SEQ ID NO:47), GHPO 1027 (SEQ ID NO:49), GHPO  
10 1099 (SEQ ID NO:51), GHPO 1151 (SEQ ID NO:53), GHPO 1275 (SEQ ID  
NO:55), GHPO 1365 (SEQ ID NO:57), GHPO 1578 (SEQ ID NO:59), GHPO  
22 (SEQ ID NO:61), GHPO 58 (SEQ ID NO:63), GHPO 200 (SEQ ID NO:65),  
GHPO 558 (SEQ ID NO:67), GHPO 563 (SEQ ID NO:69), GHPO 695 (SEQ  
ID NO:71), GHPO 699 (SEQ ID NO:73), GHPO 702 (SEQ ID NO:75), GHPO  
15 709 (SEQ ID NO:77), GHPO 741 (SEQ ID NO:79), GHPO 762 (SEQ ID  
NO:81), GHPO 827 (SEQ ID NO:83), GHPO 852 (SEQ ID NO:85), GHPO  
1013 (SEQ ID NO:87), GHPO 1020 (SEQ ID NO:89), GHPO 1031 (SEQ ID  
NO:91), GHPO 1052 (SEQ ID NO:93), GHPO 1127 (SEQ ID NO:95), GHPO  
1149 (SEQ ID NO:97), GHPO 1176 (SEQ ID NO:99), GHPO 1250 (SEQ ID  
20 NO:101), GHPO 1312 (SEQ ID NO:103), GHPO 1358 (SEQ ID NO:105),  
GHPO 1490 (SEQ ID NO:107), GHPO 1559 (SEQ ID NO:109), GHPO 1651  
(SEQ ID NO:111), GHPO 1726 (SEQ ID NO:113), GHPO 1780 (SEQ ID  
NO:115), GHPO 895 (SEQ ID NO:117), GHPO 1447 (SEQ ID NO:119),  
GHPO 28 (SEQ ID NO:121), GHPO 86 (SEQ ID NO:123), GHPO 155 (SEQ  
25 ID NO:125), GHPO 157 (SEQ ID NO:127), GHPO 237 (SEQ ID NO:129),  
GHPO 290 (SEQ ID NO:131), GHPO 293 (SEQ ID NO:133), GHPO 335

-25-

NO:1336), GHPO 1701 (SEQ ID NO:1338), GHPO 1719 (SEQ ID NO:1340), GHPO 1723 (SEQ ID NO:1342), GHPO 1732 (SEQ ID NO:1344), GHPO 1739 (SEQ ID NO:1346), GHPO 1741 (SEQ ID NO:1348), GHPO 1747 (SEQ ID NO:1350), GHPO 1749 (SEQ ID NO:1352), GHPO 1750 (SEQ ID NO:1354), GHPO 1751 (SEQ ID NO:1356), GHPO 1755 (SEQ ID NO:1358), GHPO 1771 (SEQ ID NO:1360), GHPO 1786 (SEQ ID NO:1362), and GHPO 1789 (SEQ ID NO:1364), have been identified in the *H. pylori* genome. These polypeptides can be used, for example, in vaccination methods for preventing or treating *Helicobacter* infection. For example, GHPO 1320, GHPO 523, GHPO 792, GHPO 639, GHPO 669, GHPO 992, GHPO 576, GHPO 109, GHPO 129, GHPO 234, GHPO 257, GHPO 525, GHPO 626, GHPO 1034, GHPO 1275, GHPO 1308, GHPO 1600, GHPO 1615, GHPO 536, GHPO 66, GHPO 1363, GHPO 1595, and GHPO 1166 have been shown to be protective antigens that can be used in methods for preventing *Helicobacter* infection. By “protective antigen” is meant an antigen that is capable of reducing the infection level after challenge, relative to a positive control. Absolute protection from infection, although included in the invention, is not required.

Some of the new polypeptides are secreted polypeptides that can be produced in their mature forms (*i.e.*, as polypeptides that have been exported through class II or class III secretion pathways) or as precursors that include signal peptides, which can be removed in the course of excretion/secretion by cleavage at the N-terminal end of the mature form. (The cleavage site is located at the C-terminal end of the signal peptide, adjacent to the mature form.)

According to a first aspect of the invention, there are provided isolated polynucleotides that encode the precursor and mature forms of the *Helicobacter* GHPO proteins listed above. Examples of such polynucleotides are those

-24-

GHPO 1325 (SEQ ID NO:1216), GHPO 1341 (SEQ ID NO:1218), GHPO  
1351 (SEQ ID NO:1220), GHPO 1354 (SEQ ID NO:1222), GHPO 1363 (SEQ  
ID NO:1224), GHPO 1371 (SEQ ID NO:1226), GHPO 1381 (SEQ ID  
NO:1228), GHPO 1401 (SEQ ID NO:1230), GHPO 1402 (SEQ ID NO:1232),  
GHPO 1403 (SEQ ID NO:1234), GHPO 1408 (SEQ ID NO:1236), GHPO  
5 1416 (SEQ ID NO:1238), GHPO 1420 (SEQ ID NO:1240), GHPO 1428 (SEQ  
ID NO:1242), GHPO 1437 (SEQ ID NO:1244), GHPO 1439 (SEQ ID  
NO:1246), GHPO 1460 (SEQ ID NO:1248), GHPO 1463 (SEQ ID NO:1250),  
GHPO 1472 (SEQ ID NO:1252), GHPO 1474 (SEQ ID NO:1254), GHPO  
1484 (SEQ ID NO:1256), GHPO 1489 (SEQ ID NO:1258), GHPO 1494 (SEQ  
10 ID NO:1260), GHPO 1495 (SEQ ID NO:1262), GHPO 1498 (SEQ ID  
NO:1264), GHPO 1499 (SEQ ID NO:1266), GHPO 1500 (SEQ ID NO:1268),  
GHPO 1503 (SEQ ID NO:1270), GHPO 1504 (SEQ ID NO:1272), GHPO  
1510 (SEQ ID NO:1274), GHPO 1518 (SEQ ID NO:1276), GHPO 1533 (SEQ  
ID NO:1278), GHPO 1541 (SEQ ID NO:1280), GHPO 1544 (SEQ ID  
15 NO:1282), GHPO 1548 (SEQ ID NO:1284), GHPO 1565 (SEQ ID NO:1286),  
GHPO 1575 (SEQ ID NO:1288), GHPO 1582 (SEQ ID NO:1290), GHPO  
1595 (SEQ ID NO:1292), GHPO 1597 (SEQ ID NO:1294), GHPO 1599 (SEQ  
ID NO:1296), GHPO 1601 (SEQ ID NO:1298), GHPO 1609 (SEQ ID  
NO:1300), GHPO 1613 (SEQ ID NO:1302), GHPO 1614 (SEQ ID NO:1304),  
20 GHPO 1626 (SEQ ID NO:1306), GHPO 1628 (SEQ ID NO:1308), GHPO  
1639 (SEQ ID NO:1310), GHPO 1640 (SEQ ID NO:1312), GHPO 1641 (SEQ  
ID NO:1314), GHPO 1646 (SEQ ID NO:1316), GHPO 1662 (SEQ ID  
NO:1318), GHPO 1667 (SEQ ID NO:1320), GHPO 1668 (SEQ ID NO:1322),  
GHPO 1670 (SEQ ID NO:1324), GHPO 1671 (SEQ ID NO:1326), GHPO  
25 1672 (SEQ ID NO:1328), GHPO 1678 (SEQ ID NO:1330), GHPO 1684 (SEQ  
ID NO:1332), GHPO 1695 (SEQ ID NO:1334), GHPO 1697 (SEQ ID

-23-

1033 (SEQ ID NO:1094), GHPO 1039 (SEQ ID NO:1096), GHPO 1041 (SEQ ID NO:1098), GHPO 1043 (SEQ ID NO:1100), GHPO 1044 (SEQ ID NO:1102), GHPO 1051 (SEQ ID NO:1104), GHPO 1058 (SEQ ID NO:1106), GHPO 1060 (SEQ ID NO:1108), GHPO 1075 (SEQ ID NO:1110), GHPO 1077 (SEQ ID NO:1112), GHPO 1082 (SEQ ID NO:1114), GHPO 1083 (SEQ ID NO:1116), GHPO 1086 (SEQ ID NO:1118), GHPO 1087 (SEQ ID NO:1120), GHPO 1090 (SEQ ID NO:1122), GHPO 1097 (SEQ ID NO:1124), GHPO 1098 (SEQ ID NO:1126), GHPO 1103 (SEQ ID NO:1128), GHPO 1113 (SEQ ID NO:1130), GHPO 1116 (SEQ ID NO:1132), GHPO 1123 (SEQ ID NO:1134), GHPO 1125 (SEQ ID NO:1136), GHPO 1129 (SEQ ID NO:1138), GHPO 1130 (SEQ ID NO:1140), GHPO 1134 (SEQ ID NO:1142), GHPO 1161 (SEQ ID NO:1144), GHPO 1166 (SEQ ID NO:1146), GHPO 1170 (SEQ ID NO:1148), GHPO 1175 (SEQ ID NO:1150), GHPO 1181 (SEQ ID NO:1152), GHPO 1186 (SEQ ID NO:1154), GHPO 1188 (SEQ ID NO:1156), GHPO 1191 (SEQ ID NO:1158), GHPO 1193 (SEQ ID NO:1160), GHPO 1196 (SEQ ID NO:1162), GHPO 1204 (SEQ ID NO:1164), GHPO 1210 (SEQ ID NO:1166), GHPO 1211 (SEQ ID NO:1168), GHPO 1216 (SEQ ID NO:1170), GHPO 1218 (SEQ ID NO:1172), GHPO 1220 (SEQ ID NO:1174), GHPO 1223 (SEQ ID NO:1176), GHPO 1226 (SEQ ID NO:1178), GHPO 1240 (SEQ ID NO:1180), GHPO 1246 (SEQ ID NO:1182), GHPO 1251 (SEQ ID NO:1184), GHPO 1252 (SEQ ID NO:1186), GHPO 1261 (SEQ ID NO:1188), GHPO 1265 (SEQ ID NO:1190), GHPO 1267 (SEQ ID NO:1192), GHPO 1278 (SEQ ID NO:1194), GHPO 1282 (SEQ ID NO:1196), GHPO 1283 (SEQ ID NO:1198), GHPO 1287 (SEQ ID NO:1200), GHPO 1292 (SEQ ID NO:1202), GHPO 1293 (SEQ ID NO:1204), GHPO 1302 (SEQ ID NO:1206), GHPO 1309 (SEQ ID NO:1208), GHPO 1317 (SEQ ID NO:1210), GHPO 1318 (SEQ ID NO:1212), GHPO 1321 (SEQ ID NO:1214),

-22-

583 (SEQ ID NO:966), GHPO 588 (SEQ ID NO:968), GHPO 593 (SEQ ID NO:970), GHPO 597 (SEQ ID NO:972), GHPO 598 (SEQ ID NO:974), GHPO 604 (SEQ ID NO:976), GHPO 606 (SEQ ID NO:978), GHPO 611 (SEQ ID NO:980), GHPO 612 (SEQ ID NO:982), GHPO 615 (SEQ ID NO:984), GHPO 632 (SEQ ID NO:986), GHPO 633 (SEQ ID NO:988), GHPO 637 (SEQ ID NO:990), GHPO 651 (SEQ ID NO:992), GHPO 663 (SEQ ID NO:994), GHPO 686 (SEQ ID NO:996), GHPO 693 (SEQ ID NO:998), GHPO 698 (SEQ ID NO:1000), GHPO 703 (SEQ ID NO:1002), GHPO 704 (SEQ ID NO:1004), GHPO 705 (SEQ ID NO:1006), GHPO 707 (SEQ ID NO:1008), GHPO 721 (SEQ ID NO:1010), GHPO 727 (SEQ ID NO:1012), GHPO 728 (SEQ ID NO:1014), GHPO 733 (SEQ ID NO:1016), GHPO 758 (SEQ ID NO:1018), GHPO 763 (SEQ ID NO:1020), GHPO 771 (SEQ ID NO:1022), GHPO 774 (SEQ ID NO:1024), GHPO 776 (SEQ ID NO:1026), GHPO 783 (SEQ ID NO:1028), GHPO 800 (SEQ ID NO:1030), GHPO 806 (SEQ ID NO:1032), GHPO 807 (SEQ ID NO:1034), GHPO 808 (SEQ ID NO:1036), GHPO 809 (SEQ ID NO:1038), GHPO 811 (SEQ ID NO:1040), GHPO 815 (SEQ ID NO:1042), GHPO 819 (SEQ ID NO:1044), GHPO 841 (SEQ ID NO:1046), GHPO 843 (SEQ ID NO:1048), GHPO 846 (SEQ ID NO:1050), GHPO 875 (SEQ ID NO:1052), GHPO 892 (SEQ ID NO:1054), GHPO 902 (SEQ ID NO:1056), GHPO 904 (SEQ ID NO:1058), GHPO 906 (SEQ ID NO:1060), GHPO 908 (SEQ ID NO:1062), GHPO 921 (SEQ ID NO:1064), GHPO 923 (SEQ ID NO:1066), GHPO 926 (SEQ ID NO:1068), GHPO 933 (SEQ ID NO:1070), GHPO 939 (SEQ ID NO:1072), GHPO 940 (SEQ ID NO:1074), GHPO 943 (SEQ ID NO:1076), GHPO 951 (SEQ ID NO:1078), GHPO 961 (SEQ ID NO:1080), GHPO 965 (SEQ ID NO:1082), GHPO 990 (SEQ ID NO:1084), GHPO 991 (SEQ ID NO:1086), GHPO 998 (SEQ ID NO:1088), GHPO 1001 (SEQ ID NO:1090), GHPO 1005 (SEQ ID NO:1092), GHPO

-21-

NO:830), GHPO 218 (SEQ ID NO:832), GHPO 226 (SEQ ID NO:834), GHPO  
231 (SEQ ID NO:836), GHPO 236 (SEQ ID NO:838), GHPO 239 (SEQ ID  
NO:840), GHPO 245 (SEQ ID NO:842), GHPO 246 (SEQ ID NO:844), GHPO  
248 (SEQ ID NO:846), GHPO 253 (SEQ ID NO:848), GHPO 265 (SEQ ID  
NO:850), GHPO 266 (SEQ ID NO:852), GHPO 271 (SEQ ID NO:854), GHPO  
5 272 (SEQ ID NO:856), GHPO 286 (SEQ ID NO:858), GHPO 291 (SEQ ID  
NO:860), GHPO 292 (SEQ ID NO:862), GHPO 297 (SEQ ID NO:864), GHPO  
304 (SEQ ID NO:866), GHPO 307 (SEQ ID NO:868), GHPO 324 (SEQ ID  
NO:870), GHPO 326 (SEQ ID NO:872), GHPO 331 (SEQ ID NO:874), GHPO  
343 (SEQ ID NO:876), GHPO 345 (SEQ ID NO:878), GHPO 346 (SEQ ID  
10 NO:880), GHPO 352 (SEQ ID NO:882), GHPO 355 (SEQ ID NO:884), GHPO  
363 (SEQ ID NO:886), GHPO 369 (SEQ ID NO:888), GHPO 376 (SEQ ID  
NO:890), GHPO 378 (SEQ ID NO:892), GHPO 388 (SEQ ID NO:894), GHPO  
396 (SEQ ID NO:896), GHPO 403 (SEQ ID NO:898), GHPO 410 (SEQ ID  
NO:900), GHPO 415 (SEQ ID NO:902), GHPO 421 (SEQ ID NO:904), GHPO  
15 439 (SEQ ID NO:906), GHPO 441 (SEQ ID NO:908), GHPO 443 (SEQ ID  
NO:910), GHPO 453 (SEQ ID NO:912), GHPO 455 (SEQ ID NO:914), GHPO  
464 (SEQ ID NO:916), GHPO 467 (SEQ ID NO:918), GHPO 468 (SEQ ID  
NO:920), GHPO 470 (SEQ ID NO:922), GHPO 486 (SEQ ID NO:924), GHPO  
487 (SEQ ID NO:926), GHPO 488 (SEQ ID NO:928), GHPO 489 (SEQ ID  
20 NO:930), GHPO 498 (SEQ ID NO:932), GHPO 501 (SEQ ID NO:934), GHPO  
504 (SEQ ID NO:936), GHPO 512 (SEQ ID NO:938), GHPO 517 (SEQ ID  
NO:940), GHPO 520 (SEQ ID NO:942), GHPO 528 (SEQ ID NO:944), GHPO  
530 (SEQ ID NO:946), GHPO 532 (SEQ ID NO:948), GHPO 548 (SEQ ID  
NO:950), GHPO 561 (SEQ ID NO:952), GHPO 564 (SEQ ID NO:954), GHPO  
25 572 (SEQ ID NO:956), GHPO 573 (SEQ ID NO:958), GHPO 574 (SEQ ID  
NO:960), GHPO 577 (SEQ ID NO:962), GHPO 579 (SEQ ID NO:964), GHPO

-20-

(SEQ ID NO:698), GHPO 1605 (SEQ ID NO:700), GHPO 1619 (SEQ ID NO:702), GHPO 1629 (SEQ ID NO:704), GHPO 1642 (SEQ ID NO:706), GHPO 1654 (SEQ ID NO:708), GHPO 1661 (SEQ ID NO:710), GHPO 1673 (SEQ ID NO:712), GHPO 1687 (SEQ ID NO:714), GHPO 1692 (SEQ ID NO:716), GHPO 1693 (SEQ ID NO:718), GHPO 1699 (SEQ ID NO:720),  
5 GHPO 1738 (SEQ ID NO:722), GHPO 1745 (SEQ ID NO:724), GHPO 1746 (SEQ ID NO:726), GHPO 1754 (SEQ ID NO:728), GHPO 1792 (SEQ ID NO:730), GHPO 1795 (SEQ ID NO:732), GHPO 1796 (SEQ ID NO:734), GHPO 7 (SEQ ID NO:736), GHPO 8 (SEQ ID NO:738), GHPO 9 (SEQ ID NO:740), GHPO 10 (SEQ ID NO:742), GHPO 12 (SEQ ID NO:744), GHPO  
10 25 (SEQ ID NO:746), GHPO 27 (SEQ ID NO:748), GHPO 29 (SEQ ID NO:750), GHPO 30 (SEQ ID NO:752), GHPO 37 (SEQ ID NO:754), GHPO 49 (SEQ ID NO:756), GHPO 51 (SEQ ID NO:758), GHPO 54 (SEQ ID NO:760), GHPO 65 (SEQ ID NO:762), GHPO 66 (SEQ ID NO:764), GHPO 68 (SEQ ID NO:766), GHPO 70 (SEQ ID NO:768), GHPO 77 (SEQ ID NO:770), GHPO 83 (SEQ ID NO:772), GHPO 85 (SEQ ID NO:774), GHPO  
15 87 (SEQ ID NO:776), GHPO 91 (SEQ ID NO:778), GHPO 92 (SEQ ID NO:780), GHPO 96 (SEQ ID NO:782), GHPO 97 (SEQ ID NO:784), GHPO 111 (SEQ ID NO:786), GHPO 115 (SEQ ID NO:788), GHPO 117 (SEQ ID NO:790), GHPO 123 (SEQ ID NO:792), GHPO 124 (SEQ ID NO:794), GHPO  
20 126 (SEQ ID NO:796), GHPO 127 (SEQ ID NO:798), GHPO 128 (SEQ ID NO:800), GHPO 131 (SEQ ID NO:802), GHPO 133 (SEQ ID NO:804), GHPO 140 (SEQ ID NO:806), GHPO 141 (SEQ ID NO:808), GHPO 145 (SEQ ID NO:810), GHPO 147 (SEQ ID NO:812), GHPO 166 (SEQ ID NO:814), GHPO 181 (SEQ ID NO:816), GHPO 187 (SEQ ID NO:818), GHPO 188 (SEQ ID NO:820), GHPO 192 (SEQ ID NO:822), GHPO 202 (SEQ ID NO:824), GHPO  
25 204 (SEQ ID NO:826), GHPO 205 (SEQ ID NO:828), GHPO 212 (SEQ ID

-19-

1002 (SEQ ID NO:572), GHPO 1026 (SEQ ID NO:574), GHPO 1028 (SEQ ID NO:576), GHPO 1034 (SEQ ID NO:578), GHPO 1038 (SEQ ID NO:580), GHPO 1059 (SEQ ID NO:582), GHPO 1065 (SEQ ID NO:584), GHPO 1072 (SEQ ID NO:586), GHPO 1073 (SEQ ID NO:588), GHPO 1088 (SEQ ID NO:590), GHPO 1091 (SEQ ID NO:592), GHPO 1105 (SEQ ID NO:594),  
5 GHPO 1115 (SEQ ID NO:596), GHPO 1159 (SEQ ID NO:598), GHPO 1177 (SEQ ID NO:600), GHPO 1187 (SEQ ID NO:602), GHPO 1192 (SEQ ID NO:604), GHPO 1195 (SEQ ID NO:606), GHPO 1224 (SEQ ID NO:608), GHPO 1225 (SEQ ID NO:610), GHPO 1228 (SEQ ID NO:612), GHPO 1229 (SEQ ID NO:614), GHPO 1231 (SEQ ID NO:616), GHPO 1236 (SEQ ID NO:618), GHPO 1242 (SEQ ID NO:620), GHPO 1248 (SEQ ID NO:622),  
10 GHPO 1270 (SEQ ID NO:624), GHPO 1271 (SEQ ID NO:626), GHPO 1298 (SEQ ID NO:628), GHPO 1301 (SEQ ID NO:630), GHPO 1304 (SEQ ID NO:632), GHPO 1315 (SEQ ID NO:634), GHPO 1319 (SEQ ID NO:636), GHPO 1323 (SEQ ID NO:638), GHPO 1331 (SEQ ID NO:640), GHPO 1332 (SEQ ID NO:642), GHPO 1347 (SEQ ID NO:644), GHPO 1373 (SEQ ID NO:646), GHPO 1376 (SEQ ID NO:648), GHPO 1380 (SEQ ID NO:650), GHPO 1394 (SEQ ID NO:652), GHPO 1407 (SEQ ID NO:654), GHPO 1415 (SEQ ID NO:656), GHPO 1425 (SEQ ID NO:658), GHPO 1427 (SEQ ID NO:660), GHPO 1444 (SEQ ID NO:662), GHPO 1449 (SEQ ID NO:664),  
15 GHPO 1465 (SEQ ID NO:666), GHPO 1475 (SEQ ID NO:668), GHPO 1479 (SEQ ID NO:670), GHPO 1483 (SEQ ID NO:672), GHPO 1488 (SEQ ID NO:674), GHPO 1496 (SEQ ID NO:676), GHPO 1524 (SEQ ID NO:678), GHPO 1536 (SEQ ID NO:680), GHPO 1539 (SEQ ID NO:682), GHPO 1540 (SEQ ID NO:684), GHPO 1542 (SEQ ID NO:686), GHPO 1555 (SEQ ID NO:688), GHPO 1560 (SEQ ID NO:690), GHPO 1564 (SEQ ID NO:692),  
20 GHPO 1570 (SEQ ID NO:694), GHPO 1588 (SEQ ID NO:696), GHPO 1604



-18-

NO:436), GHPO 330 (SEQ ID NO:438), GHPO 340 (SEQ ID NO:440), GHPO 342 (SEQ ID NO:442), GHPO 344 (SEQ ID NO:444), GHPO 358 (SEQ ID NO:446), GHPO 373 (SEQ ID NO:448), GHPO 382 (SEQ ID NO:450), GHPO 384 (SEQ ID NO:452), GHPO 398 (SEQ ID NO:454), GHPO 409 (SEQ ID NO:456), GHPO 422 (SEQ ID NO:458), GHPO 430 (SEQ ID NO:460), GHPO 446 (SEQ ID NO:462), GHPO 447 (SEQ ID NO:464), GHPO 450 (SEQ ID NO:466), GHPO 451 (SEQ ID NO:468), GHPO 452 (SEQ ID NO:470), GHPO 456 (SEQ ID NO:472), GHPO 461 (SEQ ID NO:474), GHPO 476 (SEQ ID NO:476), GHPO 478 (SEQ ID NO:478), GHPO 491 (SEQ ID NO:480), GHPO 511 (SEQ ID NO:482), GHPO 519 (SEQ ID NO:484), GHPO 526 (SEQ ID NO:486), GHPO 534 (SEQ ID NO:488), GHPO 536 (SEQ ID NO:490), GHPO 542 (SEQ ID NO:492), GHPO 544 (SEQ ID NO:494), GHPO 576 (SEQ ID NO:496), GHPO 578 (SEQ ID NO:498), GHPO 580 (SEQ ID NO:500), GHPO 585 (SEQ ID NO:502), GHPO 599 (SEQ ID NO:504), GHPO 639 (SEQ ID NO:506), GHPO 642 (SEQ ID NO:508), GHPO 647 (SEQ ID NO:510), GHPO 654 (SEQ ID NO:512), GHPO 669 (SEQ ID NO:514), GHPO 710 (SEQ ID NO:516), GHPO 713 (SEQ ID NO:518), GHPO 716 (SEQ ID NO:520), GHPO 718 (SEQ ID NO:522), GHPO 726 (SEQ ID NO:524), GHPO 734 (SEQ ID NO:526), GHPO 740 (SEQ ID NO:528), GHPO 770 (SEQ ID NO:530), GHPO 782 (SEQ ID NO:532), GHPO 786 (SEQ ID NO:534), GHPO 792 (SEQ ID NO:536), GHPO 797 (SEQ ID NO:538), GHPO 816 (SEQ ID NO:540), GHPO 828 (SEQ ID NO:542), GHPO 839 (SEQ ID NO:544), GHPO 840 (SEQ ID NO:546), GHPO 842 (SEQ ID NO:548), GHPO 885 (SEQ ID NO:550), GHPO 889 (SEQ ID NO:552), GHPO 903 (SEQ ID NO:554), GHPO 912 (SEQ ID NO:556), GHPO 946 (SEQ ID NO:558), GHPO 958 (SEQ ID NO:560), GHPO 968 (SEQ ID NO:562), GHPO 987 (SEQ ID NO:564), GHPO 992 (SEQ ID NO:566), GHPO 996 (SEQ ID NO:568), GHPO 997 (SEQ ID NO:570), GHPO

-17-

NO:304), GHPO 670 (SEQ ID NO:306), GHPO 739 (SEQ ID NO:308), GHPO 798 (SEQ ID NO:310), GHPO 1102 (SEQ ID NO:312), GHPO 1114 (SEQ ID NO:314), GHPO 1152 (SEQ ID NO:316), GHPO 1272 (SEQ ID NO:318), GHPO 1345 (SEQ ID NO:320), GHPO 1377 (SEQ ID NO:322), GHPO 1424 (SEQ ID NO:324), GHPO 1430 (SEQ ID NO:326), GHPO 1502 (SEQ ID NO:328), GHPO 1600 (SEQ ID NO:330), GHPO 1714 (SEQ ID NO:332), GHPO 359 (SEQ ID NO:334), GHPO 678 (SEQ ID NO:336), GHPO 708 (SEQ ID NO:338), GHPO 759 (SEQ ID NO:340), GHPO 847 (SEQ ID NO:342), GHPO 1050 (SEQ ID NO:344), GHPO 1101 (SEQ ID NO:346), GHPO 1120 (SEQ ID NO:348), GHPO 1138 (SEQ ID NO:350), GHPO 1310 (SEQ ID NO:352), GHPO 1320 (SEQ ID NO:354), GHPO 1375 (SEQ ID NO:356), GHPO 1432 (SEQ ID NO:358), GHPO 21 (SEQ ID NO:360), GHPO 282 (SEQ ID NO:362), GHPO 1089 (SEQ ID NO:364), GHPO 1141 (SEQ ID NO:366), GHPO 1280 (SEQ ID NO:368), GHPO 1608 (SEQ ID NO:370), GHPO 15 (SEQ ID NO:372), GHPO 16 (SEQ ID NO:374), GHPO 36 (SEQ ID NO:376), GHPO 38 (SEQ ID NO:378), GHPO 52 (SEQ ID NO:380), GHPO 57 (SEQ ID NO:382), GHPO 64 (SEQ ID NO:384), GHPO 79 (SEQ ID NO:386), GHPO 84 (SEQ ID NO:388), GHPO 86 (SEQ ID NO:390), GHPO 99 (SEQ ID NO:392), GHPO 106 (SEQ ID NO:394), GHPO 118 (SEQ ID NO:396), GHPO 122 (SEQ ID NO:398), GHPO 128 (SEQ ID NO:400), GHPO 138 (SEQ ID NO:402), GHPO 153 (SEQ ID NO:404), GHPO 160 (SEQ ID NO:406), GHPO 168 (SEQ ID NO:408), GHPO 179 (SEQ ID NO:410), GHPO 189 (SEQ ID NO:412), GHPO 229 (SEQ ID NO:414), GHPO 243 (SEQ ID NO:416), GHPO 244 (SEQ ID NO:418), GHPO 251 (SEQ ID NO:420), GHPO 267 (SEQ ID NO:422), GHPO 269 (SEQ ID NO:424), GHPO 279 (SEQ ID NO:426), GHPO 284 (SEQ ID NO:428), GHPO 296 (SEQ ID NO:430), GHPO 300 (SEQ ID NO:432), GHPO 305 (SEQ ID NO:434), GHPO 319 (SEQ ID

-16-

NO:174), GHPO 1506 (SEQ ID NO:176), GHPO 1543 (SEQ ID NO:178),  
GHPO 1574 (SEQ ID NO:180), GHPO 1627 (SEQ ID NO:182), GHPO 1657  
(SEQ ID NO:184), GHPO 1664 (SEQ ID NO:186), GHPO 1694 (SEQ ID  
NO:188), GHPO 1704 (SEQ ID NO:190), GHPO 1763 (SEQ ID NO:192),  
GHPO 616 (SEQ ID NO:194), GHPO 76 (SEQ ID NO:196), GHPO 109 (SEQ  
ID NO:198), GHPO 163 (SEQ ID NO:200), GHPO 169 (SEQ ID NO:202),  
GHPO 208 (SEQ ID NO:204), GHPO 219 (SEQ ID NO:206), GHPO 445  
(SEQ ID NO:208), GHPO 479 (SEQ ID NO:210), GHPO 525 (SEQ ID  
NO:212), GHPO 535 (SEQ ID NO:214), GHPO 731 (SEQ ID NO:216), GHPO  
836 (SEQ ID NO:218), GHPO 879 (SEQ ID NO:220), GHPO 881 (SEQ ID  
NO:222), GHPO 886 (SEQ ID NO:224), GHPO 893 (SEQ ID NO:226), GHPO  
894 (SEQ ID NO:228), GHPO 976 (SEQ ID NO:230), GHPO 1011 (SEQ ID  
NO:232), GHPO 1024 (SEQ ID NO:234), GHPO 1084 (SEQ ID NO:236),  
GHPO 1329 (SEQ ID NO:238), GHPO 1330 (SEQ ID NO:240), GHPO 1346  
(SEQ ID NO:242), GHPO 1360 (SEQ ID NO:244), GHPO 1388 (SEQ ID  
NO:246), GHPO 1411 (SEQ ID NO:248), GHPO 1419 (SEQ ID NO:250),  
GHPO 1446 (SEQ ID NO:252), GHPO 1469 (SEQ ID NO:254), GHPO 1501  
(SEQ ID NO:256), GHPO 1505 (SEQ ID NO:258), GHPO 1522 (SEQ ID  
NO:260), GHPO 1525 (SEQ ID NO:262), GHPO 1615 (SEQ ID NO:264),  
GHPO 1689 (SEQ ID NO:266), GHPO 1733 (SEQ ID NO:268), GHPO 18  
(SEQ ID NO:270), GHPO 139 (SEQ ID NO:272), GHPO 142 (SEQ ID  
NO:274), GHPO 250 (SEQ ID NO:276), GHPO 257 (SEQ ID NO:278), GHPO  
325 (SEQ ID NO:280), GHPO 355 (SEQ ID NO:282), GHPO 357 (SEQ ID  
NO:284), GHPO 454 (SEQ ID NO:286), GHPO 475 (SEQ ID NO:288), GHPO  
515 (SEQ ID NO:290), GHPO 527 (SEQ ID NO:292), GHPO 551 (SEQ ID  
NO:294), GHPO 602 (SEQ ID NO:296), GHPO 626 (SEQ ID NO:298), GHPO  
646 (SEQ ID NO:300), GHPO 653 (SEQ ID NO:302), GHPO 655 (SEQ ID

-15-

314 (SEQ ID NO:42), GHPO 510 (SEQ ID NO:44), GHPO 603 (SEQ ID NO:46), GHPO 937 (SEQ ID NO:48), GHPO 1027 (SEQ ID NO:50), GHPO 1099 (SEQ ID NO:52), GHPO 1151 (SEQ ID NO:54), GHPO 1275 (SEQ ID NO:56), GHPO 1365 (SEQ ID NO:58), GHPO 1578 (SEQ ID NO:60), GHPO 22 (SEQ ID NO:62), GHPO 58 (SEQ ID NO:64), GHPO 200 (SEQ ID NO:66),  
5 GHPO 558 (SEQ ID NO:68), GHPO 563 (SEQ ID NO:70), GHPO 695 (SEQ ID NO:72), GHPO 699 (SEQ ID NO:74), GHPO 702 (SEQ ID NO:76), GHPO 709 (SEQ ID NO:78), GHPO 741 (SEQ ID NO:80), GHPO 762 (SEQ ID NO:82), GHPO 827 (SEQ ID NO:84), GHPO 852 (SEQ ID NO:86), GHPO 1013 (SEQ ID NO:88), GHPO 1020 (SEQ ID NO:90), GHPO 1031 (SEQ ID NO:92), GHPO 1052 (SEQ ID NO:94), GHPO 1127 (SEQ ID NO:96), GHPO 1149 (SEQ ID NO:98), GHPO 1176 (SEQ ID NO:100), GHPO 1250 (SEQ ID NO:102), GHPO 1312 (SEQ ID NO:104), GHPO 1358 (SEQ ID NO:106), GHPO 1490 (SEQ ID NO:108), GHPO 1559 (SEQ ID NO:110), GHPO 1651 (SEQ ID NO:112), GHPO 1726 (SEQ ID NO:114), GHPO 1780 (SEQ ID NO:116), GHPO 895 (SEQ ID NO:118), GHPO 1447 (SEQ ID NO:120),  
15 GHPO 28 (SEQ ID NO:122), GHPO 86 (SEQ ID NO:124), GHPO 155 (SEQ ID NO:126), GHPO 157 (SEQ ID NO:128), GHPO 237 (SEQ ID NO:130), GHPO 290 (SEQ ID NO:132), GHPO 293 (SEQ ID NO:134), GHPO 335 (SEQ ID NO:136), GHPO 374 (SEQ ID NO:138), GHPO 442 (SEQ ID NO:140), GHPO 480 (SEQ ID NO:142), GHPO 523 (SEQ ID NO:144), GHPO 610 (SEQ ID NO:146), GHPO 675 (SEQ ID NO:148), GHPO 690 (SEQ ID NO:150), GHPO 829 (SEQ ID NO:152), GHPO 850 (SEQ ID NO:154), GHPO 876 (SEQ ID NO:156), GHPO 984 (SEQ ID NO:158), GHPO 989 (SEQ ID NO:160), GHPO 1111 (SEQ ID NO:162), GHPO 1145 (SEQ ID NO:164),  
20 GHPO 1256 (SEQ ID NO:166), GHPO 1264 (SEQ ID NO:168), GHPO 1316 (SEQ ID NO:170), GHPO 1368 (SEQ ID NO:172), GHPO 1442 (SEQ ID

-14-

of the invention. Accordingly, the present invention provides (i) methods for producing polypeptides of the invention in recombinant host systems and related expression cassettes, vectors, and transformed or transfected cells; (ii) live vaccine vectors, such as pox virus, *Salmonella typhimurium*, and *Vibrio cholerae* vectors, that contain polynucleotides of the invention (such vaccine vectors being useful in, *e.g.*, methods for preventing or treating *Helicobacter* infection) in combination with a diluent or carrier, and related pharmaceutical compositions and associated therapeutic and/or prophylactic methods; (iii) therapeutic and/or prophylactic methods involving administration of polynucleotide molecules, either in a naked form or formulated with a delivery vehicle, polypeptides or mixtures of polypeptides, or monospecific antibodies of the invention, and related pharmaceutical compositions; (iv) methods for detecting the presence of *Helicobacter* in biological samples, which can involve the use of polynucleotide molecules, monospecific antibodies, or polypeptides of the invention; and (v) methods for purifying polypeptides of the invention by antibody-based affinity chromatography.

#### Detailed Description

Open reading frames (ORFs) encoding new polypeptides, designated GHPO 35 (SEQ ID NO:2), GHPO 55 (SEQ ID NO:4), GHPO 78 (SEQ ID NO:6), GHPO 89 (SEQ ID NO:8), GHPO 129 (SEQ ID NO:10), GHPO 541 (SEQ ID NO:12), GHPO 607 (SEQ ID NO:14), GHPO 635 (SEQ ID NO:16), GHPO 701 (SEQ ID NO:18), GHPO 712 (SEQ ID NO:20), GHPO 761 (SEQ ID NO:22), GHPO 838 (SEQ ID NO:24), GHPO 1034 (SEQ ID NO:26), GHPO 1085 (SEQ ID NO:28), GHPO 1213 (SEQ ID NO:30), GHPO 1255 (SEQ ID NO:32), GHPO 1308 (SEQ ID NO:34), GHPO 1389 (SEQ ID NO:36), GHPO 1706 (SEQ ID NO:38), GHPO 234 (SEQ ID NO:40), GHPO

-13-

NO:1320), GHPO 1668 (SEQ ID NO:1322), GHPO 1670 (SEQ ID NO:1324), GHPO 1671 (SEQ ID NO:1326), GHPO 1672 (SEQ ID NO:1328), GHPO 1678 (SEQ ID NO:1330), GHPO 1684 (SEQ ID NO:1332), GHPO 1695 (SEQ ID NO:1334), GHPO 1697 (SEQ ID NO:1336), GHPO 1701 (SEQ ID NO:1338), GHPO 1719 (SEQ ID NO:1340), GHPO 1723 (SEQ ID NO:1342), GHPO 1732 (SEQ ID NO:1344), GHPO 1739 (SEQ ID NO:1346), GHPO 1741 (SEQ ID NO:1348), GHPO 1747 (SEQ ID NO:1350), GHPO 1749 (SEQ ID NO:1352), GHPO 1750 (SEQ ID NO:1354), GHPO 1751 (SEQ ID NO:1356), GHPO 1755 (SEQ ID NO:1358), GHPO 1771 (SEQ ID NO:1360), GHPO 1786 (SEQ ID NO:1362), and GHPO 1789 (SEQ ID NO:1364), which can be used, *e.g.*, in methods to prevent, treat, or diagnose *Helicobacter* infection. The sequences of polynucleotides that encode these polypeptides are shown in the sequence listing (odd numbers, up to SEQ ID NO:1363). Those skilled in the art will understand that the invention also includes polynucleotide molecules that encode mutants and derivatives of these polypeptides, which can result from the addition, deletion, or substitution of non-essential amino acids, as is described further below.

In addition to the polynucleotide molecules described above, the invention includes the corresponding polypeptides (*i.e.*, polypeptides encoded by the polynucleotide molecules of the invention, or fragments thereof), and monospecific antibodies that specifically bind to these polypeptides. The polypeptides of the invention include those having the amino acid sequences shown in the sequence listing (even numbers, up to SEQ ID NO:1363), as well as mature forms of proteins having sequences shown in the sequence listing in their unprocessed forms, and fragments thereof.

The present invention has many applications and includes expression cassettes, vectors, and cells transformed or transfected with the polynucleotides

-12-

GHPO 1287 (SEQ ID NO:1200), GHPO 1292 (SEQ ID NO:1202), GHPO  
1293 (SEQ ID NO:1204), GHPO 1302 (SEQ ID NO:1206), GHPO 1309 (SEQ  
ID NO:1208), GHPO 1317 (SEQ ID NO:1210), GHPO 1318 (SEQ ID  
NO:1212), GHPO 1321 (SEQ ID NO:1214), GHPO 1325 (SEQ ID NO:1216),  
GHPO 1341 (SEQ ID NO:1218), GHPO 1351 (SEQ ID NO:1220), GHPO  
5 1354 (SEQ ID NO:1222), GHPO 1363 (SEQ ID NO:1224), GHPO 1371 (SEQ  
ID NO:1226), GHPO 1381 (SEQ ID NO:1228), GHPO 1401 (SEQ ID  
NO:1230), GHPO 1402 (SEQ ID NO:1232), GHPO 1403 (SEQ ID NO:1234),  
GHPO 1408 (SEQ ID NO:1236), GHPO 1416 (SEQ ID NO:1238), GHPO  
1420 (SEQ ID NO:1240), GHPO 1428 (SEQ ID NO:1242), GHPO 1437 (SEQ  
10 ID NO:1244), GHPO 1439 (SEQ ID NO:1246), GHPO 1460 (SEQ ID  
NO:1248), GHPO 1463 (SEQ ID NO:1250), GHPO 1472 (SEQ ID NO:1252),  
GHPO 1474 (SEQ ID NO:1254), GHPO 1484 (SEQ ID NO:1256), GHPO  
1489 (SEQ ID NO:1258), GHPO 1494 (SEQ ID NO:1260), GHPO 1495 (SEQ  
ID NO:1262), GHPO 1498 (SEQ ID NO:1264), GHPO 1499 (SEQ ID  
15 NO:1266), GHPO 1500 (SEQ ID NO:1268), GHPO 1503 (SEQ ID NO:1270),  
GHPO 1504 (SEQ ID NO:1272), GHPO 1510 (SEQ ID NO:1274), GHPO  
1518 (SEQ ID NO:1276), GHPO 1533 (SEQ ID NO:1278), GHPO 1541 (SEQ  
ID NO:1280), GHPO 1544 (SEQ ID NO:1282), GHPO 1548 (SEQ ID  
NO:1284), GHPO 1565 (SEQ ID NO:1286), GHPO 1575 (SEQ ID NO:1288),  
20 GHPO 1582 (SEQ ID NO:1290), GHPO 1595 (SEQ ID NO:1292), GHPO  
1597 (SEQ ID NO:1294), GHPO 1599 (SEQ ID NO:1296), GHPO 1601 (SEQ  
ID NO:1298), GHPO 1609 (SEQ ID NO:1300), GHPO 1613 (SEQ ID  
NO:1302), GHPO 1614 (SEQ ID NO:1304), GHPO 1626 (SEQ ID NO:1306),  
GHPO 1628 (SEQ ID NO:1308), GHPO 1639 (SEQ ID NO:1310), GHPO  
25 1640 (SEQ ID NO:1312), GHPO 1641 (SEQ ID NO:1314), GHPO 1646 (SEQ  
ID NO:1316), GHPO 1662 (SEQ ID NO:1318), GHPO 1667 (SEQ ID

-11-

GHPO 951 (SEQ ID NO:1078), GHPO 961 (SEQ ID NO:1080), GHPO 965  
(SEQ ID NO:1082), GHPO 990 (SEQ ID NO:1084), GHPO 991 (SEQ ID  
NO:1086), GHPO 998 (SEQ ID NO:1088), GHPO 1001 (SEQ ID NO:1090),  
GHPO 1005 (SEQ ID NO:1092), GHPO 1033 (SEQ ID NO:1094), GHPO  
1039 (SEQ ID NO:1096), GHPO 1041 (SEQ ID NO:1098), GHPO 1043 (SEQ  
ID NO:1100), GHPO 1044 (SEQ ID NO:1102), GHPO 1051 (SEQ ID  
NO:1104), GHPO 1058 (SEQ ID NO:1106), GHPO 1060 (SEQ ID NO:1108),  
GHPO 1075 (SEQ ID NO:1110), GHPO 1077 (SEQ ID NO:1112), GHPO  
1082 (SEQ ID NO:1114), GHPO 1083 (SEQ ID NO:1116), GHPO 1086 (SEQ  
ID NO:1118), GHPO 1087 (SEQ ID NO:1120), GHPO 1090 (SEQ ID  
NO:1122), GHPO 1097 (SEQ ID NO:1124), GHPO 1098 (SEQ ID NO:1126),  
GHPO 1103 (SEQ ID NO:1128), GHPO 1113 (SEQ ID NO:1130), GHPO  
1116 (SEQ ID NO:1132), GHPO 1123 (SEQ ID NO:1134), GHPO 1125 (SEQ  
ID NO:1136), GHPO 1129 (SEQ ID NO:1138), GHPO 1130 (SEQ ID  
NO:1140), GHPO 1134 (SEQ ID NO:1142), GHPO 1161 (SEQ ID NO:1144),  
GHPO 1166 (SEQ ID NO:1146), GHPO 1170 (SEQ ID NO:1148), GHPO  
1175 (SEQ ID NO:1150), GHPO 1181 (SEQ ID NO:1152), GHPO 1186 (SEQ  
ID NO:1154), GHPO 1188 (SEQ ID NO:1156), GHPO 1191 (SEQ ID  
NO:1158), GHPO 1193 (SEQ ID NO:1160), GHPO 1196 (SEQ ID NO:1162),  
GHPO 1204 (SEQ ID NO:1164), GHPO 1210 (SEQ ID NO:1166), GHPO  
1211 (SEQ ID NO:1168), GHPO 1216 (SEQ ID NO:1170), GHPO 1218 (SEQ  
ID NO:1172), GHPO 1220 (SEQ ID NO:1174), GHPO 1223 (SEQ ID  
NO:1176), GHPO 1226 (SEQ ID NO:1178), GHPO 1240 (SEQ ID NO:1180),  
GHPO 1246 (SEQ ID NO:1182), GHPO 1251 (SEQ ID NO:1184), GHPO  
1252 (SEQ ID NO:1186), GHPO 1261 (SEQ ID NO:1188), GHPO 1265 (SEQ  
ID NO:1190), GHPO 1267 (SEQ ID NO:1192), GHPO 1278 (SEQ ID  
NO:1194), GHPO 1282 (SEQ ID NO:1196), GHPO 1283 (SEQ ID NO:1198),



-10-

532 (SEQ ID NO:948), GHPO 548 (SEQ ID NO:950), GHPO 561 (SEQ ID NO:952), GHPO 564 (SEQ ID NO:954), GHPO 572 (SEQ ID NO:956), GHPO 573 (SEQ ID NO:958), GHPO 574 (SEQ ID NO:960), GHPO 577 (SEQ ID NO:962), GHPO 579 (SEQ ID NO:964), GHPO 583 (SEQ ID NO:966), GHPO 588 (SEQ ID NO:968), GHPO 593 (SEQ ID NO:970), GHPO 597 (SEQ ID NO:972), GHPO 598 (SEQ ID NO:974), GHPO 604 (SEQ ID NO:976), GHPO 606 (SEQ ID NO:978), GHPO 611 (SEQ ID NO:980), GHPO 612 (SEQ ID NO:982), GHPO 615 (SEQ ID NO:984), GHPO 632 (SEQ ID NO:986), GHPO 633 (SEQ ID NO:988), GHPO 637 (SEQ ID NO:990), GHPO 651 (SEQ ID NO:992), GHPO 663 (SEQ ID NO:994), GHPO 686 (SEQ ID NO:996), GHPO 693 (SEQ ID NO:998), GHPO 698 (SEQ ID NO:1000), GHPO 703 (SEQ ID NO:1002), GHPO 704 (SEQ ID NO:1004), GHPO 705 (SEQ ID NO:1006), GHPO 707 (SEQ ID NO:1008), GHPO 721 (SEQ ID NO:1010), GHPO 727 (SEQ ID NO:1012), GHPO 728 (SEQ ID NO:1014), GHPO 733 (SEQ ID NO:1016), GHPO 758 (SEQ ID NO:1018), GHPO 763 (SEQ ID NO:1020), GHPO 771 (SEQ ID NO:1022), GHPO 774 (SEQ ID NO:1024), GHPO 776 (SEQ ID NO:1026), GHPO 783 (SEQ ID NO:1028), GHPO 800 (SEQ ID NO:1030), GHPO 806 (SEQ ID NO:1032), GHPO 807 (SEQ ID NO:1034), GHPO 808 (SEQ ID NO:1036), GHPO 809 (SEQ ID NO:1038), GHPO 811 (SEQ ID NO:1040), GHPO 815 (SEQ ID NO:1042), GHPO 819 (SEQ ID NO:1044), GHPO 841 (SEQ ID NO:1046), GHPO 843 (SEQ ID NO:1048), GHPO 846 (SEQ ID NO:1050), GHPO 875 (SEQ ID NO:1052), GHPO 892 (SEQ ID NO:1054), GHPO 902 (SEQ ID NO:1056), GHPO 904 (SEQ ID NO:1058), GHPO 906 (SEQ ID NO:1060), GHPO 908 (SEQ ID NO:1062), GHPO 921 (SEQ ID NO:1064), GHPO 923 (SEQ ID NO:1066), GHPO 926 (SEQ ID NO:1068), GHPO 933 (SEQ ID NO:1070), GHPO 939 (SEQ ID NO:1072), GHPO 940 (SEQ ID NO:1074), GHPO 943 (SEQ ID NO:1076),

-9-

NO:812), GHPO 166 (SEQ ID NO:814), GHPO 181 (SEQ ID NO:816), GHPO  
187 (SEQ ID NO:818), GHPO 188 (SEQ ID NO:820), GHPO 192 (SEQ ID  
NO:822), GHPO 202 (SEQ ID NO:824), GHPO 204 (SEQ ID NO:826), GHPO  
205 (SEQ ID NO:828), GHPO 212 (SEQ ID NO:830), GHPO 218 (SEQ ID  
NO:832), GHPO 226 (SEQ ID NO:834), GHPO 231 (SEQ ID NO:836), GHPO  
5 236 (SEQ ID NO:838), GHPO 239 (SEQ ID NO:840), GHPO 245 (SEQ ID  
NO:842), GHPO 246 (SEQ ID NO:844), GHPO 248 (SEQ ID NO:846), GHPO  
253 (SEQ ID NO:848), GHPO 265 (SEQ ID NO:850), GHPO 266 (SEQ ID  
NO:852), GHPO 271 (SEQ ID NO:854), GHPO 272 (SEQ ID NO:856), GHPO  
286 (SEQ ID NO:858), GHPO 291 (SEQ ID NO:860), GHPO 292 (SEQ ID  
10 NO:862), GHPO 297 (SEQ ID NO:864), GHPO 304 (SEQ ID NO:866), GHPO  
307 (SEQ ID NO:868), GHPO 324 (SEQ ID NO:870), GHPO 326 (SEQ ID  
NO:872), GHPO 331 (SEQ ID NO:874), GHPO 343 (SEQ ID NO:876), GHPO  
345 (SEQ ID NO:878), GHPO 346 (SEQ ID NO:880), GHPO 352 (SEQ ID  
NO:882), GHPO 355 (SEQ ID NO:884), GHPO 363 (SEQ ID NO:886), GHPO  
15 369 (SEQ ID NO:888), GHPO 376 (SEQ ID NO:890), GHPO 378 (SEQ ID  
NO:892), GHPO 388 (SEQ ID NO:894), GHPO 396 (SEQ ID NO:896), GHPO  
403 (SEQ ID NO:898), GHPO 410 (SEQ ID NO:900), GHPO 415 (SEQ ID  
NO:902), GHPO 421 (SEQ ID NO:904), GHPO 439 (SEQ ID NO:906), GHPO  
441 (SEQ ID NO:908), GHPO 443 (SEQ ID NO:910), GHPO 453 (SEQ ID  
20 NO:912), GHPO 455 (SEQ ID NO:914), GHPO 464 (SEQ ID NO:916), GHPO  
467 (SEQ ID NO:918), GHPO 468 (SEQ ID NO:920), GHPO 470 (SEQ ID  
NO:922), GHPO 486 (SEQ ID NO:924), GHPO 487 (SEQ ID NO:926), GHPO  
488 (SEQ ID NO:928), GHPO 489 (SEQ ID NO:930), GHPO 498 (SEQ ID  
NO:932), GHPO 501 (SEQ ID NO:934), GHPO 504 (SEQ ID NO:936), GHPO  
25 512 (SEQ ID NO:938), GHPO 517 (SEQ ID NO:940), GHPO 520 (SEQ ID  
NO:942), GHPO 528 (SEQ ID NO:944), GHPO 530 (SEQ ID NO:946), GHPO

-8-

NO:680), GHPO 1539 (SEQ ID NO:682), GHPO 1540 (SEQ ID NO:684),  
GHPO 1542 (SEQ ID NO:686), GHPO 1555 (SEQ ID NO:688), GHPO 1560  
(SEQ ID NO:690), GHPO 1564 (SEQ ID NO:692), GHPO 1570 (SEQ ID  
NO:694), GHPO 1588 (SEQ ID NO:696), GHPO 1604 (SEQ ID NO:698),  
GHPO 1605 (SEQ ID NO:700), GHPO 1619 (SEQ ID NO:702), GHPO 1629  
5 (SEQ ID NO:704), GHPO 1642 (SEQ ID NO:706), GHPO 1654 (SEQ ID  
NO:708), GHPO 1661 (SEQ ID NO:710), GHPO 1673 (SEQ ID NO:712),  
GHPO 1687 (SEQ ID NO:714), GHPO 1692 (SEQ ID NO:716), GHPO 1693  
(SEQ ID NO:718), GHPO 1699 (SEQ ID NO:720), GHPO 1738 (SEQ ID  
NO:722), GHPO 1745 (SEQ ID NO:724), GHPO 1746 (SEQ ID NO:726),  
10 GHPO 1754 (SEQ ID NO:728), GHPO 1792 (SEQ ID NO:730), GHPO 1795  
(SEQ ID NO:732), GHPO 1796 (SEQ ID NO:734), GHPO 7 (SEQ ID  
NO:736), GHPO 8 (SEQ ID NO:738), GHPO 9 (SEQ ID NO:740), GHPO 10  
(SEQ ID NO:742), GHPO 12 (SEQ ID NO:744), GHPO 25 (SEQ ID NO:746),  
GHPO 27 (SEQ ID NO:748), GHPO 29 (SEQ ID NO:750), GHPO 30 (SEQ ID  
15 NO:752), GHPO 37 (SEQ ID NO:754), GHPO 49 (SEQ ID NO:756), GHPO  
51 (SEQ ID NO:758), GHPO 54 (SEQ ID NO:760), GHPO 65 (SEQ ID  
NO:762), GHPO 66 (SEQ ID NO:764), GHPO 68 (SEQ ID NO:766), GHPO  
70 (SEQ ID NO:768), GHPO 77 (SEQ ID NO:770), GHPO 83 (SEQ ID  
NO:772), GHPO 85 (SEQ ID NO:774), GHPO 87 (SEQ ID NO:776), GHPO  
20 91 (SEQ ID NO:778), GHPO 92 (SEQ ID NO:780), GHPO 96 (SEQ ID  
NO:782), GHPO 97 (SEQ ID NO:784), GHPO 111 (SEQ ID NO:786), GHPO  
115 (SEQ ID NO:788), GHPO 117 (SEQ ID NO:790), GHPO 123 (SEQ ID  
NO:792), GHPO 124 (SEQ ID NO:794), GHPO 126 (SEQ ID NO:796), GHPO  
127 (SEQ ID NO:798), GHPO 128 (SEQ ID NO:800), GHPO 131 (SEQ ID  
25 NO:802), GHPO 133 (SEQ ID NO:804), GHPO 140 (SEQ ID NO:806), GHPO  
141 (SEQ ID NO:808), GHPO 145 (SEQ ID NO:810), GHPO 147 (SEQ ID

-7-

903 (SEQ ID NO:554), GHPO 912 (SEQ ID NO:556), GHPO 946 (SEQ ID NO:558), GHPO 958 (SEQ ID NO:560), GHPO 968 (SEQ ID NO:562), GHPO 987 (SEQ ID NO:564), GHPO 992 (SEQ ID NO:566), GHPO 996 (SEQ ID NO:568), GHPO 997 (SEQ ID NO:570), GHPO 1002 (SEQ ID NO:572), GHPO 1026 (SEQ ID NO:574), GHPO 1028 (SEQ ID NO:576), GHPO 1034 (SEQ ID NO:578), GHPO 1038 (SEQ ID NO:580), GHPO 1059 (SEQ ID NO:582), GHPO 1065 (SEQ ID NO:584), GHPO 1072 (SEQ ID NO:586), GHPO 1073 (SEQ ID NO:588), GHPO 1088 (SEQ ID NO:590), GHPO 1091 (SEQ ID NO:592), GHPO 1105 (SEQ ID NO:594), GHPO 1115 (SEQ ID NO:596), GHPO 1159 (SEQ ID NO:598), GHPO 1177 (SEQ ID NO:600), GHPO 1187 (SEQ ID NO:602), GHPO 1192 (SEQ ID NO:604), GHPO 1195 (SEQ ID NO:606), GHPO 1224 (SEQ ID NO:608), GHPO 1225 (SEQ ID NO:610), GHPO 1228 (SEQ ID NO:612), GHPO 1229 (SEQ ID NO:614), GHPO 1231 (SEQ ID NO:616), GHPO 1236 (SEQ ID NO:618), GHPO 1242 (SEQ ID NO:620), GHPO 1248 (SEQ ID NO:622), GHPO 1270 (SEQ ID NO:624), GHPO 1271 (SEQ ID NO:626), GHPO 1298 (SEQ ID NO:628), GHPO 1301 (SEQ ID NO:630), GHPO 1304 (SEQ ID NO:632), GHPO 1315 (SEQ ID NO:634), GHPO 1319 (SEQ ID NO:636), GHPO 1323 (SEQ ID NO:638), GHPO 1331 (SEQ ID NO:640), GHPO 1332 (SEQ ID NO:642), GHPO 1347 (SEQ ID NO:644), GHPO 1373 (SEQ ID NO:646), GHPO 1376 (SEQ ID NO:648), GHPO 1380 (SEQ ID NO:650), GHPO 1394 (SEQ ID NO:652), GHPO 1407 (SEQ ID NO:654), GHPO 1415 (SEQ ID NO:656), GHPO 1425 (SEQ ID NO:658), GHPO 1427 (SEQ ID NO:660), GHPO 1444 (SEQ ID NO:662), GHPO 1449 (SEQ ID NO:664), GHPO 1465 (SEQ ID NO:666), GHPO 1475 (SEQ ID NO:668), GHPO 1479 (SEQ ID NO:670), GHPO 1483 (SEQ ID NO:672), GHPO 1488 (SEQ ID NO:674), GHPO 1496 (SEQ ID NO:676), GHPO 1524 (SEQ ID NO:678), GHPO 1536 (SEQ ID

-6-

NO:418), GHPO 251 (SEQ ID NO:420), GHPO 267 (SEQ ID NO:422), GHPO 269 (SEQ ID NO:424), GHPO 279 (SEQ ID NO:426), GHPO 284 (SEQ ID NO:428), GHPO 296 (SEQ ID NO:430), GHPO 300 (SEQ ID NO:432), GHPO 305 (SEQ ID NO:434), GHPO 319 (SEQ ID NO:436), GHPO 330 (SEQ ID NO:438), GHPO 340 (SEQ ID NO:440), GHPO 342 (SEQ ID NO:442), GHPO 344 (SEQ ID NO:444), GHPO 358 (SEQ ID NO:446), GHPO 373 (SEQ ID NO:448), GHPO 382 (SEQ ID NO:450), GHPO 384 (SEQ ID NO:452), GHPO 398 (SEQ ID NO:454), GHPO 409 (SEQ ID NO:456), GHPO 422 (SEQ ID NO:458), GHPO 430 (SEQ ID NO:460), GHPO 446 (SEQ ID NO:462), GHPO 447 (SEQ ID NO:464), GHPO 450 (SEQ ID NO:466), GHPO 451 (SEQ ID NO:468), GHPO 452 (SEQ ID NO:470), GHPO 456 (SEQ ID NO:472), GHPO 461 (SEQ ID NO:474), GHPO 476 (SEQ ID NO:476), GHPO 478 (SEQ ID NO:478), GHPO 491 (SEQ ID NO:480), GHPO 511 (SEQ ID NO:482), GHPO 519 (SEQ ID NO:484), GHPO 526 (SEQ ID NO:486), GHPO 534 (SEQ ID NO:488), GHPO 536 (SEQ ID NO:490), GHPO 542 (SEQ ID NO:492), GHPO 544 (SEQ ID NO:494), GHPO 576 (SEQ ID NO:496), GHPO 578 (SEQ ID NO:498), GHPO 580 (SEQ ID NO:500), GHPO 585 (SEQ ID NO:502), GHPO 599 (SEQ ID NO:504), GHPO 639 (SEQ ID NO:506), GHPO 642 (SEQ ID NO:508), GHPO 647 (SEQ ID NO:510), GHPO 654 (SEQ ID NO:512), GHPO 669 (SEQ ID NO:514), GHPO 710 (SEQ ID NO:516), GHPO 713 (SEQ ID NO:518), GHPO 716 (SEQ ID NO:520), GHPO 718 (SEQ ID NO:522), GHPO 726 (SEQ ID NO:524), GHPO 734 (SEQ ID NO:526), GHPO 740 (SEQ ID NO:528), GHPO 770 (SEQ ID NO:530), GHPO 782 (SEQ ID NO:532), GHPO 786 (SEQ ID NO:534), GHPO 792 (SEQ ID NO:536), GHPO 797 (SEQ ID NO:538), GHPO 816 (SEQ ID NO:540), GHPO 828 (SEQ ID NO:542), GHPO 839 (SEQ ID NO:544), GHPO 840 (SEQ ID NO:546), GHPO 842 (SEQ ID NO:548), GHPO 885 (SEQ ID NO:550), GHPO 889 (SEQ ID NO:552), GHPO

-5-

475 (SEQ ID NO:288), GHPO 515 (SEQ ID NO:290), GHPO 527 (SEQ ID  
NO:292), GHPO 551 (SEQ ID NO:294), GHPO 602 (SEQ ID NO:296), GHPO  
626 (SEQ ID NO:298), GHPO 646 (SEQ ID NO:300), GHPO 653 (SEQ ID  
NO:302), GHPO 655 (SEQ ID NO:304), GHPO 670 (SEQ ID NO:306), GHPO  
739 (SEQ ID NO:308), GHPO 798 (SEQ ID NO:310), GHPO 1102 (SEQ ID  
5 NO:312), GHPO 1114 (SEQ ID NO:314), GHPO 1152 (SEQ ID NO:316),  
GHPO 1272 (SEQ ID NO:318), GHPO 1345 (SEQ ID NO:320), GHPO 1377  
(SEQ ID NO:322), GHPO 1424 (SEQ ID NO:324), GHPO 1430 (SEQ ID  
NO:326), GHPO 1502 (SEQ ID NO:328), GHPO 1600 (SEQ ID NO:330),  
GHPO 1714 (SEQ ID NO:332), GHPO 359 (SEQ ID NO:334), GHPO 678  
10 (SEQ ID NO:336), GHPO 708 (SEQ ID NO:338), GHPO 759 (SEQ ID  
NO:340), GHPO 847 (SEQ ID NO:342), GHPO 1050 (SEQ ID NO:344),  
GHPO 1101 (SEQ ID NO:346), GHPO 1120 (SEQ ID NO:348), GHPO 1138  
(SEQ ID NO:350), GHPO 1310 (SEQ ID NO:352), GHPO 1320 (SEQ ID  
NO:354), GHPO 1375 (SEQ ID NO:356), GHPO 1432 (SEQ ID NO:358),  
15 GHPO 21 (SEQ ID NO:360), GHPO 282 (SEQ ID NO:362), GHPO 1089  
(SEQ ID NO:364), GHPO 1141 (SEQ ID NO:366), GHPO 1280 (SEQ ID  
NO:368), GHPO 1608 (SEQ ID NO:370), GHPO 15 (SEQ ID NO:372), GHPO  
16 (SEQ ID NO:374), GHPO 36 (SEQ ID NO:376), GHPO 38 (SEQ ID  
NO:378), GHPO 52 (SEQ ID NO:380), GHPO 57 (SEQ ID NO:382), GHPO  
20 64 (SEQ ID NO:384), GHPO 79 (SEQ ID NO:386), GHPO 84 (SEQ ID  
NO:388), GHPO 86 (SEQ ID NO:390), GHPO 99 (SEQ ID NO:392), GHPO  
106 (SEQ ID NO:394), GHPO 118 (SEQ ID NO:396), GHPO 122 (SEQ ID  
NO:398), GHPO 128 (SEQ ID NO:400), GHPO 138 (SEQ ID NO:402), GHPO  
153 (SEQ ID NO:404), GHPO 160 (SEQ ID NO:406), GHPO 168 (SEQ ID  
25 NO:408), GHPO 179 (SEQ ID NO:410), GHPO 189 (SEQ ID NO:412), GHPO  
229 (SEQ ID NO:414), GHPO 243 (SEQ ID NO:416), GHPO 244 (SEQ ID

-4-

NO:158), GHPO 989 (SEQ ID NO:160), GHPO 1111 (SEQ ID NO:162),  
GHPO 1145 (SEQ ID NO:164), GHPO 1256 (SEQ ID NO:166), GHPO 1264  
(SEQ ID NO:168), GHPO 1316 (SEQ ID NO:170), GHPO 1368 (SEQ ID  
NO:172), GHPO 1442 (SEQ ID NO:174), GHPO 1506 (SEQ ID NO:176),  
GHPO 1543 (SEQ ID NO:178), GHPO 1574 (SEQ ID NO:180), GHPO 1627  
5 (SEQ ID NO:182), GHPO 1657 (SEQ ID NO:184), GHPO 1664 (SEQ ID  
NO:186), GHPO 1694 (SEQ ID NO:188), GHPO 1704 (SEQ ID NO:190),  
GHPO 1763 (SEQ ID NO:192), GHPO 616 (SEQ ID NO:194), GHPO 76  
(SEQ ID NO:196), GHPO 109 (SEQ ID NO:198), GHPO 163 (SEQ ID  
NO:200), GHPO 169 (SEQ ID NO:202), GHPO 208 (SEQ ID NO:204), GHPO  
10 219 (SEQ ID NO:206), GHPO 445 (SEQ ID NO:208), GHPO 479 (SEQ ID  
NO:210), GHPO 525 (SEQ ID NO:212), GHPO 535 (SEQ ID NO:214), GHPO  
731 (SEQ ID NO:216), GHPO 836 (SEQ ID NO:218), GHPO 879 (SEQ ID  
NO:220), GHPO 881 (SEQ ID NO:222), GHPO 886 (SEQ ID NO:224), GHPO  
893 (SEQ ID NO:226), GHPO 894 (SEQ ID NO:228), GHPO 976 (SEQ ID  
15 NO:230), GHPO 1011 (SEQ ID NO:232), GHPO 1024 (SEQ ID NO:234),  
GHPO 1084 (SEQ ID NO:236), GHPO 1329 (SEQ ID NO:238), GHPO 1330  
(SEQ ID NO:240), GHPO 1346 (SEQ ID NO:242), GHPO 1360 (SEQ ID  
NO:244), GHPO 1388 (SEQ ID NO:246), GHPO 1411 (SEQ ID NO:248),  
GHPO 1419 (SEQ ID NO:250), GHPO 1446 (SEQ ID NO:252), GHPO 1469  
20 (SEQ ID NO:254), GHPO 1501 (SEQ ID NO:256), GHPO 1505 (SEQ ID  
NO:258), GHPO 1522 (SEQ ID NO:260), GHPO 1525 (SEQ ID NO:262),  
GHPO 1615 (SEQ ID NO:264), GHPO 1689 (SEQ ID NO:266), GHPO 1733  
(SEQ ID NO:268), GHPO 18 (SEQ ID NO:270), GHPO 139 (SEQ ID  
NO:272), GHPO 142 (SEQ ID NO:274), GHPO 250 (SEQ ID NO:276), GHPO  
25 257 (SEQ ID NO:278), GHPO 325 (SEQ ID NO:280), GHPO 355 (SEQ ID  
NO:282), GHPO 357 (SEQ ID NO:284), GHPO 454 (SEQ ID NO:286), GHPO

-3-

NO:24), GHPO 1034 (SEQ ID NO:26), GHPO 1085 (SEQ ID NO:28), GHPO  
1213 (SEQ ID NO:30), GHPO 1255 (SEQ ID NO:32), GHPO 1308 (SEQ ID  
NO:34), GHPO 1389 (SEQ ID NO:36), GHPO 1706 (SEQ ID NO:38), GHPO  
234 (SEQ ID NO:40), GHPO 314 (SEQ ID NO:42), GHPO 510 (SEQ ID  
NO:44), GHPO 603 (SEQ ID NO:46), GHPO 937 (SEQ ID NO:48), GHPO  
5 1027 (SEQ ID NO:50), GHPO 1099 (SEQ ID NO:52), GHPO 1151 (SEQ ID  
NO:54), GHPO 1275 (SEQ ID NO:56), GHPO 1365 (SEQ ID NO:58), GHPO  
1578 (SEQ ID NO:60), GHPO 22 (SEQ ID NO:62), GHPO 58 (SEQ ID  
NO:64), GHPO 200 (SEQ ID NO:66), GHPO 558 (SEQ ID NO:68), GHPO  
563 (SEQ ID NO:70), GHPO 695 (SEQ ID NO:72), GHPO 699 (SEQ ID  
10 NO:74), GHPO 702 (SEQ ID NO:76), GHPO 709 (SEQ ID NO:78), GHPO  
741 (SEQ ID NO:80), GHPO 762 (SEQ ID NO:82), GHPO 827 (SEQ ID  
NO:84), GHPO 852 (SEQ ID NO:86), GHPO 1013 (SEQ ID NO:88), GHPO  
1020 (SEQ ID NO:90), GHPO 1031 (SEQ ID NO:92), GHPO 1052 (SEQ ID  
NO:94), GHPO 1127 (SEQ ID NO:96), GHPO 1149 (SEQ ID NO:98), GHPO  
15 1176 (SEQ ID NO:100), GHPO 1250 (SEQ ID NO:102), GHPO 1312 (SEQ ID  
NO:104), GHPO 1358 (SEQ ID NO:106), GHPO 1490 (SEQ ID NO:108),  
GHPO 1559 (SEQ ID NO:110), GHPO 1651 (SEQ ID NO:112), GHPO 1726  
(SEQ ID NO:114), GHPO 1780 (SEQ ID NO:116), GHPO 895 (SEQ ID  
NO:118), GHPO 1447 (SEQ ID NO:120), GHPO 28 (SEQ ID NO:122), GHPO  
20 86 (SEQ ID NO:124), GHPO 155 (SEQ ID NO:126), GHPO 157 (SEQ ID  
NO:128), GHPO 237 (SEQ ID NO:130), GHPO 290 (SEQ ID NO:132), GHPO  
293 (SEQ ID NO:134), GHPO 335 (SEQ ID NO:136), GHPO 374 (SEQ ID  
NO:138), GHPO 442 (SEQ ID NO:140), GHPO 480 (SEQ ID NO:142), GHPO  
523 (SEQ ID NO:144), GHPO 610 (SEQ ID NO:146), GHPO 675 (SEQ ID  
25 NO:148), GHPO 690 (SEQ ID NO:150), GHPO 829 (SEQ ID NO:152), GHPO  
850 (SEQ ID NO:154), GHPO 876 (SEQ ID NO:156), GHPO 984 (SEQ ID



-2-

*al.*, J. Biol. Chem. 265:9464, 1990; Evans *et al.*, Microbial Pathogenesis 10:15, 1991; Labigne *et al.*, J. Bact., 173:1920, 1991); the 87 kDa vacuolar cytotoxin (VacA) (Cover *et al.*, J. Biol. Chem. 267:10570, 1992; Phadnis *et al.*, Infect. Immun. 62:1557, 1994; WO 93/18150); a 128 kDa immunodominant antigen associated with the cytotoxin (CagA, also called TagA; WO 93/18150; U.S. Patent No. 5,403,924); 13 and 58 kDa heat shock proteins HspA and HspB (Suerbaum *et al.*, Mol. Microbiol. 14:959, 1994; WO 93/18150); a 54 kDa catalase (Hazell *et al.*, J. Gen. Microbiol. 137:57, 1991); a 15 kDa histidine-rich protein (Hpn) (Gilbert *et al.*, Infect. Immun. 63:2682, 1995); a 20 kDa membrane-associated lipoprotein (Kostrzynska *et al.*, J. Bact. 176:5938, 1994); a 30 kDa outer membrane protein (Bölin *et al.*, J. Clin. Microbiol. 33:381, 1995); a lactoferrin receptor (FR 2,724,936); and several porins, designated HopA, HopB, HopC, HopD, and HopE, which have molecular weights of 48-67 kDa (Exner *et al.*, Infect. Immun. 63:1567, 1995; Doig *et al.*, J. Bact. 177:5447, 1995). Some of these proteins have been proposed as potential vaccine antigens. In particular, urease is believed to be a vaccine candidate (WO 94/9823; WO 95/22987; WO 95/3824; Michetti *et al.*, Gastroenterology 107:1002, 1994). Nevertheless, it is thought that several antigens may ultimately be necessary in a vaccine.

### Summary of the Invention

The invention provides polynucleotide molecules that encode *Helicobacter* polypeptides, designated GHPO 35 (SEQ ID NO:2), GHPO 55 (SEQ ID NO:4), GHPO 78 (SEQ ID NO:6), GHPO 89 (SEQ ID NO:8), GHPO 129 (SEQ ID NO:10), GHPO 541 (SEQ ID NO:12), GHPO 607 (SEQ ID NO:14), GHPO 635 (SEQ ID NO:16), GHPO 701 (SEQ ID NO:18), GHPO 712 (SEQ ID NO:20), GHPO 761 (SEQ ID NO:22), GHPO 838 (SEQ ID

IDENTIFICATION OF POLYNUCLEOTIDES ENCODING NOVEL  
HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER GENOME

The invention relates to *Helicobacter* antigens and corresponding polynucleotide molecules that can be used in methods to prevent or treat *Helicobacter* infection in mammals, such as humans.

Background of the Invention

*Helicobacter* is a genus of spiral, gram-negative bacteria that colonize the gastrointestinal tracts of mammals. Several species colonize the stomach, most notably *H. pylori*, *H. heilmanii*, *H. felis*, and *H. mustelae*. Although *H. pylori* is the species most commonly associated with human infection, *H. heilmanii* and *H. felis* have also been isolated from humans, but at lower frequencies than *H. pylori*. *Helicobacter* infects over 50% of adult populations in developed countries and nearly 100% in developing countries and some Pacific rim countries, making it one of the most prevalent infections worldwide.

*Helicobacter* is routinely recovered from gastric biopsies of humans with histological evidence of gastritis and peptic ulceration. Indeed, *H. pylori* is now recognized as an important pathogen of humans, in that the chronic gastritis it causes is a risk factor for the development of peptic ulcer diseases and gastric carcinoma. It is thus highly desirable to develop safe and effective vaccines for preventing and treating *Helicobacter* infection.

A number of *Helicobacter* antigens have been characterized or isolated. These include urease, which is composed of two structural subunits of approximately 30 and 67 kDa (Hu *et al.*, Infect. Immun. 58:992, 1990; Dunn *et*

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

|    |                          |    |                                          |    |                                              |    |                          |
|----|--------------------------|----|------------------------------------------|----|----------------------------------------------|----|--------------------------|
| AL | Albania                  | ES | Spain                                    | LS | Lesotho                                      | SI | Slovenia                 |
| AM | Armenia                  | FI | Finland                                  | LT | Lithuania                                    | SK | Slovakia                 |
| AT | Austria                  | FR | France                                   | LU | Luxembourg                                   | SN | Senegal                  |
| AU | Australia                | GA | Gabon                                    | LV | Latvia                                       | SZ | Swaziland                |
| AZ | Azerbaijan               | GB | United Kingdom                           | MC | Monaco                                       | TD | Chad                     |
| BA | Bosnia and Herzegovina   | GE | Georgia                                  | MD | Republic of Moldova                          | TG | Togo                     |
| BB | Barbados                 | GH | Ghana                                    | MG | Madagascar                                   | TJ | Tajikistan               |
| BE | Belgium                  | GN | Guinea                                   | MK | The former Yugoslav<br>Republic of Macedonia | TM | Turkmenistan             |
| BF | Burkina Faso             | GR | Greece                                   |    |                                              | TR | Turkey                   |
| BG | Bulgaria                 | HU | Hungary                                  | ML | Mali                                         | TT | Trinidad and Tobago      |
| BJ | Benin                    | IE | Ireland                                  | MN | Mongolia                                     | UA | Ukraine                  |
| BR | Brazil                   | IL | Israel                                   | MR | Mauritania                                   | UG | Uganda                   |
| BY | Belarus                  | IS | Iceland                                  | MW | Malawi                                       | US | United States of America |
| CA | Canada                   | IT | Italy                                    | MX | Mexico                                       | UZ | Uzbekistan               |
| CF | Central African Republic | JP | Japan                                    | NE | Niger                                        | VN | Viet Nam                 |
| CG | Congo                    | KE | Kenya                                    | NL | Netherlands                                  | YU | Yugoslavia               |
| CH | Switzerland              | KG | Kyrgyzstan                               | NO | Norway                                       | ZW | Zimbabwe                 |
| CI | Côte d'Ivoire            | KP | Democratic People's<br>Republic of Korea | NZ | New Zealand                                  |    |                          |
| CM | Cameroon                 |    |                                          | PL | Poland                                       |    |                          |
| CN | China                    | KR | Republic of Korea                        | PT | Portugal                                     |    |                          |
| CU | Cuba                     | KZ | Kazakstan                                | RO | Romania                                      |    |                          |
| CZ | Czech Republic           | LC | Saint Lucia                              | RU | Russian Federation                           |    |                          |
| DE | Germany                  | LI | Liechtenstein                            | SD | Sudan                                        |    |                          |
| DK | Denmark                  | LK | Sri Lanka                                | SE | Sweden                                       |    |                          |
| EE | Estonia                  | LR | Liberia                                  | SG | Singapore                                    |    |                          |



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                         |                                                                                                                                           |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|-------------------------|----|------------|-------------------------|----|------------|-------------------------|----|----|------------------|--|----------|-------------------------|--|----|------------------|--|----------|-------------------------|--|----|------------------|--|----------|-------------------------|--|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>(51) International Patent Classification <sup>6</sup> :</b><br><b>A01N 43/04, A61K 31/70</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | <b>A1</b>               | <b>(11) International Publication Number:</b> <b>WO 98/43478</b><br><b>(43) International Publication Date:</b> 8 October 1998 (08.10.98) |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <b>(21) International Application Number:</b> PCT/US98/06371<br><b>(22) International Filing Date:</b> 1 April 1998 (01.04.98)<br><br><b>(30) Priority Data:</b> <table border="0" style="width: 100%;"><tr><td style="width: 30%;">08/833,457</td><td style="width: 30%;">1 April 1997 (01.04.97)</td><td style="width: 40%; text-align: right;">US</td></tr><tr><td>08/881,227</td><td>24 June 1997 (24.06.97)</td><td style="text-align: right;">US</td></tr><tr><td>08/902,615</td><td>29 July 1997 (29.07.97)</td><td style="text-align: right;">US</td></tr></table><br><b>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications</b> <table border="0" style="width: 100%;"><tr><td style="width: 30%;">US</td><td style="width: 30%;">08/833,457 (CON)</td><td style="width: 40%;"></td></tr><tr><td>Filed on</td><td>1 April 1997 (01.04.97)</td><td></td></tr><tr><td>US</td><td>08/881,227 (CON)</td><td></td></tr><tr><td>Filed on</td><td>24 June 1997 (24.06.97)</td><td></td></tr><tr><td>US</td><td>08/902,615 (CON)</td><td></td></tr><tr><td>Filed on</td><td>29 July 1997 (29.07.97)</td><td></td></tr></table><br><b>(71) Applicants (for all designated States except US):</b> MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET VACCINS S.A. [FR/FR]; 58, avenue Leclerc, F-69007 Lyon (FR). HUMAN GENOME SCIENCE, INC. [-/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). |                         | 08/833,457                                                                                                                                | 1 April 1997 (01.04.97) | US | 08/881,227 | 24 June 1997 (24.06.97) | US | 08/902,615 | 29 July 1997 (29.07.97) | US | US | 08/833,457 (CON) |  | Filed on | 1 April 1997 (01.04.97) |  | US | 08/881,227 (CON) |  | Filed on | 24 June 1997 (24.06.97) |  | US | 08/902,615 (CON) |  | Filed on | 29 July 1997 (29.07.97) |  | <b>(72) Inventors; and</b><br><b>(75) Inventors/Applicants (for US only):</b> KLEANTHOUS, Harold [GB/US]; 89 Madison Avenue, Newtonville, MA 02160 (US). AL-GARAWI, Amal [SA/US]; 32 Garrison Street #4501, Boston, MA 02114 (US). MILLER, Charles [US/US]; 32 Maple Avenue, Medford, MA 02155 (US). TOMB, Jean-François [-/US]; 3501 St. Paul Street, Baltimore, MD 21222 (US). OOMEN, Raymond, Peter [CA/CA]; R.R. #1, 5400 Lloydtown-Aurora Sideroad, Schomberg, Ontario L0G 1T0 (CA).<br><br><b>(74) Agent:</b> CLARK, Paul, T.; Clark & Elbing LLP, 176 Federal Street, Boston, MA 02110-2214 (US).<br><br><b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).<br><br><b>Published</b><br><i>With international search report.</i> |
| 08/833,457                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1 April 1997 (01.04.97) | US                                                                                                                                        |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 08/881,227                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 24 June 1997 (24.06.97) | US                                                                                                                                        |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 08/902,615                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 29 July 1997 (29.07.97) | US                                                                                                                                        |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| US                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 08/833,457 (CON)        |                                                                                                                                           |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Filed on                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1 April 1997 (01.04.97) |                                                                                                                                           |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| US                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 08/881,227 (CON)        |                                                                                                                                           |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Filed on                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 24 June 1997 (24.06.97) |                                                                                                                                           |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| US                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 08/902,615 (CON)        |                                                                                                                                           |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Filed on                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 29 July 1997 (29.07.97) |                                                                                                                                           |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <b>(54) Title:</b> IDENTIFICATION OF POLYNUCLEOTIDES ENCODING NOVEL <i>HELICOBACTER</i> POLYPEPTIDES IN THE <i>HELICOBACTER</i> GENOME<br><br><b>(57) Abstract</b> <p>The invention provides <i>Helicobacter</i> polypeptides that can be used in vaccination methods for preventing or treating <i>Helicobacter</i> infection, and polynucleotides that encode these polypeptides. The invention also provides diagnostic methods employing these polypeptides.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                         |                                                                                                                                           |                         |    |            |                         |    |            |                         |    |    |                  |  |          |                         |  |    |                  |  |          |                         |  |    |                  |  |          |                         |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |